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SUGARBEET RESEARCH

2006 REPORT

FOREWARD

SUGARBEET RESEARCH is an annual compilation of progress reports concerning research by U.S. Department of Agriculture, Agricultural Research Service investigators and other cooperators who are engaged in sugarbeet research. The report was assembled and produced at the expense of the Beet Sugar Development Foundation and is for the sole use of its members and the cooperators. Much of the data has not been sufficiently confirmed to justify general release and interpretations may be modified with additional experimentation. This report is not intended for publication and should not be used for cited reference nor quoted in publicity or advertising. Reproduction of any portion of the material contained herein will not be permitted without the specific consent of the contributors and the Beet Sugar Development Foundation.

The report presents results of investigations strengthened by contributions received under Cooperative Agreement between the USDA Agricultural Research Service and the Beet Sugar Development Foundation, along with the California Beet Growers Association, the Western Joint Research Committee, and the Sugarbeet and Education Board of Minnesota and North Dakota.

Trade names occur in this report solely to provide specific information and do not signify endorsement by the U.S. Department of Agriculture, the Beet Sugar Development Foundation or any of the cooperating organizations.

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**SUGARBEET RESEARCH
USDA-ARS – AGRICULTURAL RESEARCH STATION
SALINAS, CALIFORNIA**

2006 REPORT

SECTION A

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This research was supported in part by funds provided through the Beet Sugar Development Foundation (Projects 211, 215, 221 and 261), the California Beet Growers Association and the California Industry Research Committee.

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Hanson, L. and R.T. Lewellen. 2007. First report of stalk blight of sugar beet caused by *Fusarium solani* on the Pacific coast. Plant Disease. (in press)

See the Fort Collins section of this report.

Hayes, R.J., W.M. Wintermantel, P.A. Nicely, and E.J. Ryder. 2006. Host resistance to *Mirafiori lettuce big-vein virus* and *Lettuce big-vein associated virus* and virus sequence diversity and frequency in California. Plant Dis. 90: 233-239.

Big vein is an economically damaging disease of lettuce (*Lactuca sativa* L.) caused by the *Ospidium brassicae* vectored *Mirafiori lettuce big-vein virus* (MLBVV). *Lettuce big-vein associated virus* (LBVaV) is also frequently identified in symptomatic plants, but no causal relationship has been demonstrated. Although big vein is a perennial problem in the US, the extent of MLBVV and LBVaV infection and diversity is unknown. Lettuce cultivars partially resistant to big vein reduce losses, but do not eliminate disease. While *L. virosa* L. does not develop big vein symptoms, it has not been tested for infection with MLBVV or LBVaV. Lettuce cultivars Great Lakes 65, Pavane, Margarita, and *L. virosa* accession IVT280 were evaluated for big vein incidence and virus infection in inoculated greenhouse trials. Additional lettuce samples were collected from field sites in California, classified for symptom severity and evaluated for virus infection. Reverse transcription-polymerase chain reaction and nucleotide sequencing were used to determine infection with MLBVV and LBVaV, and sequence diversity among viral isolates, respectively. Infections with MLBVV and MLBVV/LBVaV were dependent on big vein symptom expression in California production areas and isolates were closely related to those found in Europe and Japan. Partial big vein resistance was identified in Margarita and Pavane; however, MLBVV infection was found in asymptomatic plants. *L. virosa* IVT280 remained symptomless and virus free, suggesting that it is immune to MLBVV and LBVaV.

Lewellen, R.T. 2007. Registration of CN927-202, CN926-11-3-22, and CN921-306 Sugarbeet Cyst Nematode Resistant Sugarbeet Lines. Crop Registrations Journal (accepted 1/04/07)

Sugarbeet (*Beta vulgaris* L.) breeding lines CN927-202 (Reg. no. GP- , PI 640420), CN926-11-3-22 (Reg. no. GP- , PI 640421), and CN921-306 (Reg. no. GP- , PI 640422) are partially inbred lines that appear to have moderate to high resistance to sugarbeet cyst nematode (SBCN) (*Heterodera schachtii* Schmidt). These lines were developed by the USDA-ARS in cooperation with the Beet Sugar Development Foundation (BSDF) and the California Beet Growers Association. They were released in 2006. For these lines, the

source of resistance appears to be *B. vulgaris* L. subsp. *maritima* (L.) Arcang germplasm from composite cross C50 (PI 564243) (Lewellen and Whitney, 1993) through C51 (PI 593694) (Lewellen, 2000), also called breeding line R22 (PI 590791) in the Salinas breeding program. These three partially inbred lines have C51 parentage in common. Because C51 was developed from a composite cross involving about 60 accessions of *B. vulgaris* subsp. *maritima*, the original wild beet source of resistance to SBCN could not be identified. Nor to date is the exact inheritance of this SBCN resistance known, but it appears to be one or a few major genes with dominant gene action; i.e., the experimental hybrids with these or similar lines and sources have nearly the same level of resistance to SBCN as the lines themselves (Lewellen and Pakish, 2005). The allelic relationships among these three lines for their resistance to SBCN also have yet to be determined. Neither is the genic or allelic relationship to the SBCN resistance segregating in CN12 (PI 636338) (Lewellen, 2006a) and likely from WB242 (PI 546413) and CN72 (PI 636339) (Lewellen, 2006a) released in 2005 known. This resistance is not the *Hs-I^{pro-1}* gene transferred to sugarbeet from the hard-seeded species *B. procumbens* Moq. (section Beta Procumbens) (Savitsky, 1975).

CN927-202 is homozygous for red hypocotyls (*RR*), multigerm (*MM*), self-fertile (*S*), segregates for genetic male sterility (*a₁a₁*), and has a high frequency of *Rz1* for resistance to *Beet necrotic yellow vein virus* (BNYVV), the cause of rhizomania. CN927-202 was selected from C927-4 (PI 628756) (Lewellen, 2004). CN927-202 theoretically has 12.5% of its germplasm from *B. vulgaris* subsp. *maritima*. Wild beets were initially crossed to breeding line C54 (PI 590802) at Salinas in 1984 to produce population R22 (=C50). After multiple cycles of improvement for agronomic type and resistance to rhizomania and virus yellows (caused by *Beet yellows virus* and *Beet chlorosis virus*), improved R22 (=C51) was crossed to an early version of C931 (PI 636340) (Lewellen, 2006b) to produce population 5921 in 1995. Population 5921 was again backcrossed to C931 population to produce population 6927. Individual plants of 6927 were selfed in 1997 to produce a set of *S*₁ progenies from which 7927-4 was selected. After intraline recombination and improvement, 1927-4 was produced and released as C927-4 in 2002. Because in field tests at Salinas and Brawley, CA, there appeared to be high resistance to an unidentified soil-borne problem, which was subsequently identified as *H. schachtii*, C927-4 was selfed to produce *S*₁ progenies including 2927-4-202. Progeny 2927-4-202 was selected after being tested at Salinas and Brawley under rhizomania and SBCN conditions and observed to have relatively high performance, particularly under SBCN conditions (Lewellen and Pakish, 2005). The *S*₁ progeny 2927-4-202 was bulk increased in 2004 to produce 4927-202. A second bulk increase was made in 2005 to produce 5927-202, released as CN927-202.

As line 4927-202, CN927-202 was tested at Salinas and Brawley under rhizomania and severe SBCN conditions. It gave high per se and experimental hybrid performance for sugar yield, suggesting it had resistance to both rhizomania and SBCN. In 2004-2005, individual plants of 4927-202 were evaluated in greenhouse tests for reaction in *H. schachtii* infested soil. Compared to susceptible checks and based on cyst counts, 10 out of 10 plants produced relatively low numbers of nematodes. In subsequent tests in the greenhouse in 2005 and 2006, plants in this line again showed moderate to high

resistance to cyst nematode and matured cysts appeared to be partially filled. In 2004-2005 tests at Brawley under severe nematode conditions but free of BNYVV, the experimental hybrid 4927-202H50 = { F₁CMS[C790-68CMS (Lewellen and Skoyen, 1987) x C790-15 (Lewellen, 1994)] x CN927-202} yielded 12500 kg ha⁻¹ sugar (lsd .05=1040) and 14.83% sucrose (lsd .05=0.56) with 0% bolting (lsd .05=1.3) compared to the mean of six advanced experimental and semi-commercial hybrids with *Hs-1^{pro-1}* resistance from *B. procumbens* of 10640 kg ha⁻¹ sugar, 13.90% sucrose, and 0.4% bolting. In this same test the mean of the two most widely grown commercial hybrids in the Imperial Valley was 8300 kg ha⁻¹ sugar, 14.40% sucrose, and 0% bolting. The canopy score used to assess general plant health at harvest was 1.1 (lsd .05=0.5) for CN927-202H50, 2.6 for the mean of the six semi-commercial *Hs-1^{pro-1}* hybrids, and 3.5 for the mean of the two commercial hybrids based on a scale of 1 to 5 where 1 = estimate of expected appearance under healthy conditions and 5 = very poor appearance and/or dead. Soil cores were taken from field plots in mid-season on January 25, 2005, and total counts of *H. schachtii* made. For CN927-202H50, the counts were 34 eggs+larvae gram⁻¹ of soil, for the mean of three of the *Hs-1^{pro-1}* hybrids checked, 20 eggs+larvae gram⁻¹ of soil, and for the two commercial hybrids, 65 eggs+larvae gram⁻¹ of soil. In an adjacent test of lines per se, CN927-202 had better sugar yield performance than any other entry including the commercial hybrid checks, suggesting highly effective field resistance to SBCN.

CN927-202 may approach parental line usefulness when hybrids are grown under SBCN conditions. At this time, however, CN927-202 is primarily being released as a source of resistance to SBCN derived from *B. vulgaris* subsp. *maritima*. CN927-202 segregates for reaction to *Fusarium* spp. that causes stalk blight and crown and root rot.

CN926-11-3-22 is homozygous for green hypocotyls (*rr*), multigerm (*MM*), self-fertile (*S^f*), and has a high frequency of *Rz1* for resistance to BNYVV. CN926-11-3-22 was developed specifically because of its apparent resistance to *H. schachtii*. It is estimated that C926-11-3-22 has about 2% of its germplasm descending from *B. vulgaris* subsp. *maritima* through C51. C51 was crossed to C37 (PI590715) (Lewellen et al., 1985) in 1992 to produce the equivalent of a BC₁F₁ population. After four additional backcrosses to recurrent sugarbeet population C931 involving selection for plant type, components of yield, and resistance to rhizomania, BC₅ F₁ population 7926 was produced in 1997. After one cycle of recombination, population 8926 was produced. Tests at Brawley under high temperature, rhizomania conditions showed that at a low frequency, plants with unusually high vigor and performance occurred within this population. In an attempt to isolate and understand this response under the Brawley test conditions, individual plants from population 8926 were selfed. One of these S₁ progenies, called 9926-11, segregated for this resistance response in progeny tests in 2000. Individual plants from 9926-11 were selfed and one S₂ progeny 1926-11-3 selected. From 1926-11-3, the S₃ progeny 2926-11-3-22 was produced and tested at Brawley in 2003. Based upon its reaction to what by then was believed to be resistance to SBCN, the S₃ was increased in bulk to produce 4926-11-3-22. Line 4926-11-3-22 was tested in the field at Brawley and in the greenhouse at Salinas in 2005. An experimental hybrid 4926-11-3-22H5 = [C833-5CMS (Lewellen, 2002) x CN926-11-3-22] was also produced and evaluated in field trials at

Brawley. Plants from partially inbred line 4926-11-3-22 were increased at Salinas in 2005 to produce line 5926-11-3-22, released as CN926-11-3-22. Line CN926-11-3-22 and its experimental hybrid are continuing to be evaluated at Salinas and in disease nursery trials.

CN926-11-3-22 may be homozygous for resistance to *H. schachtii*. In tests in the greenhouse in *H. schachtii* infested soil, 10 out of 10 plants showed low rates of nematode reproduction based on cyst counts as compared to susceptible checks. In the same field test at Brawley mentioned above for CN927-202 in which the hybrid of CN927-202 yielded 12500 kg ha⁻¹ sugar, the experimental hybrid of CN926-11-3-22 gave 11900 kg ha⁻¹ sugar, 15.4% sucrose, and 0% bolting, and had a canopy score of 1.4. Just like CN927-202, in the adjacent test at Brawley of lines per se, partially inbred CN926-11-3-22 was not significantly different in yield compared to the hybrid checks. In a companion nondiseased trial at Brawley, the experimental hybrid CN926-11-3-22H5 was nearly equal to the mean of the SBCN susceptible commercial hybrid checks for sugar yield and superior for sucrose concentration. Greenhouse tests under SBCN conditions suggested that CN926-11-3-22 was more resistant to *F. oxysporum* f.sp. *betae* than were entries derived from C927-4.

CN926-11-3-22 approaches commercial parental line traits when the hybrids are grown under both diseased (SBCN and/or rhizomania) and nondiseased conditions. Tests to determine reactions to other diseases and pests are underway. CN926-11-3-22 may have the same or different source of resistance to SBCN as CN927-202, both likely coming from wild sea beet. Hybrids produced with CN926-11-3-22 may be useful in regional, national, and international trials to evaluate the efficacy and usefulness of this source of resistance to reduce damage from cyst nematode.

CN921-306 is homozygous for green hypocotyls (*rr*), multigerm (*MM*), self-fertile (*S*^f), and has a high frequency of *Rz1* for resistance to BNYVV. CN921-306 was specifically identified and selected because of its apparent resistance to *H. schachtii*. It is estimated that CN921-306 has about 27% of its germplasm from *B. vulgaris* subsp. *maritima* sources. Unlike CN927-202 and CN926-11-3-22, CN921-306 retains obvious wild beet traits. It is easier bolting and segregates for annualism (*B*). Seed stalks are lax and readily lodge. One of the wild beet components of CN921-306 came through C51. The other sources are C26 (PI610488) (Lewellen, 2000) and C27 (PI610489) (Lewellen, 2000). C26 and C27 are improved populations that are approximately half sugarbeet and half *B. vulgaris* subsp. *maritima* from collections made in France, UK, Ireland, and northern Europe (Panella and Lewellen, 2006). Genetic male-sterile plants from population 8926 (see CN926-11-3-22 above) were crossed to C26 and C27 in 2000 to produce population 0921. Population 0921 was selected for resistance to rhizomania and improved for agronomic traits and components of sugar yield to produce population 2921 in 2002. Population 2921 segregated at a low frequency in tests at Brawley for high vigor under high temperature, SBCN/rhizomania conditions similar to the source populations of CN927-202 and C926-11-3-22. Individual plants from 2921 were selfed and based upon progeny tests in 2004, S₁ progeny 3921-306 was increased to produce 5921-306, released as CN921-306. Less is known about CN921-306 except that in the S₁

progeny tests, it was superior in yield performance and apparent resistance to SBCN compared to C927-4. In greenhouse SBCN tests at Salinas in 2004-2005, 8 out of 10 plants showed moderate to high resistance to *H. schachtii*. In 2006 tests, again about 80% of the plants had relatively low cyst counts. The relationship of this resistance to that found in CN927-202 and CN926-11-3-22 has not been determined. Currently, populations are being searched for specific molecular genetic markers in this and the CN927-202, CN12, and CN72 sources of SBCN resistance. CN921-306 may be useful as a potential source of resistance to cyst nematode that may or may not be different from other released sources.

Lewellen, R.T., H.-Y. Liu, A.M. Gillen, and C.A. Strausbaugh. 2007. Performance of rhizomania resistant sugarbeet under normal and resistance-breaking strains of *Beet necrotic yellow vein virus*. Proc. American Society Sugar Beet Technologists, March 1-4, 2007, Salt Lake City, UT.

Rhizomania in sugarbeet (*Beta vulgaris*) is caused by *Beet necrotic yellow vein virus* (BNYVV). In current commercial cultivars, resistance to BNYVV is conditioned primarily by the allele *Rz1*. Since 2003, observations indicate that *Rz1* has been compromised by resistance-breaking strains of BNYVV (RB-BNYVV). A second resistance gene *Rz2* originally identified in *B. vulgaris* spp. *maritima* (WB42) appears to provide partial resistance to the resistance-breaking strains.

Sugarbeet cultivars with single and combinations of resistance genes were evaluated in baited plant greenhouse tests based on ELISA values. These cultivars and other experimental hybrids and breeding lines were evaluated in field trials at Salinas and Brawley, CA and Kimberly, ID under BNYVV noninfested and infested conditions. Infested conditions included both normal and RB-BNYVV strains.

The performance in the field substantiated the baited plant results. Significant interactions occurred for components of yield between cultivars (source of resistance) and strains of BNYVV. The *Rz1* allele gave a high level of protection against normal BNYVV but was defeated by the RB-BNYVV strains originating from the Imperial Valley of California. The *Rz2* allele either alone or in combination with *Rz1* provided partial resistance to the RB-BNYVV strains. The *Rz1* allele appeared to continue to provide some protection to losses caused by the resistance-breaking strains. However, this apparent partial protection may have been due to mixed normal and RB-BNYVV strains occurring in the field trials. The performance of the *Rz1* entry showed a continuous gradation from fully resistant to fully susceptible, depending upon the history and severity of the RB-BNYVV infestation. Resistance in C28 (C79-4) introgressed into sugarbeet from PI 206407 (resembling Swiss chard) did not condition resistance to RB-BNYVV. Resistance in WB41 introgressed into sugarbeet (C79-2) and reported to be *Rz3* conditioned partial resistance to all BNYVV strains tested. Quantitatively inherited resistance selected against normal strains also provided partial protection against losses to the resistance-breaking strain.

Because of the demonstrated vulnerability of single, major genes, the search is being continued for additional sources of resistance. A promising source is from WB151 and other *B. vulgaris* spp. *maritima* accessions and populations. At this time it is not known if the resistance conditioned by these sources from wild beet is the same or different from the known *Rz2* and *Rz3* factors.

Liu, H.-Y. and R.T. Lewellen. 2006. Distribution and molecular analysis of resistance-breaking isolates of *Beet necrotic yellow vein virus* in the United States. *Phytopathology* 96: S69, 2006.

Beet necrotic yellow vein virus (BNYVV) is the causal agent of rhizomania disease of sugar beet (*Beta vulgaris* L.). The virus is transmitted by the plasmodiophorid *Polymyxa betae*. The disease can only be controlled effectively by the use of partially resistant cultivars. During 2003 and 2004 in the Imperial Valley of California, partially resistant sugar beet cultivars with *Rz1* allele seemed to be compromised. Distinct BNYVV isolates have been identified from these plants. These isolates do not contain RNA-5 as determined by RT-PCR. From the banding patterns of single-strand conformation polymorphism and sequence analyses we concluded that the resistance-breaking BNYVV isolates from Imperial Valley had likely evolved from the original existing A-type. Rhizomania infested sugar beet fields throughout the United States were surveyed in 2004-2005. Our soil survey indicated that the resistance-breaking isolates not only existed in the Imperial Valley and San Joaquin Valley of California but also in Colorado, Idaho, Minnesota, Nebraska, and Oregon. Out of all the soil samples we tested, 92.5% of 'Beta 6600' (*rz1rz1rz1*), 77.5% of 'Beta 4430R' (*Rz1rz1*), 45.0% of 'Beta G017R' (*Rz2rz2*), and 15.0% of 'KWS Angelina' (*Rz1rz1+Rz2rz2*) were infected with BNYVV. Analyses of the deduced amino acid sequence of coat protein and P-25 protein of resistance-breaking BNYVV isolates revealed the high percentage of identity with non-resistance-breaking BNYVV isolates (99.9% and >98.0% respectively). The P-25 proteins in all isolates consisted of 219 amino acid residues and there was a maximum of 10 amino acid differences. The variable amino acids in P-25 proteins were located at the residues of 67 and 68. In the United States, the two amino acids found in the non-resistance-breaking isolates were conserved (AC). The resistance-breaking isolates were variable including AF, AL, SY, VC, VL, as well as AC. we cannot depend on the change of these two amino acids to absolute differentiate resistance-breaking and non-resistance-breaking isolates of BNYVV.

Panella, L. and R.T. Lewellen. 2007. Broadening the genetic base of sugar beet: introgression from wild relatives. *Euphytica* 154:383-400. DOI 10.1007/s10681-006-9209-1

See the Fort Collins section of this report.

Rush, C. M., H.Y. Liu, R.T. Lewellen, and R. Acosta-Leal. 2006. The continuing saga of rhizomania of sugar beets in the United States. *Plant Dis* 90:4-15.

Rhizomania caused by *Beet necrotic yellow vein virus* (BNYVV) is the most important soil-borne virus disease of sugar beet worldwide. Since 1984 when discovered, the gene *Rz1* has provided a high level of resistance. In 2002 in the Imperial Valley of California, cultivars with *Rz1* resistance began to show severe symptoms of rhizomania. In subsequent years, these resistance breaking isolates occurred in additional fields and threaten to completely defeat the *Rz1* resistance. This feature article in Plant Disease on these resistance breaking strains in sugar beet combines a summation of the rhizomania disease and published research up to present. It also reports new research findings on the virology of the resistance breaking strains, the search for new sources of resistance within *Beta vulgaris* germplasm resources, the national distribution of these strains, and their relationship to the phenomenon of “blinkers” in sugar beet fields with resistant cultivars. This paper also discusses the prospects and research underway to manage this continuing threat to the US sugar beet industry.

Schoelz, J.E., B.E. Wiggins, W.M. Wintermantel and K. Ross. 2006. Introgression of a tombusvirus resistance locus from *N. edwardsonii* var. Columbia to *N. clevelandii*. *Phytopathology* 96: 453-459.

A new variety of *Nicotiana*, *N. edwardsonii* var. Columbia, was evaluated for its capacity to serve as a new source for virus resistant genes. Columbia was developed from a hybridization between *N. glutinosa* and *N. clevelandii*, the same parents used for the formation of the original *N. edwardsonii*. However, in contrast to the original *N. edwardsonii*, crosses between Columbia and either of its parents are fertile. Thus, the inheritance of virus resistance genes present in *N. glutinosa* could be characterized by using Columbia as a bridge plant in crosses with the susceptible parent, *N. clevelandii*. To determine how virus resistance genes would segregate in interspecific crosses between Columbia and *N. clevelandii*, we followed the fate of the *N* gene, a single dominant gene that specifies resistance to *Tobacco mosaic virus* (TMV). Our genetic evidence indicated that the entire chromosome containing the *N* gene was introgressed into *N. clevelandii* to create an additional line, designated *N. clevelandii* line 19. Although line 19 was homozygous for resistance to TMV, it remained susceptible to *Tomato bushy stunt virus* (TBSV) and *Cauliflower mosaic virus* (CaMV) strain W260, indicating that resistance to these viruses must reside on other *N. glutinosa* chromosomes. We also developed a second addition line, *N. clevelandii* line 36, which was homozygous for resistance to TBSV. Line 36 was susceptible to TMV and CaMV strain W260, but was resistant to other tombusviruses, including *Cucumber necrosis virus*, *Cymbidium ringspot virus*, *Lettuce necrotic stunt virus*, and *Carnation Italian ringspot virus*.

Stevens, M., H.-Y. Liu, O. Lemaire. 2006. Virus Diseases. In A. Philip Draycott (ed.) *Sugar Beet*. pp. 256-285 (Book chapter). Blackwell Publishing Ltd, Oxford, United Kingdom.

Sugar beet is susceptible to a number of different viruses that are transmitted by either insects, fungi, nematodes, seed and/or physical contact. All of these viruses have the ability to decrease the potential yield of the root crop as well as affect the extractability of sugar by the processor. Certain viruses such as *Beet necrotic yellow vein virus* (BNYVV), the causal agent of rhizomania, have decimated sugar yields in intense sugar beet producing regions of the world and this virus can dictate where beet can be grown if partially resistant varieties are not grown. With the advance in molecular biology most of the economically important sugar beet viruses have been fully characterised and their DNA or RNA genomes sequenced. This has been particularly useful in understanding how these viruses interact with plants and their vectors, and how they can be better controlled in the future. Such advances have enabled the development of highly specific and sensitive serological and molecular diagnostic methods that have helped to clarify the taxonomic position of certain viruses and their strains, such as the virus yellows complex, as well enabling the identification of new viral species and how sugar beet viruses can interact in the same plant.

Tzanetakis, I.E., W.M. Wintermantel, A.A. Cortez, J.E. Barnes, S.M. Barrett, M.P. Bolda, and R.R. Martin. 2006. Epidemiology of Strawberry Pallidosis Associated Virus and Occurrence of Pallidosis Disease in North America. Plant Disease 90:1343-1346.

Strawberry pallidosis associated virus (SPaV) was found closely associated with pallidosis disease. The modes of transmission of the virus were studied, including pollen, seed (achene) and whitefly transmission. Three whitefly species were tested for their ability to transmit Strawberry pallidosis associated virus but only the greenhouse whitefly, *Trialeurodes vaporariorum*, was identified as a vector of the virus. Testing strawberries for Strawberry pallidosis associated virus and *Beet pseudo yellows virus*, a second crinivirus associated with pallidosis disease, in strawberry producing areas in North America, confirmed a high incidence of both viruses in areas where high populations of whiteflies were present. Infection rates as high as 90% for Strawberry pallidosis associated virus and 60% for *Beet pseudo yellows virus* were observed when plants exhibiting decline symptoms were tested. Lower rates of infection were found in regions where whiteflies were absent or found in low numbers. The role of these criniviruses in the strawberry decline observed over the past few years along the western coast of North America was examined.

Weiland, J.J., N. Nagl, J.M. McGrath, L.W. Panella, R.T. Lewellen. 2007. Molecular genetic tagging of *Beta vulgaris* ssp. *maritima*-derived resistance to the sugar beet cyst nematode *Heterodera schachtii*. Plant & Animal Genome XV Annual Conference, Jan. 13-17, 2007, San Diego, CA

See Fargo and/or East Lansing section of this report.

Wintermantel, W.M. 2006. Vector specificity of criniviruses in tomato and virus competitiveness during mixed infection. Proceedings of the 4th International Bemisia Workshop, Hawks Cay Resort, Duck Key, FL, Dec. 3-6, 2006.

Tomato chlorosis virus (ToCV), family *Closteroviridae*, genus *Crinivirus*, causes interveinal chlorosis, leaf brittleness and limited necrotic flecking or leaf bronzing on tomato leaves. ToCV can cause a decline in plant vigor and reduce fruit yield; it is emerging as a serious production problem for field and greenhouse tomato growers, and has been increasing in prevalence in many parts of the world. ToCV has a moderately wide host range, infecting 24 host plant species in seven families. The virus is unique among known whitefly-transmitted viruses, due to its ability to be transmitted by four whitefly vectors from two genera. Studies demonstrated that transmission efficiency and virus persistence in the vector varies significantly among the different whitefly vectors. *Trialeurodes abutilonea* and *Bemisia tabaci* biotype B are highly efficient vectors of ToCV. *B. tabaci* biotype A and *T. vaporariorum* are less efficient vectors, but are fully capable of transmission. ToCV persists for up to 5 days in *T. abutilonea*, 2 days in *B. tabaci* biotype B, and only 1 day in *B. tabaci* biotype A and *T. vaporariorum*. ToCV is closely related to another crinivirus, *Tomato infectious chlorosis crinivirus* (TICV). TICV and ToCV produce identical symptoms on tomato, but TICV differs from ToCV in that it is transmitted exclusively by *T. vaporariorum*. Geographical distribution of TICV and ToCV depends on distribution of the whitefly vectors. In some parts of the world both viruses have been found together in tomato, indicating that infection by one crinivirus does not prevent infection by a second. Crinivirus epidemiology is impacted not only by vector-movement of viruses, but also by factors such as virus competitiveness in host plants. It is likely that competitiveness of each virus varies among different host plant species, and may be influenced by factors such as plant age or which virus became established first. Alternatively, co-infection may increase the potential for genetic recombination or pseudo-recombination between related crinivirus species, and may contribute to selection pressure leading to emergence of new strains or species with altered host range, symptomatology or vector specificity. In order to elucidate the effects of co-infection on crinivirus vector specificity and accumulation, we established *Physalis wrightii* and *Nicotiana benthamiana* source plants, containing either TICV alone, ToCV alone, or both viruses together. *T. vaporariorum* and *T. abutilonea* were allowed to feed separately on all virus sources, as well as virus-free plants for 24 hours, then were transferred to young host plants. Symptomatic plants were tested by northern hybridization and quantitative RT-PCR, and indicated some host-specific differences in accumulation by TICV and ToCV. Interestingly, transmission of TICV from mixed infections by the non-vector, *T. abutilonea* was confirmed in two of fifty-six plants.

Wintermantel, W.M., S. Fuentes, C. Chuquillanqui, and L.F. Salazar. First Report of Beet pseudo-yellows virus and Strawberry pallidosis associated virus in Strawberry in Peru. Plant Disease 90: 1457.

During a 2006 survey for the presence of criniviruses in Peru, large numbers of greenhouse whitefly (*Trialeurodes vaporariorum*) were observed infesting strawberry

(*Fragaria* × *ananassa*) fields near Huaral on the central coast of Peru. Plants exhibited a wide range of symptoms including stunting and reddening of leaves. These symptoms are characteristic of those induced by the presence of the criniviruses *Beet pseudo-yellows virus* (BPYV) and/or Strawberry pallidosis associated virus (SPaV) together with any of a number of different strawberry-infecting viruses (1,3). The virus complex causes older leaves to develop a red color, vein and petiole reddening, roots become stunted, and plants fail to develop. Leaf samples with varying symptoms were collected from 22 plants from 2 fields, each planted with a different cultivar. Total nucleic acid was extracted, spotted onto positively charged nylon membranes, and tested by hybridization with probes specific to the minor coat protein (CPm) gene of BPYV (2) and coat protein (CP) gene of SPaV (4). Results identified the presence of BPYV, SPaV, or both viruses in mixed infections in symptomatic strawberry, while control plants were infected with each virus individually. No signal was detected in virus-free strawberry. Secondary confirmation was obtained using probes specific to the RNA-dependent RNA polymerase (RdRp) genes of SPaV and BPYV. The SPaV probe corresponded to nucleotides 6116–6599 of SPaV RNA1 (GenBank Accession No. NC_005895), whereas the BPYV probe corresponded to nucleotides 6076–6447 of BPYV RNA1 (GenBank Accession No. NC_005209). All probes were generated by reverse-transcription polymerase chain reaction (RT-PCR) amplification using sequence-specific primers, cloning of RT-PCR products into pGEM-T Easy (Promega, Madison, WI), confirmation by sequencing, and expression as digoxigenin-labeled transcript probes (Roche, Indianapolis, IN). Field 1, containing cv. Fern Sancho, had the largest number of symptomatic and infected plants (5 of 12 BPYV, 6 of 12 SPaV, and 4 of 12 with both). Only 1 of 10 plants from field 2 containing cv. Tajo Holandesa was infected, but with both SPaV and BPYV. BPYV and SPaV are transmitted by the greenhouse whitefly (*T. vaporariorum*), although BPYV is transmitted much more efficiently and has a broader host range than SPaV (4). Movement of these viruses in Peru is likely a result of both propagation by runners and vector transmission. To our knowledge, this is the first report of either virus in Peru.

Wintermantel, W.M., R.C. Grube and A.G. Anchieta. 2006. Biology and genetics of lettuce dieback disease and Lettuce necrotic stunt virus. *Phytopathology* 96:S124.

Lettuce dieback, a new soil-borne disease of lettuce, emerged in the 1990s to cause severe losses for lettuce production in the western United States. The disease is caused by *Tomato bushy stunt virus* (TBSV) and the recently described tombusvirus, Lettuce necrotic stunt virus (LNSV). The complete genome of LNSV was sequenced, compared with genomes of other tombusviruses, and was found to be related to but distinct from TBSV. Both LNSV and TBSV can infect lettuce through the soil in the absence of fungal vectors. Fields with high disease incidence are usually poorly drained, and field and greenhouse tests determined that elevated soil salinity, as measured by electrical conductivity led to increased frequency of diseased plants. Neither virus appears to be transmissible through seed embryos, however, seed coat transmission occurred at low levels when plants were tested as seedlings for the presence of virus. The ability to detect virus in seedlings, however, does not always lead to development of disease symptoms. Resistance based on a single dominant gene, *Tvr1*, is widespread among commercial crisphead lettuce cultivars, and resistance has also been identified for other lettuce types.

LNSV and TBSV can accumulate in seedlings of both resistant and susceptible cultivars based on ELISA, but resistant varieties do not develop disease symptoms, and virus accumulation is rarely detectable in resistant plants from the field.

Wintermantel, W.M. and R.J. Hayes. 2006. Host resistance to *Mirafiori lettuce big-vein virus* and virus sequence diversity in the western United States. *Phytopathology* 96:S124

Big vein is an economically damaging disease of lettuce (*Lactuca sativa*) caused by the *Olpidium brassicae* vectored *Mirafiori lettuce big-vein virus* (MLBVV). Although big vein is a perennial problem in the US, the extent of MLBVV infection and diversity was unknown. Lettuce cultivars partially resistant to big vein reduce losses, but do not eliminate disease. While the wild relative, *L. virosa*, does not develop big vein symptoms, it had not been tested for infection with MLBVV. Lettuce cultivars Great Lakes 65, Pavane, Margarita, and *L. virosa* accession IVT280 were evaluated for big vein incidence and virus infection in inoculated greenhouse trials. In addition, lettuce samples were collected from field sites in California and Arizona, classified for symptom severity and evaluated for virus infection and isolate diversity by RT-PCR and nucleotide sequencing. Infections with MLBVV were correlated with big vein field symptoms and virus isolates were closely related to those from Europe and Japan. Partial big vein resistance was identified in Margarita and Pavane; however, MLBVV infection was found in asymptomatic plants. Variation for symptom expression and MLBVV accumulation occurred among *L. virosa* accessions. Accession IVT280 remained symptomless and in most cases virus free, suggesting it is a strong source of resistance.

Wintermantel, W.M. and S.R. Kaffka. 2006. Sugarbeet performance with curly top is related to virus accumulation and age at infection. *Plant Disease* 90: 657-662.

Resistance to curly top disease caused by *Beet curly top virus* (BCTV) and related curtoviruses has been important to sustainable sugar beet (*Beta vulgaris*) production in the western United States for most of the last century. Recent advances in sugarbeet genetics have led to the development of high-yielding cultivars, but these cultivars have little resistance to curly top disease. These cultivars are highly effective when disease management practices or environmental factors minimize curly top incidence, but can result in significant losses in years with early infection or abundant curly top. A greenhouse assay has been developed to rapidly test cultivars for a broad array of factors affecting performance in the presence of curly top. Previous studies have shown that sugarbeet plants were more susceptible and losses more severe when seedlings were infected by BCTV, but less severe when plants were larger at the time of infection. To evaluate more precisely the relationship between age at infection, disease severity, virus accumulation and yield loss in modern cultivars that were not bred for curly top resistance, individual sugarbeet plants varying in degree of resistance and susceptibility to curly top were inoculated by viruliferous beet leafhoppers (*Circulifer tenellus*) when

plants had 2, 4 or 6 true leaves, and maintained in a greenhouse for 6 weeks. When plants were inoculated at the 2 leaf stage, all cultivars became severely stunted with high disease ratings and similar rates of symptom development, regardless of resistance or susceptibility of the cultivar. Plants inoculated at 4 and 6 leaf stages exhibited increasing separation between resistant and susceptible phenotypes, with highly resistant cultivars performing well with low disease ratings and increased plant weights relative to susceptible cultivars. High yielding cultivars performed only slightly better than the susceptible control cultivar. Results from greenhouse trials matched those from field trials conducted under heavy curly top pressure. Importantly, low virus concentration was directly correlated with lower disease ratings and higher plant weight, while elevated virus concentrations corresponded to higher disease ratings and lower weights. This demonstrates a rapid greenhouse assay involving multiple traits can provide a rapid and effective means of selecting cultivars with improved curly top control, and could lead to more rapid incorporation of resistance into high-yielding sugarbeet.

Wintermantel, W.M. and G.C. Wisler. 2006. Vector Specificity, Host Range and Genetic Diversity of *Tomato Chlorosis Virus*. *Plant Disease* 90: 814-819.

Tomato chlorosis virus (ToCV), family *Closteroviridae*, genus *Crinivirus*, causes interveinal chlorosis, leaf brittleness and limited necrotic flecking or leaf bronzing on tomato leaves. ToCV can cause a decline in plant vigor and reduce fruit yield; it is emerging as a serious production problem for field and greenhouse tomato growers, and has been increasing in prevalence in many parts of the world. The virus is unique among known whitefly-transmitted viruses, due to its ability to be transmitted by four whitefly vectors from two genera. Studies demonstrated that transmission efficiency and virus persistence in the vector varies significantly among the different whitefly vectors. *Trialeurodes abutilonea* and *Bemisia tabaci* biotype B are highly efficient vectors of ToCV. *B. tabaci* biotype A and *T. vaporariorum* are less efficient vectors, but are fully capable of transmission. ToCV persists for up to 5 days in *T. abutilonea*, 2 days in *B. tabaci* biotype B, and only 1 day in *B. tabaci* biotype A and *T. vaporariorum*. ToCV has a moderately wide host range, infecting 24 host plant species in seven families. A portion of the coat protein coding region of five geographically diverse ToCV isolates was compared and found to be highly conserved. This information, coupled with existing information on conservation within the heat shock protein 70 homologue coding region suggests many ToCV isolates throughout the world are related very closely, and may have been distributed on plant material.

Book Chapter:

Mutschler, M.A. and W.M. Wintermantel. 2006. Reducing virus associated crop loss through resistance to insect vectors. In: *Natural resistance mechanisms of plants to viruses*. Loebenstein, G. and Carr, J.P. eds. Springer, New York. pp 241-260.

STUDY OF NEW PATHOTYPES OF RHIZOMANIA IN THE UNITED STATES

(Project 261)

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SUMMARY:

During the survey of resistance-breaking isolates of *Beet necrotic yellow vein virus* (BNYVV) through out the sugar beet growing areas in the United States, BNYVV and Beet oak-leaf virus (BOLV) occurred often concurrently in the same area and sometimes in the same sugar beet plant. To determine the possibility of interactions between the two *Polymyxa betae* transmitted viruses tests were conducted. Soils infested with cultures of aviruliferous *P. betae* and viruliferous *P. betae* carrying resistance-breaking BNYVV and BOLV, alone and in combination, were compared with noninfested soil for their effects on plant fresh weight and virus content as measured by enzyme-linked immunosorbent assay (ELISA). The *Rz* genes that confer resistance to BNYVV did not confer resistance to BOLV. BNYVV ELISA values were significantly higher in single infections than in mixed infections with BOLV, in both the rhizomania-resistant and -susceptible cultivars. In contrast, ELISA values of BOLV were not significantly different between single and mixed infections in both the rhizomania-resistant and -susceptible cultivars. Results indicated that BOLV may suppress BNYVV in mixed infections. Soils infested with *P. betae* significantly reduced fresh weight of seedlings regardless of whether they were with or without one or both viruses.

INTRODUCTION:

Beet necrotic yellow vein virus (BNYVV) is a member of the genus *Benyvirus* (Tamada, 1999 and Torrance and Mayo, 1997) and it causes the disease known as rhizomania. It is the most important sugar beet virus and is transmitted by the plasmodiophorid, *Polymyxa betae* Keskin (Fujusawa and Sugimoto, 1976, Abe and Tamada, 1986 and Barr, 1992). BNYVV was first described in Italy in 1959. In the United States, the virus was first identified in California in 1984 (Duffus et al., 1984) but now occurs in every major sugar beet production region in the country (Rush, et al., 2006).

Rhizomania has caused major reduction in sugar beet root yield and sugar content. As soon as rhizomania was identified in North America, the USDA Agricultural Research Service in Salinas, California began an extensive screening of genetic resources to identify potential sources of resistance to BNYVV and incorporate resistance into sugar beet germplasm (Biancardi, et al., 2002). *Rz1* is a single dominant resistant gene for BNYVV (Lewellen, et al., 1987) and is the only major gene resistances identified within commercial sugar beet (Biancardi, et al., 2002; Scholten and Lange, 2000). The second resistant gene, derived from wild beet (WB42) designated as *Rz2* (Scholten et al., 1996, 1999), was shown to be different from *Rz1* and conferred a higher level of resistance (Panella and Lewellen, 2006). Recently, a third resistance gene *Rz3* has been reported

which is linked to *Rz1* and *Rz2* on chromosome III (Gidner et al., 2005). Plants with combined *Rz1* and *Rz2* or *Rz3* in a heterozygous condition have lower virus titer than with *Rz1* alone. At present time, the resistant cultivars have been the only economical way to control this devastating disease.

In 2002-2003, rhizomania resistant *Rz1* cultivars began to express severe symptoms of rhizomania in the Imperial Valley of California. We soon verified that certain isolates of BNYVV from the Imperial Valley had overcome genetic resistance (Liu, et al., 2005). Since 2003, not only did the resistance-breaking BNYVV appear in the Imperial Valley, but also in other sugar beet growing regions in the United States (Liu and Lewellen, 2007).

During the survey for resistance-breaking BNYVV isolates in the United States, Beet oak-leaf virus (BOLV) (Liu, et al., 2003) was frequently found co-infected with BNYVV in the same field and sometimes in the same sugar beet plant. BOLV was first isolated from rhizomania infested fields in California. Infected sugar beet leaves showed oak-leaf pattern symptoms different from rhizomania. BOLV is serologically distinct from BNYVV, *Beet soil-borne mosaic virus* (BSBMV), and *Beet soil-borne virus* (BSBV). The host range of BOLV is similar to BNYVV and BSBMV mostly infecting Chenopodiaceous plants. BOLV has been purified from spinach (*Spinacia oleracea*) plants. Virus particles were 20 nm wide and ranged from 80 to 640 nm in lengths. BOLV is transmitted by *P. betae*. The molecular mass of the capsid protein was estimated to be 46.0 kDa. A polyclonal antibody from rabbits has been produced and can be used in ELISA, western blot, and immunogold labeling tests. BOLV appears to be wide spread in U.S. It has been found also in Colorado, Michigan, Minnesota, Nebraska, and Wyoming. In contrast to BNYVV, little is known about the effect of BOLV on yield and sugar content in sugar beet.

The objectives of this study were to determine if the *Rz* BNYVV resistant genes confer resistance to BOLV and to determine the effects of *P. betae*, resistance-breaking BNYVV isolates and BOLV alone and in combination, on growth and relative ELISA values in sugar beet.

MATERIALS AND METHODS:

Inoculum preparation. Resistance-breaking BNYVV isolates were collected from the Imperial Valley, California. BOLV isolates were collected from Salinas, California. BNYVV and BOLV isolates were mechanically inoculated to systemic host *Beta macrocarpa* or spinach (*Spinacia oleracea*) which was planted in sterilized soil. After showing systemic infection, virus-free *P. betae* was incorporated into the soil. One month later, the infected roots and soil were used for inoculum. The aviruliferous *P. betae* was obtained from river sand that was collected from eastern Wyoming. Roots from seedlings grown in soil containing this *P. betae* isolate were repeatedly tested by enzyme-linked immunosorbent assay (ELISA) for the presence of these two soil-borne viruses, making sure no viruses were detected. All virus infested soils and virus-free soils were tested prior to these studies to confirm the presence or absence of the desired viruses.

Soil test. One part of soil samples was mixed with nine parts of autoclaved builder's sand to facilitate ease of root removal at harvest. Greenhouse benches were washed in 10% sodium hypochlorite prior to use. Pots were new 280-ml Styrofoam cups. The soil test procedures were described previously (Liu, et al., 2005). Sugar beet cultivars used in experiments that were resistant to rhizomania included Beta 4430 R (*Rz1rz1*), Beta G017 R (*Rz2rz2*), and KWS Angelina (*Rz1rz1* + *Rz2rz2*) and a triploid rhizomania-susceptible Beta 6600 (*rz1rz1rz1*). Pots were arranged on greenhouse benches in a randomized complete block design with three replications for each treatment. Greenhouse was maintained between 15 and 24 C without supplemental light. The soil treatments consisted of: (i) sterilized soil; (ii) *P. betae*-infested soil; (iii) BNYVV-infested soil; (iv) BOLV-infested soil; and (v) BNYVV- and BOLV-infested soil, mixed in equal parts. Roots from these pots were harvested. The seedlings in each pot were counted and weighted and the roots tested for relative concentration of BNYVV and BOLV by ELISA after 3, 5, 7, and 9 weeks post emergence of seedlings.

Enzyme-linked immunosorbent assay (ELISA). Samples were prepared by washing roots of seedlings from each pot to remove soil. Root tissue (0.2 g from each root mass) was placed in sample extraction bags containing 2 ml of extraction buffer (0.05 M phosphate-buffered saline, pH 7.2, 0.5% Tween 20, 0.4% dry milk powder) and homogenized with a hand-held roller press (Agdia, Inc.). Expressed sap (100 µl per well) was added to duplicate wells of a microtiter plate. Each plate also contained controls including sap from BNYVV-infected beet roots, BOLV-infected beet roots, and healthy beet roots.

Double antibody sandwich ELISA (Clark and Adams, 1977) was used. Purified IgG made to BNYVV and BOLV (1mg/ml) were used to coat microtiter plates at a 1/1000 dilution. Alkaline phosphatase-conjugated anti-BNYVV/BOLV IgG was added to wells (1/1000 dilution). Alkaline phosphatase substrate (Sigma Chemical, St. Louis, MO) was used at a ratio of 5 mg/8.3 ml of substrate buffer. Absorbance readings (A_{405nm}) were made 1 hr after the addition of substrate using a Bio-Tek EL312e microplate reader (Winooski, VT). Analysis of variance was run to determine statistical differences among treatment means.

RESULTS:

Statistical analyses. The means squares and levels of significance from the analyses of variance for the variables are shown in Table 1. The main effect means for cultivars, soil treatments, and harvest dates are shown in Table 2. To illustrate specific results, interaction means are shown in Table 3, 4, and 5.

Effects of *P. betae* on sugar beet. In greenhouse pot culture, the mean effect of virus-free *P. betae* caused a significant reduction in sugar beet growth (Table 2), as measured by the average weight per plant. The most significant reduction in growth of sugar beet cultivars was 'Beta 4430R' with BNYVV-*Rz1* resistant gene and 'KWS Angelina' with both *Rz1* and *Rz2* resistant genes. For BNYVV susceptible variety 'Beta 6600' and 'Beta G017R' with *Rz2* resistant gene there were no significant reductions on plant weight (Table 4).

Table 1. Mean squares from analyses of variance for enzyme-linked immunosorbent assay value for *Beet necrotic yellow vein virus* (BNYVV) and Beet oak-leaf virus (BOLV), and average fresh weight per plant for four cultivars grown under five soil treatments and four harvest dates.

Source	Mean Squares ^u			
	df	BNYVV ^v	BOLV ^v	Weight (g) ^w
Cultivar (C) ^x	3	3.294 **	2.057 ns	0.127 **
Soil Treatment (ST) ^y	4	197.709 **	86.076 **	0.013 **
C X ST	12	0.794 ns	1.468 ns	0.002 ns
Harvest Date (HD) ^z	3	11.593 **	5.587 **	0.018 **
C X HD	9	4.359 ns	0.548 ns	0.006 *
ST X HD	12	3.315 **	2.608 *	0.001 ns
C X ST X HD	36	14.948 ns	0.693 ns	0.003 ns
Error	158	90.397	1.267	0.002

^u Completely random design with three repetitions; ns = not significant; * and ** indicate significance at the $P \leq 0.05$ and 0.01 levels, respectively, according to the *F* test.

^v Values represent the ratio of the absorbance at 405 nm reading for BNYVV or BOLV over the corresponding healthy absorbance value.

^w Average fresh weight per plant.

^x Rhizomania susceptible cultivar without known resistant gene: Beta 6600, rhizomania resistant cultivars: Beta 4430R, Beta G017R, and KWS Angelina with *Rz1*, *Rz2*, and *Rz1+Rz2* resistant genes, respectively.

^y Sterilized soil, soil with non-viruliferous *Polymyxa betae*, BNYVV viruliferous *P. betae*, BOLV viruliferous *P. betae*, and BNYVV and BOLV viruliferous *P. betae*.

^z 3, 5, 7, and 9 weeks post germination.

Mixed infections with BNYVV and BOLV. In both BNYVV-resistant and –susceptible cultivars, ELISA values for BNYVV from roots were significantly reduced in mixed infections with BOLV compared to single infections with BNYVV (Table 3). In contrast, ELISA values from roots infected BOLV alone or in mix infections with BNYVV there were not significantly different in both BNYVV-resistant and –susceptible cultivars except in KWS Angelina. In KWS Angelina, ELISA values of BOLV were significantly reduced in mixed infections with BNYVV compared to single infections with BOLV.

Rhizomania resistance genes. Resistance to BNYVV conferred by *Rz1*, *Rz2*, and *Rz1 + Rz2* alleles did not show resistance to resistance-breaking BNYVV isolates and also did not confer resistance to BOLV in sugar beet in greenhouse pot cultures (Table 3). ELISA values for BNYVV in the rhizomania-susceptible cultivar (Beta 6600) and rhizomania resistant cultivars (Beta 4430R, Beta G017R or KWS Angelina) were not significant different. ELISA values for BOLV were also not significantly different on all four sugar beet cultivars tested.

Table 2. Main effect treatment means for enzyme-linked immunosorbent assay values for *Beet necrotic yellow vein virus* (BNYVV), *Beet oak-leaf virus* (BOLV), and average plant fresh weight evaluated for four cultivars over five soil treatments and four harvest dates.

Treatments	BNYVV ^y	BOLV ^y	Weight (g)
Grand mean	2.737	2.085	0.258
Cultivar ^z			
Beta 6600 (<i>rz1rz1rz1</i>)	2.920 a	2.161 a	0.326 a
Beta 4430 R (<i>Rz1rz1</i>)	2.950 a	2.300 a	0.227 c
G017 R (<i>Rz2rz2</i>)	2.603 b	1.875 a	0.231 c
KWS Angelina (<i>Rz1rz1</i> + <i>Rz2rz2</i>)	2.477 b	2.003 a	0.250 b
Soil treatment			
Noninfested	1.001 d	0.978 c	0.278 a
Polymyxa betae	1.784 c	1.220 c	0.237 c
BNYVV	5.439 a	1.155 c	0.263 ab
BOLV	1.111 d	3.786 a	0.267 a
BNYVV + BOLV	4.352 b	3.286 b	0.246 bc
Harvest date			
Week 3	2.576 bc	1.668 b	0.235 c
Week 5	3.350 a	2.398 a	0.263 ab
Week 7	2.708 b	2.170 a	0.258 b
Week 9	2.316 c	2.103 a	0.277 a

^y Values represent the ratio of the absorbance at 405 nm reading for BNYVV or BOLV over the corresponding healthy absorbance value. Means within columns followed by a different letter are significant at $P \leq 0.05$ according to the Duncan's multiple range test.^z Rhizomania susceptible cultivar without known resistant gene: Beta 6600, rhizomania resistant cultivars: Beta 4430R, Beta G017R, and KWS Angelina with *Rz1*, *Rz2*, and *Rz1+Rz2* resistant genes, respectively.

Table 3. Enzyme-linked immunosorbent assay value interaction means among cultivars^y and soil treatments for *Beet necrotic yellow vein virus* (BNYVV) and *Beet oak-leaf virus* (BOLV).^z

Treatment interactions	BNYVV	BOLV
Beta 6600-BNYVV soil	5.628 a (+)	1.167 b (-)
-BOLV soil	1.069 c (-)	3.740 a (+)
-BNYVV + BOLV soil	4.825 b (+)	3.745 a (+)
Beta 4430 R-BNYVV soil	5.559 a (+)	1.137 b (-)
-BOLV soil	1.201 c (-)	4.141 a (+)
-BNYVV + BOLV soil	4.614 b (+)	4.063 a (+)
G017 R-BNYVV soil	5.310 a (+)	1.134 b (-)
-BOLV soil	1.088 c (-)	3.677 a (+)
-BNYVV + BOLV soil	3.804 b (+)	2.987 a (-)
KWS Angelina-BNYVV soil	5.259 a (+)	1.182 c (-)
-BOLV soil	1.087 c (-)	3.584 a (+)
-BNYVV + BOLV soil	4.165 b (+)	2.349 b (-)

^y Rhizomania susceptible cultivar without known resistant gene: Beta 6600, rhizomania resistant cultivars: Beta 4430R, Beta G017R, and KWS Angelina with *Rz1*, *Rz2*, and *Rz1+Rz2* resistant genes, respectively.

^z Values represent the ratio of the absorbance at 405 nm reading for BNYVV or BOLV over the corresponding healthy absorbance value. Means within columns followed by a different letter are significant at $P \leq 0.05$ according to the Duncan's multiple range test. Ratio of ≥ 3 times the healthy mean are considered positive (+). Means are for 12 pots across four dates of harvest and three repetitions.

Table 4. Effects of aviruliferous *Polymyxa betae*-infested soil on plant weight in rhizomania-susceptible and-resistant sugar beet cultivars ^y

Sugar beet Cultivar ^z	Average weight per plant (g)	
	Non-infested soil	<i>Polymyxa betae</i> infested soil
Beta 6600	0.475 a	0.349 b
Beta 4430R	0.508 a	0.350 b
Beta G017R	0.463 a	0.298 b
KWS Angelina	0.442 a	0.229 b

^y Means are the 12 pots across four harvest dates and three repetitions. Means within rows of each test followed by a different letter are significant at $P \leq 0.05$ according to the Duncan's multiple range test.

^z Rhizomania susceptible cultivar without known resistant gene: Beta 6600, rhizomania resistant cultivars: Beta 4430R, Beta G017R, and KWS Angelina with *Rz1*, *Rz2*, and *Rz1+Rz2* resistant genes, respectively.

Table 5. Effects of viruliferous *Polymyxa betae*-infested soil with *Beet necrotic yellow vein virus* (BNYVV), *Beet oak-leaf virus* (BOLV), and BNYVV + BOLV on plant weight in rhizomania-susceptible and-resistant sugar beet cultivars.

Sugar beet cultivar ^y	Average weight per plant (g) ^z		
	BNYVV	BOLV	BNYVV + BOLV
Beta 6600	0.341 a	0.343 a	0.295 b
Beta 4430	0.235 a	0.225 a	0.222 a
Beta G017R	0.230 a	0.244 a	0.237 a
KWS Angelina	0.246 a	0.257 a	0.230 a

^y Rhizomania susceptible cultivar without known resistant gene: Beta 6600, rhizomania resistant cultivars: Beta 4430R, Beta G017R, and KWS Angelina with *Rz1*, *Rz2*, and *Rz1+Rz2* resistant genes, respectively.

^z Means are the 12 pots across four harvest dates and three repetitions. Means within rows of each test followed by a different letter are significant at $P \leq 0.05$ according to the Duncan's multiple range test.

DISCUSSION:

Several important conclusions were made from this research including the effects of (i) *P. betae*, (ii) BNYVV or BOLV single infection, and (iii) BNYVV and BOLV mixed infections on growth of sugar beet and virus content in greenhouse pot culture. The use of ELISA for detection of BNYVV (Gerik, et al., 1987) is highly reliable, and has been accepted as the sugar beet industry standard for confirmation of rhizomania-infested fields since the late 1980s (Gerik, et al., 1987, Wisler, et al., 1994, Wisler, et al., 1999). Highly specific antisera developed at the USDA-ARS in Salinas gives low absorbance values for negative samples. Absorbance values at least three times greater than healthy controls are required to achieve a positive score. Purified antiserum was highly selective in identifying BNYVV or BOLV infection in the sugar beet roots. The root samples from non-infested soil and aviruliferous *P. betae* soil treatments were negative to both BNYVV and BOLV in ELISA tests, which indicated that both soil samples were virus-free. In BNYVV or BOLV soil, root samples were only positive to BNYVV or BOLV, which proved these soil samples contained only one virus and were not contaminated with the other virus (Table 2).

BNYVV ELISA values were significantly higher in susceptible cultivars and cultivars with *Rz1* resistant gene than cultivars containing *Rz2* or *Rz1* and *Rz2* resistant genes (Table 2). These results coincided with our soil survey results. Cultivars with *Rz1* resistant gene have been used in the fields for sometime and the resistance-breaking BNYVV isolates could have developed or been selected that defeat the *Rz1* resistant gene.

Based on the results presented in this paper, BNYVV and BOLV are serologically distinct. The *Rz* genes conferring resistance to BNYVV do not confer resistance to BOLV (Table 3), clearly demonstrating that BOLV is distinct from BNYVV.

Reduction in seedling weight occurred when sugar beet seedlings are grown in *P. betae* infested soil compared with non-infested soil (Table 4). Two BNYVV resistant cultivars, Beta 4430 and KWS Angelina, had a significant reduction in seedling weight when grown in *P. betae* infested soil. This outcome revealed that *Rz1* and *Rz2* resistant genes condition resistant to BNYVV and not to *P. betae*.

Resistance-breaking BNYVV alone accumulates equally in both rhizomania-resistant and -susceptible cultivars. When BNYVV existed in mixed infections with BOLV, the level of BNYVV was significantly reduced in all cultivars tested. However, the level of BOLV remains the same no matter if it is a single infection or in mixed infections with BNYVV (Table 3). BOLV seems to suppress BNYVV in mixed infections. Rhizomania infection causes a significant reduction in root yield and sugar content (Lewellen and Biancardi, 1990; Tamada and Baba, 1973; and Wisler et al., 1999). In contrast, BOLV has been observed in beets in the United States (Liu, et al., 2003), but the effects of this virus on beet production are largely unknown. If BOLV caused no or little effect on sugar beet yield, BOLV may be useful for suppressing BNYVV in heavily infested rhizomania fields.

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IDENTIFICATION OF NOVEL SOURCES OF RESISTANCE TO BCTV FOR BIOREMEDIATION OR GENETIC ENGINEERING

(Project 221)

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Research Sponsor:

California Beet Growers Association and California Industry Research Committee

Introduction:

In recent years curly top disease, caused by *Beet curly top virus* (BCTV), re-emerged in California, resulting in significant economic losses for sugarbeet production in the San Joaquin Valley. Curly top has affected California agriculture for over a century, and no cost effective control methods have been developed that effectively and reliably prevent losses. During the summer of 2001, *Beet curly top virus* (BCTV) reemerged as an important, economically damaging pathogen of sugarbeet, tomato, and pepper throughout widespread areas of the western United States. These areas included California, the Snake River Valley of Idaho and the southwestern desert of west Texas and New Mexico. More recently curly top has been problematic in the Rocky Mountain region. The wide host range of BCTV, abundance of the beet leafhopper vector (*Circulifer tenellus*), and increasing acreage of uncultivated land in some areas is making curly top management increasingly difficult. The present California management strategy focuses on the large-scale use of insecticides to control the leafhopper vector in rangeland, and the use of insecticidal treatments on crops.

In an effort to control the beet leafhopper, and indirectly BCTV, California growers (all affected crops) pay \$1.5 million annually (2004 figures) for the spraying of 80,000-200,000 acres of uncultivated land with insecticide. The insecticide applications are directed at the overwintering breeding hosts (annual and perennial weeds) of the leafhopper to decrease the spring populations of the vector. Many California growers have become heavily dependent on the spray program. Although it is somewhat difficult to measure the efficacy of the insecticide treatments, this control measure is thought to work well in certain years and locations, and be inadequate in others. This was demonstrated in 2001 and 2003, when in spite of the heavy application of insecticide to leafhopper overwintering grounds, leafhopper populations and curly top disease incidence reached levels not seen for over a decade. Such outbreaks occur periodically and usually continue for a few years as was observed this decade, depending largely on environmental conditions, but also influenced by available weed and crop hosts, cropping patterns and management practices to name a few. Since the leafhopper vector needs only a brief feeding interval to introduce the virus into a healthy plant, treating sugarbeet with insecticides will not effectively block virus transmission, but may reduce overall numbers of leafhoppers.

The inability to manage curly top through traditional means necessitates the use of novel approaches, including molecular genetics. These methods have shown promise with related

viruses in other hosts, and should be effective for curly top in sugarbeet as well. New advances in technology are leading to approaches that may ultimately be useful for biotechnology-based control. It is in the best interest of the sugarbeet industry to explore new avenues for virus control and prevention, as this may ultimately reduce reliance on chemical control of the beet leafhopper, and lead to effective management of a virus that has been a chronic problem for over a century.

Background on methodology: Many plants induce a natural process known as virus-induced gene silencing (VIGS) upon infection by viruses. VIGS causes selective, specific degradation of viral genome sequences, as well as any additional sequences inserted into it. This can occur either during or after production of RNA. A number of different structural features on nucleic acids have been implicated as possible triggers. These include abnormal double stranded RNA molecules (double stranded RNA is something that is produced during RNA virus replication), tandem insertions of the same DNA sequence, and specific structural features on the nucleic acids to name a few. VIGS can initiate even in the first cell the virus infects, preventing whole plant infection, and in many transgenic systems it has been demonstrated that the silencing signal can be transmitted systemically throughout the plant. Recent studies have shown that when small pieces of DNA corresponding to a target gene present in transgenic plants are blasted into a leaf (using a device called a gene gun that essentially shoots DNA into a leaf), systemic silencing (suppression) of the target gene can be detected 2 to 3 days after bombardment. Even though the small pieces of DNA that were delivered by the gene gun only occurred in a few cells, the target gene was suppressed throughout the plant. Although most studies on gene silencing have been done with RNA viruses, silencing also occurs with DNA viruses. BCTV is a DNA virus, however it does produce RNA as a template for synthesis of virus proteins. Recent studies indicated that silencing based approaches have been effective for other geminiviruses (BCTV is also a geminivirus), such as *African cassava mosaic virus* and *Tomato yellow leaf curl virus*. As a result, it may be possible to develop methods to suppress infection by BCTV using similar approaches and a common virus-based vector for delivery of constructs to plants for testing.

Our initial goal is to develop strategies for control of BCTV in sugarbeet using VIGS. Ultimately we wish to develop methodologies that will allow this system to be delivered to plants using both traditional plant transformation and using alternate methodologies that might be effective even without the development of GMO sugarbeet; however, the first step is to demonstrate the effectiveness of the method for controlling this important viral disease. Once the resistance-inducing constructs are identified, we intend to work on novel methods for delivery to crops in the field.

Objectives:

1. Develop small synthetic DNA constructs capable of interfering with the BCTV (curly top) infection process, based on current knowledge of “gene silencing.” Improve upon existing constructs using slightly modified DNA constructs and develop new constructs.
2. Insert these constructs into a virus-based vector capable of delivering constructs to sugarbeet and other plants used in experimentation.

3. Test constructs on test host plants (*N. benthamiana*) and sugarbeet to determine the effectiveness of each construct in preventing infection and virus accumulation.
4. Deliver constructs to sugarbeet through either genetic engineering or using a mechanical delivery system to essentially “vaccinate” young plants against curly top.

Brief overview of progress to date:

Progress has been made demonstrating that two genetic constructs can reduce severity of curly top in the model host, *Nicotiana benthamiana* when treated 3 days prior to curtovirus inoculation. One construct appears to exhibit nearly complete control of *Beet mild curly top virus* (BMCTV) if sufficient time for activation of gene silencing occurs prior to exposure to BMCTV. Success for control of *Beet severe curly top virus* (BSCTV) was less impressive, but results suggest only minor modifications may be needed to achieve complete control of both viruses. Additional constructs are in development with further testing of new/modified constructs anticipated by summer 2007.

Project Accomplishments and Results from the Current Funding Period:

Objectives 1 through 3:

Constructs were designed based on viral sequences critical to virus replication and host infection, and include structures demonstrated to be effective inducers of gene silencing. The silencing constructs designed to date target sequences involved in virus replication. Studies concluded last spring (2006) tested 3 types of constructs using the approaches listed in Objective 2, including; a small positive strand sequence, a small negative strand (or antisense) sequence, and a construct producing a structure known as a hairpin. Results demonstrated some control with both the hairpin and the antisense constructs, but no differences from untreated controls with the positive strand construct. Although both the hairpin and antisense constructs reduced severity of curly top symptoms on *Nicotiana benthamiana* (experimental host commonly used for studies such as these), control was not sufficient. As a result, we chose two approaches to improve our control of BCTV.

The first approach was to develop additional constructs to determine if sequences other than those used in initial studies would be more effective. The second was to use an alternate delivery method that may be more effective in the *Nicotiana* system for induction of virus induced gene silencing than the systems we have been using to date. During the summer of 2006 we signed an agreement with Yale University to obtain a different gene delivery system based on *Tobacco rattle virus* (TRV). The TRV vector was specifically designed for use in members of the *Solanaceae*. Our previous systems (described in Objective 2 of 2006 Proposal) were known to work on solanaceous hosts for other types of testing, but had to be adapted for the specific needs of this project, whereas this TRV system was expected to be more suited to our use and would hopefully provide more complete control, rather than the partial control observed during Year 1 of this project. We inserted our two previously successful constructs, BMCTV hairpin and

BSCTV antisense, into the new vector with only minor sequence modifications. These are now known as pTRV-hp25 and pTRV-CFHC1, respectively. The first set of tests with these constructs was completed in early November 2006 and results were extremely promising.

Plants were inoculated mechanically with the TRV vector carrying either a “hairpin” construct designed against BMCTV in which the inserted sequence assembles in the form of a hairpin, or an “antisense” construct, in which the inserted sequence consists of the reverse complement of a segment derived from the replication associated protein of BSCTV. Three days following treatment, untreated plants and plants treated with either of the two constructs were inoculated with either BSCTV or BMCTV. Symptom development (leaf curling, twisting, discoloration and stunting) was observed over a period of 5 weeks, and plant height was determined as an indicator of infection severity. Results indicate that in some cases, control was dramatic and highly effective, while in others it was less effective. Much of this depended on the similarity between the construct used for control and the inoculated virus. Both constructs were most effective on the virus from which the resistance construct was derived and less effective against the divergent virus. The construct pTRV-HP25 was the most effective overall. With this construct, resistance was nearly complete in some treated plants inoculated with BMCTV, with minimal symptom development and very little stunting (Fig. 1). In other plants, control was not as dramatic, suggesting that perhaps silencing was not activated in some plants by the time virus replication began accelerating. This divergence is reflected by contrasts shown between silenced plants and those that did not appear to have been silenced for BMCTV (Fig. 2). Cumulative data for plants silenced as well as those not silenced is shown in the column “all plants.” There was very little difference in plant growth between pTRV-hp25 silenced plants and untreated controls (Figs. 1&2), as well as few symptoms on silenced pTRV-HP25-treated plants, whereas untreated plants inoculated with BMCTV exhibited severe stunting and leaf curling (Fig. 1). Importantly, we were unable to detect BMCTV in BMCTV-inoculated plants treated with pTRV-HP25, whereas plants inoculated with BMCTV, but not treated with pTRV-hp25 contained high levels of virus, based on serological virus detection tests (data not shown). Control of BSCTV with the pTRV-HP25 was not effective (data not shown). In order for control to be effective against both curtovirus species it will most likely be necessary to design a similar construct to similar region of the viral genome that is conserved between the two primary curtovirus species affecting agriculture in California. These efforts are described later on in this report.

Treatment of plants with pTRV-CFHC1 also showed some promise, but control was not as impressive as for the pTRV-HP25. Treatment of *N. benthamiana* 3 days prior to inoculation with BSCTV led to some decrease in stunting severity, but this was incomplete (Figs. 3&4). Plants still developed substantial symptoms, but were not as severely affected as untreated plants. Like the results observed for pTRV-HP25, it appeared that silencing was not effectively activated in all plants, as illustrated by some plants uniformly exhibiting reduced symptom severity (Fig. 3). This is further illustrated by separate columns for “all plants,” silenced, and not silenced plants in Figure 4. Unlike the results of pTRV-HP25 on BMCTV infection described

Figure 1. Effectiveness of pTRV-hp25 in controlling BMCTV on *N. benthamiana*.

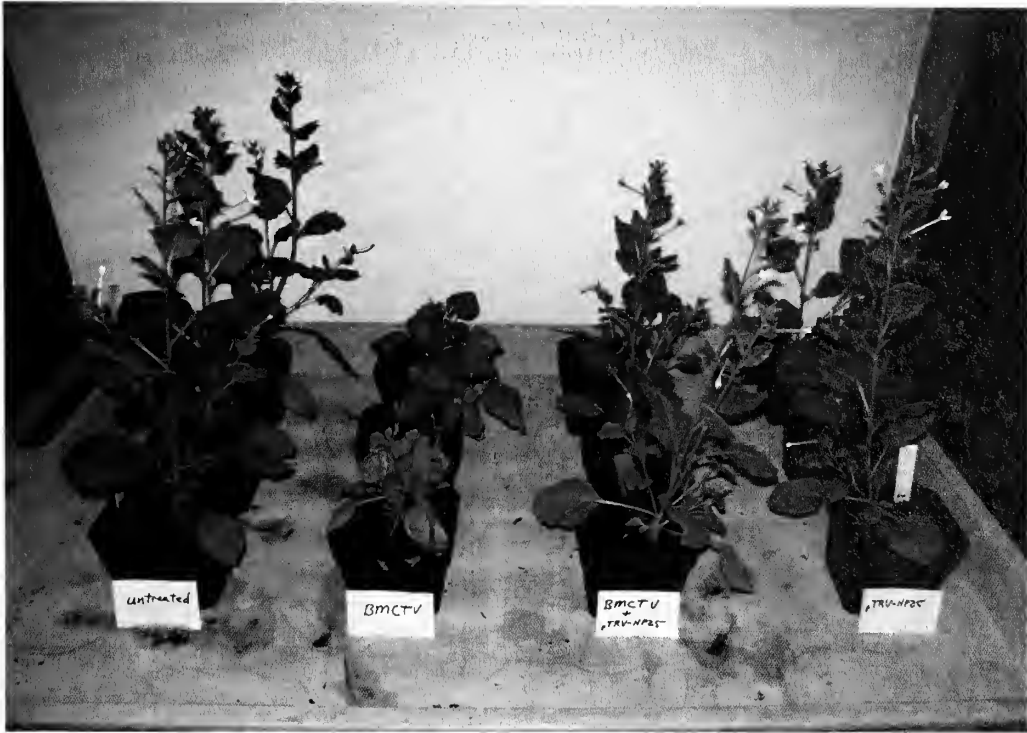


Figure 2. Height (cm) of *N. benthamiana* infected with BMCTV following treatment with pTRV-HP25 at 5 weeks following BMCTV inoculation. Treatment with pTRV-HP25 occurred 3 days prior to BMCTV inoculation. Results with treated plants are separated by those exhibiting silencing and those that did not. This most likely reflects whether sufficient silencing activation occurred prior to virus inoculation. Cumulative data for all plants is illustrated in the column “all plants.”

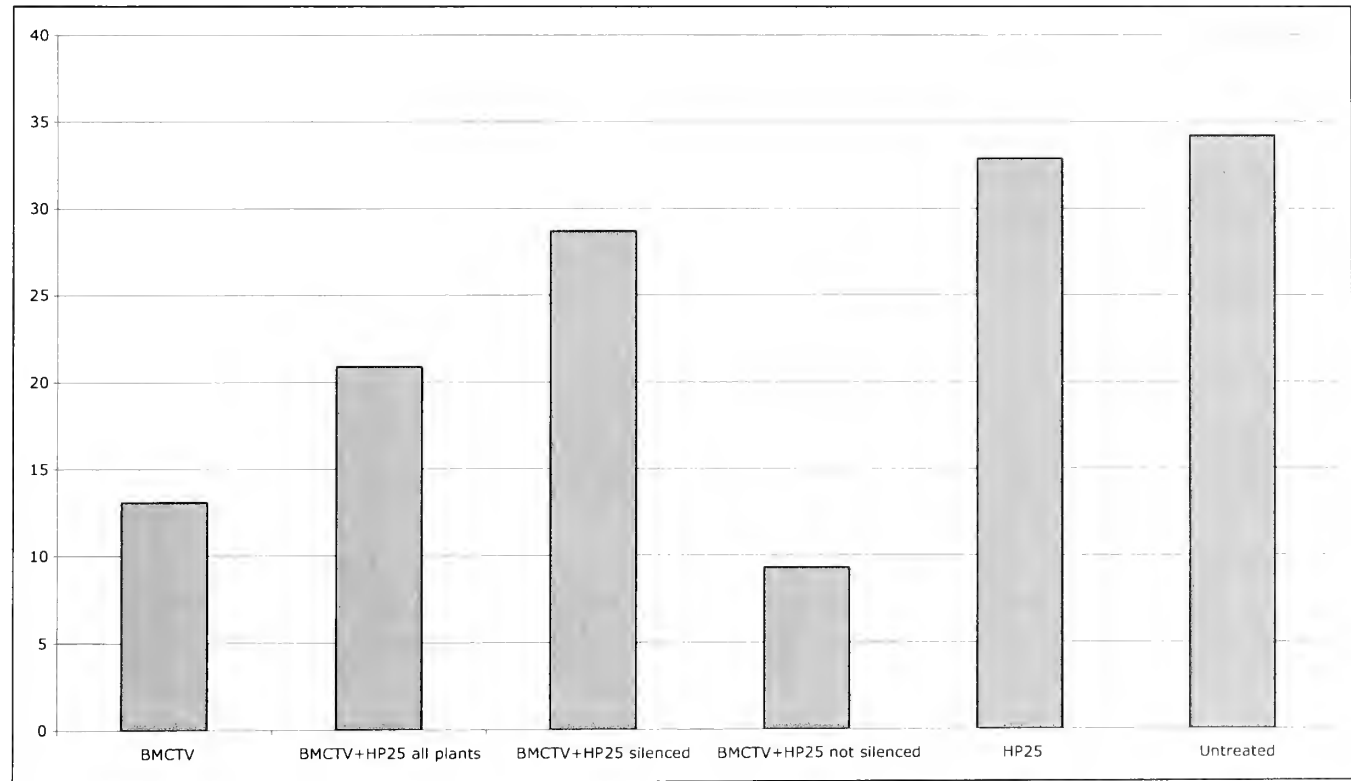
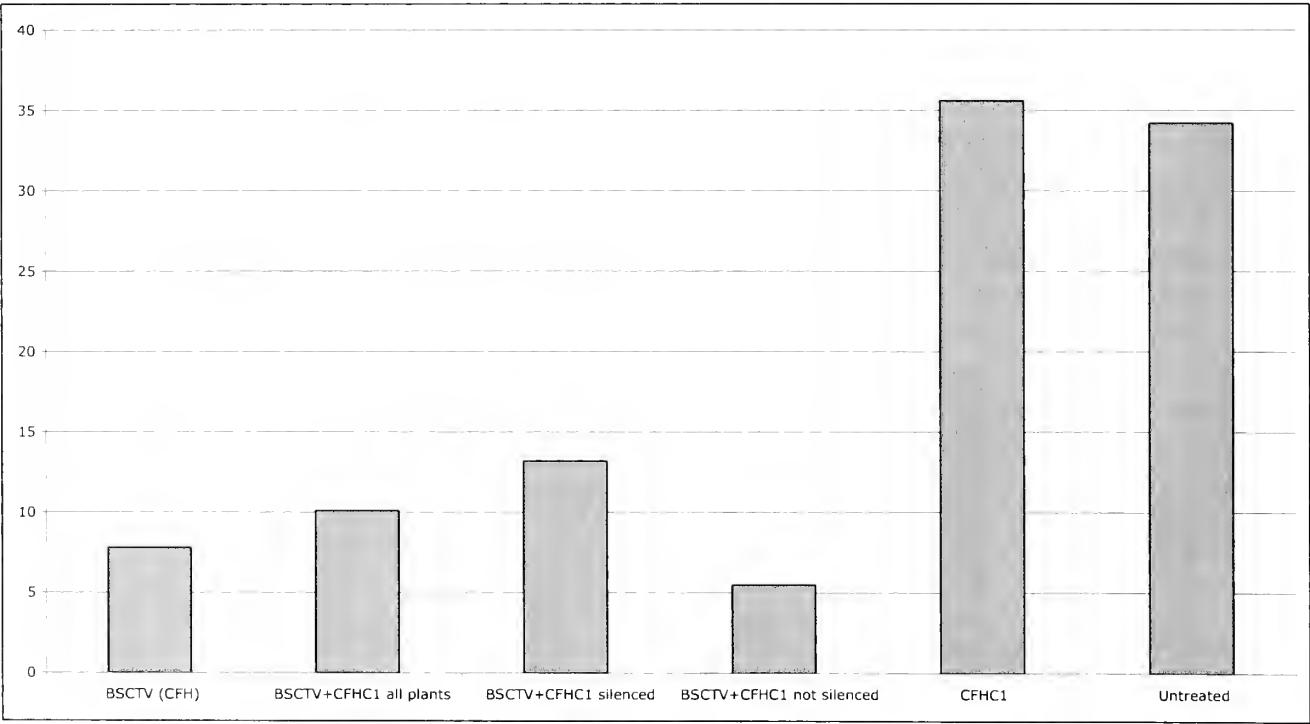


Figure 3. Effectiveness of pTRV-CFHC1 in controlling BSCTV on *N. benthamiana*.



Figure 4. Height (cm) of *N. benthamiana* infected with BSCTV (aka. CFH strain) following treatment with pTRV-CFHC1 at 5 weeks after BSCTV inoculation. Treatment with pTRV-CFHC1 occurred 3 days prior to BSCTV inoculation. Results with treated plants are separated by those exhibiting silencing and those that did not. This most likely reflects whether sufficient silencing activation occurred prior to virus inoculation. Cumulative data for all plants is illustrated in the column “all plants.”



above, we were still able to detect BSCTV in BSCTV-inoculated plants treated with pTRV-CFHC1 (data not shown). This is not surprising, since the silencing was only partially effective with this construct. As with pTRV-HP25, effectiveness of pTRV-CFHC1 was most effective for BSCTV, the source of origin for the transgene. Little difference was observed between treated and untreated plants for pTRV-CFHC1 inoculated with BMCTV (data not shown). This experiment was repeated in Feb-March 2007), however resistance was not as strong as in the initial experiment (data not shown). We are pleased with the success to date, and anticipate the next several months should allow us to follow these results with additional constructs that may be effective against both major curtovirus species, allowing progress to begin on Objective 4.

Based on the success of the studies to date, we are developing new constructs using sequences conserved between both of the predominant forms of curly top, BSCTV and BMCTV. Since the constructs seem to work well against viruses from which the construct sequence was derived, and less well against the virus from which it was not derived, even though the two are fairly close in sequence similarity, we are focusing on areas within the same gene sharing exact sequence identity between both BSCTV and BMCTV. We anticipate that the new constructs will be completed this spring with testing this summer. Hopefully these new constructs will be effective not against one, but against both viruses responsible for curly top in California and the western U.S.

Objective 4: Deliver constructs to sugarbeet through either genetic engineering or using a mechanical delivery system to essentially “vaccinate” plants against curly top.

Development of field delivery systems will begin upon conclusion of construct testing for silencing-based control of both BSCTV and BMCTV (Objective 3). If the new constructs described in the above paragraph provide effective control, as suggested by the above data with pTRV-HP25, we hope to begin work on this objective in the fall of 2007 with continuation of this objective into 2008.

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DEVELOPMENT OF SUGARBEET BREEDING LINES AND GERMPLASM (211,215)

R.T. LEWELLEN

CY91 – CY91 segregates for hypocotyl color, resistance to rhizomania caused by BNYVV conditioned by Rz1. It is moderately resistant to powdery mildew caused by *Erysiphe betae* and to *Erwinia carotovora beta vasculorum*. CY91 is intermediate to moderately susceptible to curly top virus. It is moderately nonbolting.

As a line, CY91 produces a canopy with a tendency to stay dark green throughout the growing season. It is uncertain if this is because of its resistance to virus yellows or resistance to other unidentified disease or nutrient stresses. It has intermediate to high root and sugar yield with good sucrose concentration.

CY91 has undergone two cycles of population improvement by full-sib recurrent selection. Full-sib progenies were evaluated at Salinas in replicated yield and nursery trials. Cycle 1 families were evaluated for sucrose concentration and sugar yield under combined rhizomania and BChV inoculated conditions. Cycle 2 families were evaluated for sucrose concentration and sugar yield under rhizomania and BYV inoculated conditions. Progenies in both cycles were evaluated for bolting tendency in over-wintered tests. For cycle 1, 17 full-sib families were recombined to produce seed lot Y191. For cycle 2, 10 full-sib families were recombined to produce seed lot Y691, released as CY91. Between cycles 1 and 2, mass selection of individual roots was made for combined resistance to rhizomania, *Erwinia*, and powdery mildew to produce the cycle 1, synthesis 2 called Y391 that was the source of the second cycle full-sib families. Other versions similar to CY91 were produced and evaluated including Y591 and Y791(I). CY91 was derived from broadly based composite population that combined germplasm from long-term breeding projects at Salinas for resistance to virus yellows, rhizomania, powdery mildew, *Erwinia*, and bolting tendency. It includes germplasm from lines released in the past as C78, C80, C69, C67, C72, C81-22 and C76-89. From these sources, it is estimated that 3-4% of the germplasm was derived from *B. vulgaris* subsp *maritima*.

CY91 may provide a source of resistance to virus yellows, rhizomania and bolting in an advanced and productive background.

In addition to the cycle 2 synthetic released or CY91, six of the full-sib families were increased individually. Each of these six progeny lines trace to the two plants in the paircross. These elite families may have greater potential as source material than the recombined synthetic CY91 and desired individual traits will not have been diluted by the other families. By making these

variable as a subset of the recombined components of CY91, breeders will have the opportunity to further evaluate these materials and make their own critical decisions. These six lines are listed below with a very brief description: where SI = selection index for all traits and all highly favorable would total 14; MM = multiterm; Rz1 = resistant or segregating for resistance to rhizomania; SY = highest sugar yield among all full-sib families tests; %S = high % sugar relative to test mean; H%S = highest % sugar ; VYR = highest or best virus yellow resistance; PMR = powdery mildew resistant of slow-mildewing types; and NB = best nonbolting tendency.

CY91-405 – MM, Rz1, VYR, %S, PMR, SY, SI = 6

CY91-416 – MM, Rz1, VYR, H%S, PMR, SY, SI = 8

CY91-429 – MM, Rz1, VYR, H%S, PMR, SI = 6

CY91-453 – MM, Rz1, mod. VYR, %S, mod. PMR, SY, SI = 8

CY91-466 - MM, Rz1, VYR, H%S, PMR, SY, NB, SI = 7

CY91-507 – MM, Rz1, VYR, %S, PMR, SI = 8

CY952-222, CY953-217, C954-210 – These lines may provide resistance to virus yellows (BYV & BChV) combined with resistance to rhizomania and good GCA for % sugar and sugar yield. These lines are increases of S₁ progenies derived from F₁ hybrids between self-fertile x self-sterile breeding lines and populations. Self-sterile breeding lines have a long history of population improvement at Salinas for combined disease resistance. However, at Salinas as in most environments, self-sterile genotypes will not set sufficient seed to run S₁ progeny tests for disease evaluation and recurrent selection. By crossing genetic-male-sterile (aa) plants from a self-fertile population to a self-sterile one, favorable trait can be combined and the subsequent F₁ hybrid plants (Aa) selfed. After S₁ progeny testing, the selected S₁ progenies can be recombined (aa x A). CY952-222, CY953-217, and CY954-210 were selected from population hybrids between the self-fertile populations CZ25, C931, and C941 crossed to breeding line Y90. Y90 is an improved breeding line similar to CY91. These lines have shown high GCA for sugar yield and high % sugar in experimental hybrids at Salinas and Brawley, California.

C79-9-2, C79-9-3, and C79-9-4 – being released with H.-Y. Liu, are moderately based, self-sterile (SsSs), multiterm (MM), sugarbeet (*Beta vulgaris* L.) lines that segregate for resistance to rhizomania (undertermined Rz gene) caused by *Beet necrotic yellow vein virus* (BNYVV). They segregate for hypocotyl color (*R₁rr*). It is anticipated that these lines will have most traits similar to C37 (PI 590715), which was the original recurrent parent for C79-9 (PI 593668).

C79-9-2 is an improved breeding line developed from C79-9. In 2003, C79-9 was selected by mass selection for resistance to normal rhizomania, caused by a non-resistance-breaking strain of BNYVV. The criteria of selection were lack of classical rhizomania symptoms, root size and

shape, and sucrose concentration. The seed increase was called R437. IN 2005, line R437 was grown under Imperial Valley strain of BNYVV (IV-BNYVV). The criteria of selection of mother roots was the same as in 2003 to produce line R637 being released as C79-9-2. C79-9-2 will have an enriched source of resistance to IV-BNYVV. The resistance to rhizomania was introgressed to sugarbeet from WB151 (PI 546397), *B. vulgaris* subsp. *maritima* wild beet accession from Denmark. This resistance to IV_BNYVV is probably not *Rz1*, and it's allelic or locus relationship may be different from *Rz2* or *Rz3* and has yet to be determined. Field tests show that resistance is to all known strains of BNYVV and in preliminary testing appeared to have higher efficacy than in similar breeding lines with *Rz1*, *Rz2*, or *Rz3*.

C79-9-3 is an increase of two full-sib families extracted from breeding line R437 and evaluated in a progeny test under IV-BNYVV conditions in 2005. The highest performing two progenies were selected and recombined in 2006 to produce R637-303, released as C79-9-3. These two families had greater than 90% resistant plants, a lower disease index, and higher sugar yield than their source R437 and the best overall performance of any other materials in the progeny test.

C79-9-4 should be similar to C79-9-3 but was increased by recombining three additional full-sib families evaluated in the progeny test to produce R637-304, released as C79-9-4. These three families had an average of 68% resistant plants to IV-BNYVV, significantly lower sugar yield, but higher sucrose concentration.

These lines are being released because of their apparently high resistance to IV-BNYVV. Their primary usefulness may be as enhanced sources for resistance to IV_BNYVV and for genetic and marker analyses.

C890-3-41 – being released with **H.-Y. Liu**, is a narrowly based self-fertile (*Sf/Sf*) line that segregates for monogermity (*M_:mm*), O-type, and resistance to IV-BNYVV. It is the increase of one S1 family from C890-2/3 (PI 593702). Plants from C890-2/3 were randomly selfed and the S1 progenies evaluated for resistance to IV-BNYVV in the field at Salinas, CA. The increase of this one selected progeny was called 6812-41 and is being released as C890-3-41. In the progeny test under IV_BNYVV conditions, this line had 75% resistant plants, a low disease index, and good sugar concentration and yield. C89-3-41 is descended from C79-2 (PI 593661) and C79-3 (PI 593662) through C89-2/3 with resistance to rhizomania from WB41 (PI 546384) or WB42 (PI 546385). The resistance gene is likely *Rz2* or *Rz3*. From C890-3-41 it may be possible to directly select a monogerm, O-type inbred line with homozygous resistance to IV-BNYVV and high agronomic and multiple disease resistance characteristics. A CMS counterpart called C890-3-41CMS will be distributed with the maintainer.

C842-34, C842-59 and C842-86 – being released with **A. Gillen** and **C. Strausbaugh**, are narrowly based, self-fertile (*Sf/Sf*), monogerm (*mm*), O-type sugarbeet (*Beta vulgaris* L.) lines that may segregate for genetic male sterility (*alal*) and resistance to rhizomania (*Rz1*) and have high resistance to *Curly top virus* (CTV) as measured in the BSDF nursery at Kimberly, ID. All of these lines were derived from C842 (PI 634217), a monogerm, self-fertile, genetic-male-sterile facilitated, random-mated population as selfed progeny families. The individual S1

progeny families were evaluated in a replicated progeny test at Kimberly, ID under CTV inoculated conditions. The source population C842 was developed by recombining the best monogerm, O-type, curly-top (CT) resistant, nonbolting inbred lines developed over the past 50 years at Salinas including C562 (PI 590847), C546 (PI 590649), C718 (PI 590849), C762-17 (PI 560130) and others with population C869 (PI 628754). Resistance to rhizomania caused by *Beet necrotic yellow vein virus* (BNYVV) was derived from moderately CTV resistant C869.

C842-34 released from seed lot 8642-434 and tested as 4842-434 is the increase of one S1 family with seed from both pollen-fertile (*Al*₁) and genetic-male-sterile (*alal*) plants harvested in bulk. It should be O-type and monogerm, but bigerm seeds may occur on primary branches. In the CT test, C842-34 was scored 2.0, with the mean of the S1 progenies scored 3.6 with a range of 1.3 to 7.0. Susceptible check SP7322-0 was scored 7.0.

C842-59 released from seed lot 6842-459 and tested as 4842-459 is the increase of one S1 family with the same history as C842-34. In the CT test, C842-59 was scored 2.0.

C842-86 released from seed lot 6842-486 and tested as 4842-486 is the increase of one S1 family with the same history as C842-34. In the CT test, C842-86 was scored 1.3 and was the most CT resistant progeny family.

At the time seed is distributed of these three monogerm, O-type CT resistant lines, seed of each of thei F1CMS hybrids with C833-5CMS (PI 615523) will be distributed to facilitate hybrid production and performance testing. These lines may be useful individually as a source of high CT resistance combined with resistance to rhizomania or recombined to produce an improved source population for resistance to CTV.

INDEX OF VARIETY TRIALS

SALINAS, CA

(2006)

U.S. AGRICULTURAL RESEARCH STATION

Tests were located in two field plot areas at Salinas and two at Brawley, CA. Disease nurseries were also used in Idaho, Colorado, Michigan and Minnesota. Tests at Brawley (Imperial Valley) were planted in September 2005, and harvested in June, 2006. Tests at Salinas were planted from May through August, 2006, and harvested from September through December. Tests at Spence Field (Salinas) were under rhizomania conditions. Herbicides Nortron, Pyramin, Betamix, Progress, and Poast were used in the trials. Bayleton at 2lbs material/acre was used for powdery mildew control. Lorsban-4E was applied for aphid and other insect control. The specific planting and harvest dates as well as plot size and design are shown on each test summary.

Tests are listed in the main Table of Contents for Salinas by types of material and evaluation. As an aid to find test summaries, they are listed below by ascending test (planting date) number and cross- referenced to the page number. Tests shown as n/a are not available or not included in this report.

TEST NO.	NO. ENTRIES	TEST DESCRIPTION	PAGE NO.
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Rhizomania, Powdery Mildew, Yield & Evaluation Tests, Spence Field, May 2006

Lines and Progenies

106	48	Evaluation of Plant Introductions	A139
206	24	Fargo & Fort Collins lines	A42
306	48	East Lansing lines	A43
406	64	Coded powdery mildew	n/a
506	48	Powdery mildew/SBCN lines	A47(i)
606	128	S ₁ progeny test popn-849mm.....	A71
706	96	S ₁ progeny test popn-943MM.....	A46
806	48	Monogerm populations and lines.....	A69
906	48	Multigerm progeny lines.....	A40(i)
1006	8	Mother root selection	n/a

Lines and Hybrids

1106	12	SBCN/RZM sources of resistance	A87
1206	48	SBCN/RZM hybrids	A84
1306	12	C78/3 experimental hybrids.....	A79
1406	72	Company coded rhizomania.....	A97
1506	72	California coded rhizomania.....	A92
1606	12	Sources of resistance, lines	A40
1706	24	Sources of resistance, hybrids.....	A75
1706-2	6	C28 hybrids	A83
1806	24	Topcross and population hybrids	A77(i)
1906	48	Lines and populations	A37
2006	48	Testcross hybrids of progeny lines.....	A72

Lines and Hybrids (cont.)

2106	12	Sources of resistance, hybrids	A77
2206	12	Y91 experimental hybrids	A81

Rhizomania, Cercospora, Yield & Evaluation

3106	64	Lines and hybrids	A50
3206	72	CR11-88 progeny test	A55

IV-BNYVV Strain Tests, Hartnell Field, May 2006

4106	24	Sources of resistance	n/a
4206	16	Sources of resistance, lines	A59
4306	16	Sources of resistance, hybrids	A88
4406	48	Lines and populations	A61
4506	24	Sources of resistance, hybrids	A90
4606	24	Progeny lines	A65
4706	24	Fargo & EL accessions	A67

IMPERIAL VALLEY, BRAWLEY, CA, 2005-2006

Non-diseased Yield Tests, Field J

B106	24	Topcross hybrids	A103
B206	48	Hybrids with SBCN/RZM resistance	A105
B306	48	Experimental hybrids	A108

Sugargeet Cyst Nematode Tests, Field K

B406	24	Hybrids with SBCN resistance	A111
B506	24	Hybrids with SBCN resistance	A113
B606	48	Lines with SBCN resistance	A116
B706	96	Progeny families	A120

Sugarbeet Cyst Nematode Tests, Field K (S)

B806	32	Observation of lines	n/a
B906	128	Selfed progenies from CN12	n/a
B1006	96	Selfed progenies from CN72	n/a
B1106	64	Fort Collins SBCN resistant lines	n/a
B1206	80	Progeny test of C927-4 lines	n/a
B1306	48	Progeny from CN926-#'s	n/a

BEET CURLY TOP NURSERY, BSDF, KIMBERLY, ID, 2006

USDA-CT		Curly top evaluation	A125
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DISEASE NURSERY EVALUATIONS IN ID, MN, CO, & MI

FC-Rhizoc	20	Reaction to Rhizoctonia AG-2-2	A132
SHK-BTS	36	Shakopee evaluation Cercospora	A132
SHK-BTS	36	Shakopee evaluation Aphanomyces	A132
EL-CLS	36	Michigan Cercospora leaf spot Evaluation	A135
ID-RZM	72	Rhizomania/Verticillium, Heyburn, ID	A136

TEST 1906. PERFORMANCE OF LINES & POPULATIONS UNDER RHIZOMANIA, SALINAS, CA, 2006

48 entries x 8 reps., RCB(e)
1-row plots, 22 ft. long

Planted: May 4, 2006
Harvested: October 2-3, 2006

Variety	Description	Acre Yield		Sucrose %	Soluble Solids %	RJAP %	Beets/ 100'	Foliar Foliar	
		Sugar Lbs	Beets Tons					Color ¹ Score	Seq ² Score
Hybrid checks									
Beta 4430R	Betaseed, 8-21-03 Rz1	11891	37.95	15.63	19.09	81.8	131	1.5	1.3
Roberta	Betaseed, 3/06 pelleted rzrrz	7420	27.28	13.59	16.90	80.4	130	3.9	4.1
Angelina	Betaseed (KWS), 3/06 Rz1+Rz2	12813	38.95	16.45	20.30	81.0	137	1.3	1.4
Phoenix	Holly Hybrids, 3-10-06 Rz1	9785	32.89	14.94	18.61	80.2	136	1.6	1.8
MM,O.P. lines									
EL-SP7322-0	Inc. SP7322-0, 4/05	5595	21.55	12.96	16.59	78.1	123	3.9	4.0
Z510	Inc. Z210, (Polish %S composite)	9021	25.94	17.39	21.19	82.1	123	3.0	3.3
R578	RZM R378 Iso, (C78/3)	9624	30.94	15.56	20.10	77.4	133	1.8	1.6
P529	PMR-RZM P429, (CP05)	10389	33.40	15.55	19.84	78.4	132	1.9	1.9
P530	PMR-RZM P430, CP06	9769	32.40	15.09	18.98	79.5	130	2.0	1.6
P518-6	PMR-RZM P418-6, CP08	8716	28.99	15.01	19.64	76.4	129	1.9	1.5
P507/8	PMR-RZM P407/8, CP07	9667	30.89	15.65	19.86	78.8	135	1.5	1.5
05-C37	Inc. 04-C37	8131	27.74	14.68	18.52	79.2	130	2.6	2.6
P527	PMR-RZM P427, CP03	8928	30.20	14.79	19.08	77.6	135	1.6	1.6
P528	PMR-RZM P428, CP04	10408	35.05	14.85	19.19	77.4	123	2.6	2.6
05-US75	Inc. 03-US75	7329	28.04	13.13	17.19	76.3	132	3.1	3.1
05-US22/3	Inc. 02-US22/3	7452	24.35	15.31	19.19	79.8	140	3.4	3.4
Y591 (CY91)	IRZM-½ Y391	10184	31.80	16.01	20.33	78.8	133	1.0	1.4
R539	Inc. R039, C39R (Quantitative)	8742	29.69	14.73	18.77	78.4	120	1.4	1.3
P531CT	PMR-RZM P431CT, CP09CT	9811	30.79	15.95	20.29	78.6	126	2.6	2.6
Y595	RZM Y95(C) (C1,Syn1,FSs)	10142	32.89	15.43	19.64	78.6	120	1.9	1.9
R481-22	RZM R181-22, (C81-22)	9984	30.89	16.15	20.23	79.8	112	1.6	1.8
R522	IRZM-½ R522(sp), C51	9062	31.09	14.60	19.39	75.3	131	1.6	1.8
R521	IRZM-½ R321,R021 (C51,C26,C27)	9904	32.72	15.11	19.31	78.3	124	1.4	1.5
R540	IRZM-½ R940,R840,R740 (C79-#s)	10502	34.85	15.06	19.64	76.7	130	1.3	1.3

(cont.)

Variety	Description	Acre yield		Sucrose %	Soluble Solids %	RJAP %	Beets/ 100'	Foliar	
		Sugar Lbs	Beets Tons					Color	Seq
MM, O.P. lines (cont.)									
R525	IRZM-8 R325, R324, R324/5, R337	9361	31.36	14.95	19.58	76.4	129	2.6	2.6
R541/2	IRZM-8 R641, R642 (WB169, WB258)	8895	31.00	14.38	18.39	78.2	124	2.0	2.3
Y577	IRZM-8 Y277, Y375 (SB x Bvm)	10164	32.46	15.65	20.05	78.1	134	1.8	1.9
MM populations with FC gp									
05-FC1036	RZM 04-FC1028, 1037, 1038aa x A, (FC, EL, Salinas LSR sources)	10327	32.95	15.66	19.92	78.7	121	1.9	2.3
05-FC1022	RZM-CR-8 20031022 (C931 x FC _{Rhizoc})	9362	27.76	16.91	21.15	80.0	120	2.4	2.4
05-FC1018	RZM-CR-8 20031018 (C931 x FC709-2)	8323	25.73	16.15	20.45	79.0	128	2.5	2.8
05-FC1019	RZM-CR-8 20031019 (FC712 x C931)	10060	31.34	16.00	19.79	80.8	128	2.4	2.5
N524	Inc. N424(g) (seg. Hslprol)	6919	23.43	14.79	19.46	76.0	110	1.5	1.4
MM, S ^f , A:aa populations									
5944	S ₁ (C1,2,3)aa x A, (C1, Syn1 S1s)	11053	33.10	16.71	21.45	77.9	125	2.0	1.8
5933	933(C)aa x A, (Colorado x Salinas)	10693	33.33	16.04	20.27	79.1	128	1.4	1.3
4931	RZM 3931aa x A, C931	10659	33.05	16.11	20.34	79.3	124	2.3	2.1
4941	RZM 3941aa x A, C941	10376	33.44	15.50	19.80	78.3	118	1.3	1.4
CR411	RZM CR311aa x A, CR11	9769	32.96	14.79	19.34	76.5	110	1.5	1.8
Z425	RZM Z325aa x A, CZ25/2	11421	35.15	16.23	20.65	78.6	124	2.0	2.3
N412 (Sp)	N312, N212-#(C)aa x A, CN12	9406	31.60	14.89	18.85	79.0	108	1.4	1.4
N472 (Sp)	N372, N272-#(C)aa x A, CN72	9279	31.58	14.65	19.04	76.9	116	1.1	1.1
4921	RZM-ER-8 2921 (C51, C26, C27 SF)	10660	34.47	15.46	19.69	78.5	130	1.3	1.4
4943	RZM 3943aa x A, (C1, Syn2 S1s)	10642	32.25	16.50	21.08	78.3	123	1.8	1.8
05-FC1030-15 (Sp)	03-FC1030-15aa x A	8663	26.80	16.17	20.71	78.1	119	2.4	2.5
05-FC1030-16 (Sp)	03-FC1030-16aa x A	9028	29.23	15.45	19.44	79.5	132	2.9	2.9
R524-2/3	Inc. R324-213, -215, -222, -223 (WB41, 42) RZ2, RZ3?	8881	28.88	15.38	19.95	77.1	139	2.8	2.6

(cont.)

Variety	Description	Acre Yield		Soluble		RJAP	Beets/ 100'	Foliar Foliar	
		Sugar	Beets	Sucrose	Solids			Color	Seq
		Lbs	Tons	%	%			Score	Score
MM, S ^f , A:aa populations (cont.)									
R524-302	Inc. R324-302, -306 (WB41) Rz3?	8623	28.77	14.99	19.74	75.9	132	3.1	3.4
R525-301	Inc. R325-301, -302 (WB42) Rz2?	8417	27.15	15.51	20.34	76.3	138	3.0	3.1
R537-302	Inc. R337-302 (WB151) Rz?	9877	30.60	16.15	20.81	77.6	132	2.4	2.6
Mean		9502.6	30.83	15.39	19.63	78.4	126.8	2.1	2.1
LSD (.05)		835.5	2.44	0.58	0.64	2.0	12.0	0.5	0.5
C.V. (%)		8.9	8.04	3.83	3.30	2.6	9.6	24.2	25.1
F value		18.7**	15.53**	17.60**	19.53**	4.7**	3.2**	16.4**	16.3**

NOTES:

Test 1906 was grown under moderate rhizomania. In 2006, no corresponding nondiseased tests were grown for comparison. March and April in 2006 were very wet and it was not possible to plant the nondiseased tests on a timely basis. Test 1906 was harvested by machine so individual roots were not scored for reaction to rhizomania. Powdery mildew was controlled. There was little evidence of other important diseases or pests. Susceptible checks for rhizomania include: Roberta, SP7322-0, Z510, C37, US75, US22/3; Other lines have Rz1 resistance except R540, R525, R541/2, R524-2/3, R524-302, R525-301, and R537-302 that may have Rz2 or other from Beta vulgaris subsp maritima accessions.

Test 1906 was grown under conventional BNYVV conditions. For similar test under combined conventional BNYVV and Cercospora leaf spot conditions see test 3106. For performance under IV-BNYVV conditions, see tests 4206 thru 4606. Also see tests 506, 806, & 906 for performance of lines and populations under conventional BNYVV.

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

TEST 1606. RHIZOMANIA EVALUATION OF LINES FOR SOURCES OF RESISTANCE, SALINAS, CA, 2006

12 entries x 8 reps., RCB
1-row plots, 22 ft. long

Planted: May 4, 2006
Harvested: October 5, 2006

Variety	RZM Resist	Description	Acre Yield		Sucrose %	Soluble Solids %	RJAP %	Beets/ 100'		Foliar Color ¹ Score	Foliar Seq ² Score
			Sugar Lbs	Beets Tons				No.			
C37 Background											
05-C37	--	Inc. 04-C37	6861	23.39	14.64	18.51	79.1	120		3.0	3.0
R540	C79-#	IRZM-% R940,R840,R740	10080	33.13	15.21	19.65	77.4	134		1.5	1.3
R525	C79-2,3; WB41,42	IRZM-% R325,R324,...	9465	30.15	15.69	19.88	78.9	119		2.4	2.5
R541/2	C79-10,11; WB169,258										
		IRZM-% R641,R642,...	8843	30.31	14.61	18.76	77.9	134		2.4	2.4
Differential Checks											
Angelina	R ₁ +R ₂	Betaseed, 3-20-06	12643	38.09	16.59	20.56	80.7	129		1.0	1.1
Roberta	rzrz	Betaseed, 3-20-06	6151	22.48	13.66	17.27	79.1	125		3.9	4.0
Beta G017R	Rz2	Betaseed	11500	34.33	16.73	20.84	80.3	137		1.1	1.4
Beta 4430R	Rz1	Betaseed	12001	36.14	16.61	20.60	80.6	139		1.5	1.9
Breeding Lines											
R521	Bvm	IRZM-% R321,R021	9577	31.25	15.31	19.40	79.0	136		1.8	1.8
R539	Q	Inc. R039, C39R	8126	26.62	15.27	19.10	80.0	115		1.6	1.5
Y577	Rz1,Bvm	IRZM-% Y277, Y375	10248	32.20	15.93	20.24	78.7	137		1.8	1.9
R537-302	C79-9; WB151	Inc. R337-302 (WB151)	10000	30.03	16.67	21.19	78.7	131		2.0	2.1
Mean			9624.5	30.68	15.58	19.67	79.2	129.7		2.0	2.1
LSD (.05)			1052.9	3.22	0.50	0.56	1.7	10.9		0.5	0.5
C.V. (%)			11.0	10.53	3.21	2.88	2.1	8.4		24.6	23.9
F value			27.1**	17.04**	30.58**	31.76**	2.9**	4.2**		22.2**	22.3**

Notes: Normal BNYVV at Spence field. Moderate rhizomania. See tests 4206 thru 4506 for performance under IV-BNYVV.

¹Foliar color due to rhizomania. 1 = all normal green; 2 = +25% yellowish; 3 = +50% yellowish; 4 = +75% yellowish; 5 = 100% yellowish.

²Foliar segregation pattern for rhizomania. 1 = all green; 2 = +25% yellowish (1-25%); 3 = 50:50 green: yellowish; 4 = +75% yellowish (75-99%); 5 = all yellowish.

TEST 906. EVALUATION OF MULTIGERM PROGENY LINES UNDER RHIZOMANIA, SALINAS, CA, 2006

48 entries x 4 reps., sequential
1-row plots, 11 ft. long

Planted: May 5, 2006
Harvested: October 12, 2006

Variety	Description	Acre Yield		Soluble Solids	RJAP	Beets/ 100'	Powdery Foliar		Seg
		Sugar Lbs	Beets Tons				Mildew	Color	
				%	%	No.	Mean	Score	Score
<u>Checks</u>									
Angelina	Betaseed (KWS), 3/06 pelleted	16414	47.35	17.38	21.27	81.7	143	5.0	1.5
Roberta	Betaseed (KWS), 3/06 pelleted	7855	26.60	14.75	18.65	79.1	143	1.3	4.5
Beta4430R	Betaseed	14278	41.71	17.10	21.17	80.8	155	0.8	2.0
Phoenix	Holly Hybrids, 3-10-06	11265	35.06	16.05	19.58	82.0	139	1.3	2.3
<u>Lines and populations with Rz1, Rz2, and other resistance in C37 background</u>									
05-C37	Inc. 04-C37 ck. (rzrz)	7740	26.19	14.82	19.00	78.0	136	5.0	3.8
R540	IRZM-8 R940, R840, R740 (C79-#)	12308	39.70	15.52	20.10	77.3	139	1.0	1.8
R521	IRZM-8 R321, R021 (Bvm x C37)	11644	36.27	16.08	20.60	78.0	141	0.5	1.3
R578 (Iso)	RZM R378(Iso), (C78/3)	12088	36.47	16.55	20.92	79.1	143	1.3	1.8
<u>Multigerm, O.P., progeny lines</u>									
R524-302	Inc. R324-302, -306 (WB41)	9688	30.83	15.67	20.88	75.1	150	6.3	4.0
R525-301	Inc. R325-301, -302 (WB42)	9319	29.02	16.02	20.55	78.0	141	5.8	3.5
R524-2/3	Inc. R324-213, -215, -222, -223 (WB41,42)	9713	31.23	15.55	20.45	76.0	134	3.0	3.3
R537-302	Inc. R337-302 (WB151)	11621	34.66	16.77	21.77	77.0	136	1.3	2.8
Y575-305	Inc. Y375-305	10520	33.65	15.63	19.88	78.6	132	0.3	1.3
Y575-311	Inc. Y375-311	9194	29.42	15.60	20.33	76.8	134	0.3	2.5
Y590-40 (Iso)	RZM Y390-40	11573	33.65	17.17	21.92	78.4	132	0.8	2.3
R481-22	RZM R181-22, (C81-22)Rz1,VYR	11319	33.65	16.80	21.27	79.0	141	0.0	2.0
<u>Multigerm, S^f, Aa progeny lines increased from Sls selected from F1 hybrids for % sugar, virus yellows, rhizomania</u>									
R578H23 -308	Inc. R378H23 -308 (A,aa)	10434	30.83	16.92	22.45	75.4	143	0.0	3.0
-312	-312 (A,aa)	11072	32.44	17.08	21.80	78.3	143	0.5	3.8
-320	-320 (A,aa)	9439	27.20	17.35	22.48	77.2	141	0.0	3.0
-325	-325 (A,aa)	9351	26.60	17.58	22.40	78.5	130	0.0	3.3

TEST 906. EVALUATION OF MULTIGERM PROGENY LINES UNDER RHIZOMANIA, SALINAS, CA, 2006

(cont.)

Variety	Description	Acre Yield		Beets/ 100'	Soluble Solids	Sucrose	RJAP	Powdery Mildew		Foliar Color	Foliar Seg
		Sugar	Beets					Mean	Score		
		Lbs	Tons					%	No.		
Multigerm, S ^f , Aa progeny lines (cont.)											
R578H40 -306	Inc. R378H40 -306 (A,aa)	10346	28.21	18.35	22.98	80.0	141	0.0	2.8	2.8	
-312	-312 (A,aa)	10197	29.82	17.10	22.42	76.2	139	0.0	3.5	3.0	
-324	-324 (A,aa)	9585	28.61	16.77	21.25	79.1	134	0.0	2.5	2.3	
R578H41 -301	Inc. Y391H41 -301 (A,aa)	11035	32.04	17.23	21.65	79.6	130	0.0	2.0	2.0	
Y591H23 -311	Inc. Y391H23 -311 (A,aa)	10842	31.84	17.00	22.52	75.5	148	0.0	3.3	3.0	
-313	-313 (A,aa)	10067	28.61	17.58	22.65	77.6	139	0.3	2.5	2.5	
-314	-314 (A,aa)	11305	33.05	17.05	21.77	78.3	139	0.3	3.0	2.8	
-322	-322 (A,aa)	8428	23.58	17.85	22.67	78.7	134	0.0	3.0	3.0	
5943-9-6	Inc. 3943-9-6 (A,aa)	11988	34.66	17.30	22.88	75.7	136	0.0	3.3	3.3	
5943-9-7	Inc. 3943-9-7 (A,aa)	12835	37.28	17.23	22.33	77.2	134	0.0	2.3	2.5	
5943-19-312	Inc. 3943-19-312 (A,aa)	10487	30.63	17.10	21.85	78.3	145	0.0	1.5	1.5	
5943-35-301	Inc. 3943-35-301 (A,aa)	12862	36.27	17.70	22.58	78.4	127	0.5	2.5	2.5	
5943-35-318	Inc. 3943-35-318 (A,aa)	11145	31.84	17.50	22.60	77.5	134	0.0	3.0	3.3	
5930-19-312	Inc. 3930-19-312 (A,aa)	12379	36.27	17.08	21.88	78.1	143	0.0	2.0	2.3	
5930-19-325	Inc. 3930-19-325 (A,aa)	8980	29.22	15.38	19.83	77.6	141	0.0	1.0	1.0	
5930-35-312	Inc. 3930-35-312 (A,aa)	9731	26.80	18.20	23.33	78.0	134	0.0	3.8	4.3	
Z525-9-307	Inc. Z325-9-307 (A,aa)	10387	29.62	17.55	23.05	76.2	145	0.0	3.5	3.8	
Z525-9-308	Inc. Z325-9-308 (A,aa)	9396	26.60	17.67	23.02	76.8	143	0.0	3.8	4.3	
5936-10-310	Inc. 3936-10-310 (A,aa)	10244	31.64	16.23	20.75	78.2	148	0.0	1.0	1.0	
5936-16-313	Inc. 3936-16-313 (A,aa)	9255	25.79	18.10	22.88	79.3	139	0.0	2.8	2.5	
Multigerm, S ^f , Aa, CR progeny lines selected for resistance to Cercospora and rhizomania											
CR509-1-312	Inc. CR301-1-312 (A,aa)	8827	26.80	16.48	22.10	74.6	141	0.3	1.8	1.8	
CR510-2-305	Inc. CR310-2-305 (A,aa)	10723	35.26	15.18	20.20	75.1	141	0.3	3.3	3.3	
CR511-7-302	Inc. CR311-7-303,-304 (A,aa)	7812	25.59	15.15	20.27	74.8	136	0.0	1.8	1.8	
CR511-88	RZM CR311-88 (A,aa), (CR11-88)	11103	36.47	15.25	19.48	78.3	132	1.3	2.0	1.5	

TEST 906. EVALUATION OF MULTIGERM PROGENY LINES UNDER RHIZOMANIA, SALINAS, CA, 2006

(cont.)

Variety	Description	Acre Yield		Beets	Tons	Sucrose	Soluble Solids	RJAP	100'	Beets/	Powdery Mildew		Foliar	
		Sugar	Beets								Mean	Score	Color	Seg
		Lbs		%	%	No.	Mean	Score	Score					
<u>Checks</u>														
5930-35	Inc. 2930-35, (C930-35)	10409	31.43	16.58	22.08	75.1	143	1.3	3.0	3.0				
Z510	Inc. Z210 %S Polish acc.	9981	27.40	18.20	22.38	81.3	141	3.8	4.0	4.0				
C28	90060149-0 (Syngenta)	9743	34.86	13.95	18.42	75.7	139	2.0	3.0	3.0				
4931	RZM 3931aa x A (C931)	12747	38.49	16.55	20.92	79.1	130	0.8	2.0	2.3				
Mean		10618.2	31.90	16.66	21.42	77.8	139.0	0.9	2.7	2.7				
LSD (.05)		1826.0	5.34	0.78	1.05	2.6	20.1	0.9	0.9	1.0				
C.V. (%)		12.3	11.97	3.35	3.51	2.4	10.4	66.9	25.5	25.4				
F value		6.3**	6.14**	13.51**	11.21**	3.8**	0.6NS	26.8**	6.7**	6.7**				

Notes: Progeny lines increased from S1 and FS progenies evaluated in prior years and selected on the basis of disease resistance, % sugar, sugar yield, etc. aa x A = increase through aa genetic ms plants. (A,aa) = bulk increase of both aa and A_ plants. See tests 1306,1806, 1906, and 2206 for hybrid performance.

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3= light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

TEST 206. EVALUATION OF FARGO & FORT COLLINS LINES FOR RHIZOMANIA, SALINAS, CA, 2006

24 entries x 4 reps., sequential
1-row plots, 11 ft. long

Planted: May 5, 2006
Harvested: November 1, 2006

Variety	Description	Acre Yield		Soluble Stand Harv				DI	%R (0-3)	%R (0-4)	Foliar		PM
		Sugar Lbs	Beets Tons	Sucrose %	Solids %	Count	No.				Color Score	Seg Score	
C37 Checks													
05-C37	Inc. 04-C37, rzrz	6975	21.75	16.02	20.15	15	15	4.6	22.4	31.2	3.8	4.0	5.0
R540	IRZM-% R940,R840,R740	11169	34.25	16.33	20.77	15	14	3.3	81.5	89.0	1.5	1.8	2.0
R521	IRZM-% R321,R021	11182	32.67	17.10	21.45	15	14	3.1	85.1	95.8	1.5	1.5	1.8
4747	Inc. 0747 (C37 SFSf)	7312	23.98	15.27	19.40	15	15	4.7	19.6	24.7	4.0	4.5	4.8
R481-22	RZM R181-22, (C81-22)	12179	33.92	17.98	22.55	13	13	3.0	87.7	94.2	2.3	1.5	0.8
Fargo accessions													
04N0090	L53/PI546420//L19, 4/10/06	4251	12.20	17.55	22.52	14	14	4.7	25.3	28.8	5.0	5.0	2.9
04N0091	L53/PI546420//L19	3622	11.66	15.52	19.40	14	13	5.4	5.0	11.0	4.3	4.8	3.5
01N0056	3747/Bvm(Denmark)	4211	13.48	15.67	19.80	8	8	5.1	15.6	15.6	4.5	4.8	2.7
04N0106	3747/Bvm(Belgium)	5367	17.03	15.77	20.35	10	9	5.2	12.7	17.6	2.8	3.0	2.2
04N0107	3747/Bvm(Ireland)	5169	15.91	16.17	19.83	5	5	4.9	15.4	31.7	3.5	4.0	1.3
03N0082	R376-43/PI540689(Belgium)	8157	27.05	15.05	19.63	14	13	4.4	39.5	49.1	2.5	2.5	1.6
04N0093	R376-43/PI540682 (Den)	8623	28.31	15.27	19.67	10	8	3.4	75.0	79.2	2.0	1.8	1.8
04N0095	R376-43/PI540593 (Fr)	7148	21.42	16.63	20.60	11	11	3.7	69.0	76.5	3.0	2.8	2.7
04N0096	R376-43/PI540579 (Fr)	7791	25.33	15.45	19.85	13	13	5.0	20.5	32.0	2.5	2.3	0.4
04N0097	R376-43/PI518418 (Ire)	4803	16.37	14.45	18.23	12	12	5.5	9.0	11.1	4.5	4.0	2.0
04N0098	R376-43/PI540582 (Den)	6560	21.47	15.27	20.25	11	11	5.0	29.4	33.8	2.5	2.0	1.6
04N0100	R376-43/PI540578 (Fr)	5524	17.55	15.68	20.70	11	11	4.9	29.3	33.6	2.8	2.8	1.0
04N0101	R376-43/PI540659 (Fr)	9449	33.61	14.13	18.45	12	11	3.9	59.8	64.7	3.0	3.0	1.6

TEST 206. EVALUATION OF FARGO & FORT COLLINS LINES FOR RHIZOMANIA, SALINAS, CA, 2006

(cont.)

Variety	Description	Acre Yield		Soluble Solids		Stand Harv		DI	%R (0-3)	%R (0-4)	Foliar		PM
		Beets		Sucrose		Count					Color		
		Sugar Lbs	Tons	%	No.	%	No.				Score	Seg	
Fargo accessions (cont.)													
05N0155	R376-43/PI540678 (Den)	10036	30.54	16.48	21.05	13	13	3.7	65.1	76.6	1.5	1.5	0.8
04N0068	F1016/961009H2 (Root maggot res)	5707	16.66	17.20	21.85	13	11	4.6	33.7	40.3	4.8	4.8	4.2
Fort Collins accessions													
20051007H01-X C833H5CMS x 01-FC1014-22,2/17/06													
		10414	29.93	17.40	22.23	15	14	3.4	73.5	84.1	2.3	1.5	1.8
20051007HOMS	Rhizoc. 03-FC1014-22	9023	25.57	17.67	22.60	16	16	3.7	59.7	68.8	2.3	2.5	1.3
20051007HOPF	Rhizoc. 03-FC1014-22	6214	17.75	17.52	23.08	15	14	4.1	38.0	57.9	2.3	2.0	1.0
05-FC1022	RZM-CR-½ 20031022	9530	26.80	17.78	22.50	13	13	3.9	52.8	62.5	2.8	3.0	1.4
Mean													
LSD (.05)		7517.3	23.13	16.22	20.70	12.5	12.2	4.3	42.7	50.4	3.0	3.0	2.1
C.V. (%)		1805.8	5.72	1.23	1.53	2.5	2.5	0.7	23.1	24.8	1.1	1.0	1.1
F value		17.0	17.53	5.39	5.24	14.4	14.6	11.7	38.4	34.8	25.8	24.7	37.9
		14.8**	12.67**	6.36**	6.40**	7.9**	8.4**	9.5**	10.6**	10.0**	7.6**	11.0**	9.8**

Notes: See test 4706 under IV-BNYVV. Test 206 was under moderate rhizomania (normal BNYVV).

R481-22 was released as C81-22 and has R376-43 as one of its components. C81-22 was selected for $\frac{1}{2}$ sugar and sugar yield combined with resistance to rhizomania (Rz1) and virus yellows. 4747 is an increase of population 3747 used by Devon Doney at Fargo. 4747 is the Sf, A_{aa}, MM, rz1rz1 version of C37 (SsSs, MM, AA, rz1rz1, CTR, VYR, NB). R540 is C37 type with resistance to rhizomania from WB41 & WB42 (Rz2 and/or Rz2/Rz3). R521 is about 37% WB from the total collections of McFarlane and Doney.

TEST 306. EVALUATION OF EAST LANSING LINES FOR RHIZOMANIA, SALINAS, CA, 2006

48 entries x 4 reps., sequential
1-row plots, 11 ft. long

Planted: May 5, 2006
Harvested: November 1, 2006

Variety	Description	Acre Yield		Soluble Stand Harv				%R (0-3)	%R (0-4)	Foliar		PM	
		Sugar	Beets	Sucrose	Solids	Count	Count			Color	Seg		
		Lbs	Tons	%	%	No.	No.	%	%	Score	Score		
Checks													
Z510	Inc. Z210 (Polish gp)	8257	21.54	19.20	24.10	14	14	4.6	29.6	41.1	3.3	3.0	3.2
EL-SP7322-0	SP22-0, 4/05	4415	15.17	14.52	18.60	15	14	5.1	12.1	15.6	4.0	4.0	2.8
EL-C869	C869 Salem(UXBSCo), 4/05	10630	32.57	16.30	20.58	16	15	3.1	89.4	96.6	1.3	1.0	2.2
5849	Inc. 4849-#(C)mm (A,aa)	9630	27.69	17.42	21.95	14	14	3.2	84.8	96.1	1.3	1.0	2.0
4842(Iso)	RZM-% 2842 (A,aa)	9211	28.11	16.40	21.10	13	13	3.1	86.6	98.3	1.0	1.3	2.7
4850	Inc. 2252-2MmAA	9049	24.61	18.38	23.83	15	14	3.1	94.6	97.7	2.3	2.0	1.3
EL accessions													
EL06- 2	C869 x WB879m, 3/21/06	3417	10.93	15.57	20.65	14	12	4.9	12.3	18.7	2.3	2.5	2.2
EL06- 3		6257	19.63	15.88	20.63	13	13	4.4	36.5	44.3	2.5	2.3	2.8
EL06- 5		6494	18.88	17.20	21.15	14	12	3.7	65.3	73.7	2.8	2.5	2.3
- 6		4373	14.11	15.50	19.85	13	12	4.9	20.8	20.8	3.0	3.5	2.3
- 7		9885	28.22	17.35	21.83	14	14	3.5	73.5	78.5	1.5	1.3	2.2
- 8		3277	11.25	14.52	20.05	14	12	4.7	28.5	30.6	2.5	2.0	2.7
- 9.		1844	6.05	15.38	21.35	13	10	5.5	11.3	14.1	2.8	2.5	1.9
EL accessions													
EL06-10	C869 x WB185	4396	13.90	15.70	21.35	15	14	4.0	53.4	58.4	2.0	1.5	1.5
-11		4254	13.47	15.85	22.20	17	15	3.7	66.5	71.8	2.5	2.3	0.9
-13		4114	12.73	16.13	22.23	15	14	3.9	58.6	68.7	1.8	1.8	1.3
EL06-14	SP6822-0 x WB879	6395	19.94	15.95	20.08	13	12	4.6	35.1	37.6	3.5	3.3	2.1
-15		7352	22.91	15.88	20.05	15	15	4.0	56.8	60.2	2.5	2.5	2.1
-16		4327	13.58	15.75	20.45	16	15	4.7	30.2	31.8	2.8	3.0	1.5
-17		6064	19.31	15.70	19.98	14	13	4.7	28.3	35.7	3.5	3.3	1.8

(cont.)

Variety	Description	Acre Yield		Soluble Stand Harv		%R (0-3)		%R (0-4)		Foliar		Foliar	
		Sugar	Beets	Sucrose	Solids	Count	Count	DI	%	Color	Seg	Score	PM
		Lbs	Tons	%	%	No.	No.	%	%	Score	Score	Score	Score
EL accessions (cont.)													
EL06-18	SP6822-0 x WB879	4610	14.32	16.02	20.83	16	15	4.7	32.6	39.5	3.0	2.8	2.8
-19		5813	17.82	16.27	20.48	13	13	4.3	35.2	43.1	2.8	2.8	2.2
-20		5348	16.76	15.95	20.10	13	11	4.4	37.0	41.7	3.5	3.3	2.4
-21		5006	15.70	15.95	20.52	14	14	4.9	14.0	17.6	3.3	2.8	1.4
-22		4347	14.22	15.30	19.45	14	13	5.7	4.2	6.1	4.0	4.3	1.2
-23		4854	15.70	15.57	19.73	14	13	4.8	26.8	30.9	3.3	2.8	1.3
-24		3745	12.09	15.48	20.85	12	12	4.4	37.8	42.6	3.0	2.8	1.2
-25		3925	12.31	15.93	20.73	14	14	5.1	12.7	18.6	3.3	3.0	2.6
-26		4168	13.26	15.70	20.42	15	14	5.4	8.5	12.0	3.0	3.3	3.1
-27		6824	21.22	16.10	20.02	13	12	4.2	47.4	57.4	2.5	2.3	2.4
Checks													
EL-C869	C869, 4/05	11221	34.48	16.25	20.90	16	15	3.0	95.2	98.4	1.0	1.0	2.5
EL-SP7322-0	SP22-0, 4/05	4532	15.06	14.93	19.40	13	12	5.2	11.5	11.5	5.0	4.8	2.2
EL accessions													
EL06-29	C869 x SP6822-0	3402	11.14	15.17	22.63	14	13	3.2	90.6	93.1	1.8	1.5	1.1
-30		2251	6.47	18.42	24.02	12	10	4.1	48.8	55.0	2.5	2.3	0.8
EL06-32	Smooth Root, H %S x EL0204	9084	27.16	16.63	20.48	13	12	4.4	39.1	43.1	3.8	3.3	3.1
-33		11062	33.95	16.27	20.55	15	15	3.1	85.0	98.3	1.0	1.0	2.8
-34		10427	31.93	16.33	20.15	14	14	3.2	82.5	92.9	1.8	1.8	2.6
-35		10881	35.01	15.57	19.83	13	13	3.3	79.6	88.9	1.8	1.8	2.3
-36		10509	31.61	16.60	20.67	14	12	3.3	79.8	85.4	2.0	2.3	2.8
-37		8498	28.22	15.00	18.77	13	12	3.8	53.8	78.0	2.5	2.3	1.3
-38		6202	20.37	15.20	19.25	11	10	4.8	20.8	25.4	3.0	2.8	2.2
-39		6541	20.26	16.07	20.67	7	7	3.5	71.3	80.6	2.5	2.5	1.3

TEST 306. EVALUATION OF EAST LANSING LINES FOR RHIZOMANIA, SALINAS, CA, 2006

(cont.)

Variety	Description	Acre Yield		Soluble Solids		Stand Count		DI	%R (0-3)	%R (0-4)	Foliar		PM
		Sugar	Beets	Sucrose	Solids	Count	No.				Color	Seg	
EL accessions (cont.)													
EL06-40	Smooth Root, H %S x EL0204												
	9910	30.13	16.50	21.15	13	13	3.8	61.1	67.0	2.3	1.8	3.3	
-41	9010	28.22	15.93	20.00	13	12	3.8	58.6	66.0	2.8	2.5	1.7	
	7045	21.64	16.27	20.50	15	14	4.8	20.8	24.6	3.3	3.3	2.8	
-43	8831	26.95	16.42	20.65	15	15	4.5	34.0	40.5	2.8	2.8	3.3	
Traditional EL													
EL06-44	EL53	22.17	15.15	19.58	14	13	4.2	44.1	51.9	2.8	3.3	3.3	
-45	EL55	16.76	13.02	16.60	14	12	5.2	14.6	16.7	3.5	3.0	2.9	
Mean		6516.4	20.20	16.01	20.64	13.7	12.9	4.2	46.3	52.4	2.6	2.5	2.2
LSD (.05)		1679.7	4.79	1.32	1.63	2.4	2.7	0.6	23.1	20.5	1.0	0.9	1.1
C.V. (%)		18.4	16.98	5.91	5.65	12.7	15.0	9.6	35.8	28.0	26.0	25.8	37.5
F value		19.2**	20.28**	4.62**	5.17**	3.2**	3.0**	13.7**	10.9**	15.8**	6.2**	7.0**	2.9**

Notes: Moderate rhizomania (normal BNYVV). Hand harvested and scored for rhizomania on scale of 0 to 9 where 9 = severe. Foliar color = canopy rating from 1 to 5 for normal green to pale yellow = 5. Foliar segregation = frequency of green : pale yellow plants where 5 = 100% pale yellow.

TEST 706. S₁ PROGENY TEST FROM POPN-943 FOR %SUGAR & SUGAR YIELD PERFORMANCE UNDER RHIZOMANIA, SALINAS, CA, 2006

96 entries x 4 reps., sequential
1-row plots, 11 ft. long

Planted: May 5, 2006

Harvested: October 17 & 18, 2006

Variety	Description	Acre Yield		Soluble Solids	Sucrose	Beets/ 100'	RJAP	No.	Powdery Foliar		Seg
		Sugar	Beets						Mildew	Color	
		Lbs	Tons						%	Score	
Checks											
R481-22	RZM R181-22, (C81-22)VYR	11105	33.05	16.80	21.23	79.2	127	0.8	1.3	1.5	
R578H23-308	Inc. R378H23-308 (A,aa)	8955	27.02	16.55	21.55	76.8	127	0.3	2.3	2.8	
R578H40-306	Inc. R378H40-306 (A,aa)	10106	27.81	18.17	23.27	78.1	127	0.3	2.3	2.8	
Y591H23-311	Inc. Y392H23-311 (A,aa)	10210	29.02	17.58	22.08	79.6	132	0.0	2.0	3.0	
5943-9-6	Inc. 3943-9-6 (A,aa)	9814	27.20	18.10	23.35	77.6	136	0.3	2.0	3.0	
Z510	Inc. Z210(%S Polish composite)	11674	30.14	19.35	23.48	82.4	130	4.3	2.8	3.5	
S ₁ 's from RZM 4943⊗, 90 S ₁ s											
5943 -#'s	range	7404-	22.37-	15.32-	19.95-	75.3-	105-	0.0-	1.0-	1.0-	
		12862	40.30	19.60	23.85	82.9	141	4.8	3.8	4.3	
Mean		10553.4	26.89	15.47	19.74	69.7	112.0	0.5	1.8	2.1	
Mean											
LSD (.05)		10538.2	30.34	17.41	22.22	78.37	126.5	0.6	2.0	2.4	
C.V. (%)		1763.5	5.02	0.88	1.07	2.63	21.3	1.1	0.8	0.9	
F value		12.0	11.88	3.65	3.45	2.41	12.1	141.7	29.1	26.2	
		3.3**	3.85**	6.28**	5.67**	2.31**	1.3NS	4.3**	4.1**	5.6**	

Population 4943 is comprised of progeny families selected for performance and resistance to rhizomania and virus yellows. Approximately 25% of popn-943 is germplasm from high % sugar Polish accessions, similar to Z510, and 75% germplasm from breeding lines and populations such as C78/3 and C931. After a cycle of recombination among previously selected S₁ families, individual plants from popn-943 were selfed to produce the above S₁ progenies. In 2007, 5943-# S₁ progenies will be selected based upon % sugar and overall performance under rhizomania conditions and recombined to form popn-943 cycle 2, Syn 1. The ultimate goal is to produce a population with combined resistance to virus yellows, curly top, rhizomania, etc. and high sucrose concentration and sugar yield performance.

(cont.)

Variety	Description	Acre Yield		Beets	Sucrose	Soluble Solids	RJAP	Beets/ 100'	Powdery Foliar		Foliar			
		Sugar	Beets						Mildew	Color				
		Lbs	Tons						%	%		No.	Mean	Score

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

TEST 506. EVALUATION UNDER RHIZOMANIA OF PMR/SBCN RESISTANT LINES AND PROGENIES FOR PERFORMANCE & PM,
SALINAS, CA, 2006

48 entries x 4 reps., sequential
1-row plots, 11 ft. long

Planted: May 5, 2006
Harvested: October 20, 2006

Variety	Description	Acre Yield		Sucrose %	Soluble Solids %	RJAP %	Beets/ 100'	Powdery Foliar Mildew		Foliar Seg	
		Sugar	Beets					Mean	Score	Color	Score
		Lbs	Tons								
<u>Checks</u>											
05-C37	Inc. 04-C37	8334	26.40	15.70	20.02	78.5	141	6.3	4.0	4.0	4.0
P527	PMR-RZM P427, CP03	9783	30.02	16.30	20.72	78.7	136	0.6	2.3	2.3	2.8
P528	PMR-RZM P428, CP04	10575	33.13	15.95	20.45	78.0	134	0.8	2.8	2.8	3.0
US H11	10/4/02	7928	26.80	14.77	19.17	77.1	150	6.1	4.8	4.8	4.8
<u>Angelina</u>											
	Betaseed(KWS), 3/20/06, pelleted	15113	41.71	18.13	22.22	81.6	127	5.0	1.5	1.5	1.5
R578 (Iso)	RZM R378, (C78/3)	11533	34.09	16.92	21.90	77.3	136	0.8	2.0	2.0	2.5
P529	PMR-RZM P429, (CP05)	11628	34.76	16.68	21.55	77.4	125	0.0	1.8	2.0	2.0
P530	PMR-RZM P430, (CP06)	10646	32.04	16.63	20.88	79.6	127	0.4	2.5	2.5	2.8
<u>P518-6</u>											
P518-6	PMR-RZM P418-6, (CP08)	9626	29.42	16.33	21.00	77.7	127	0.8	3.0	3.0	2.8
P507/8	PMR-RZM P407/8, (CP07)	10489	31.03	16.95	21.75	77.9	134	0.1	2.0	2.0	2.0
N412 (Sp)	N312,N212-#(C)aa x A, (CN12)	11625	34.86	16.67	21.33	78.2	132	0.0	2.0	2.0	2.3
N472 (Sp)	N372,N272-#(C)aa x A, (CN72)	11567	35.58	16.27	20.92	77.7	139	0.6	2.0	2.0	2.0
<u>Roberta</u>											
Roberta	Betaseed, 3/20/06, pelleted	7150	23.58	15.18	18.80	80.7	143	1.1	5.0	5.0	5.0
Beta G017R	Betaseed, 4/22/05	14699	41.31	17.80	21.90	81.3	157	1.9	1.3	1.3	1.5
Beta 4430R	Betaseed, 3/28/06	14158	39.70	17.83	22.25	80.2	152	0.5	1.8	1.8	2.0
Phoenix	Holly Hybrids, 3/10/06	12129	36.01	16.88	20.80	81.1	130	1.8	2.5	2.5	2.5
<u>Progeny lines</u>											
N572-233	RZM N472-233 (NR,rzrz)	6398	19.85	16.02	21.08	76.0	152	0.8	2.0	2.0	2.0
5926-11-3-22	RZM 4926-11-3-22 (NR,Rz1)	8556	24.38	17.52	22.75	77.0	148	0.1	1.3	1.3	1.0
N512-11	RZM N412-11 (NR,Rz1)	9841	28.09	17.52	23.58	74.4	141	0.0	3.0	3.0	3.3
N512-13	RZM N412-13 (NS,rzrz)	4437	14.61	15.18	20.52	73.9	127	0.0	2.3	2.3	2.3
<u>P529-305</u>											
P529-305	Inc. P329-305 (NT,PmPm,Rz1)	11462	32.04	17.90	22.27	80.4	136	0.0	2.3	2.3	1.8
P507-303	Inc. P307-303 (NT,PmPm,Rz1)	11239	32.24	17.45	22.27	78.4	136	0.0	2.0	2.0	2.0
P507-304	Inc. P307-304 (NS,PmPm,Rz1)	10054	29.46	17.00	21.48	79.3	136	0.5	2.5	2.5	3.0
P507-306	Inc. P307-306 (NT,PmPm,Rz1)	10630	31.03	17.13	22.40	76.5	134	0.0	1.8	1.8	1.8

TEST 506. EVALUATION UNDER RHIZOMANIA OF PMR/SBCN RESISTANT LINES AND PROGENIES FOR PERFORMANCE & PM,
SALINAS, CA, 2006

(cont.)

Variety	Description	Acre Yield		Soluble Solids	Sucrose	RJAP	Beets/ 100'	Powdery Mildew		Foliar	
		Sugar	Beets					Mean	Score	Color	Seg
		Lbs	Tons					%	No.	%	Score
Progeny lines (cont.)											
P507-308	Inc. P307-308 (NR, PmPm, Rz1)	10851	30.99	22.02	17.50	79.4	143	0.0	1.8	1.8	1.8
P507-311	Inc. P307-311 (NR, PmPm, Rz1)	11276	32.64	22.52	17.27	76.7	130	0.0	2.0	2.0	2.3
P507/8	PMR-RZM P407/8, CP07	12236	36.47	21.65	16.77	77.5	134	0.0	2.0	2.0	2.0
3927-4	RZM 2927-4 (A,aa) (NR)	10080	30.83	20.65	16.35	79.2	132	0.9	3.3	3.3	3.3
5927-202	Inc. 4927-202 (NR)	10079	29.50	21.88	17.08	78.1	125	0.9	1.8	1.8	2.0
5927-4-302	Inc. 3927-4-302 (NR)	10389	29.82	22.38	17.42	77.9	125	1.0	1.3	1.3	1.5
5927-4-303	Inc. 3927-4-303 (NR)	8633	27.26	20.45	15.85	77.5	141	3.9	3.0	3.0	3.3
5927-4-307	Inc. 3927-4-307 (NS)	10442	33.65	19.80	15.52	78.4	139	2.1	2.8	2.8	2.5
5927-4-309	Inc. 3927-4-309 (NS, Rz1)	11107	32.66	21.95	16.98	77.4	143	2.4	2.5	2.5	2.3
5921-306	Inc. 3921-306 (NR, Rz1)	10317	29.82	23.10	17.30	74.9	132	0.8	1.3	1.3	1.8
4921	RZM-ER-8 2921 (A,aa)	12729	37.88	21.35	16.80	78.7	139	1.6	2.0	2.0	2.3
Y577	IRZM-8 Y277, Y375	12931	38.28	21.67	16.85	77.7	134	0.8	2.0	2.0	2.0
Y575-305	Inc. Y375-305 (NT)	10351	31.03	21.15	16.65	78.7	132	0.4	1.5	1.5	1.8
Y575-311	Inc. Y375-311 (NT)	9184	27.40	21.70	16.73	77.1	118	0.5	3.0	3.0	3.0
Y595	RZM Y95(C)	10804	32.24	21.55	16.73	77.6	123	0.1	3.0	3.0	2.8
P531CT (Iso)	PMR-RZM P431CT	10592	30.63	22.25	17.25	77.6	134	0.1	3.0	3.0	2.5
P531CT (Sp)	PMR-RZM P431CT, (CP09CT)	10530	31.43	21.60	16.77	77.7	130	0.0	3.0	3.0	3.0
R521	IRZM-8 R321, R021	11170	34.05	21.17	16.42	77.6	132	0.9	2.0	2.0	2.3
R522	IRZM-8 R522, (C51)	11313	34.86	21.42	16.23	75.7	134	0.8	2.5	2.5	2.3
R539	Inc. R039 (C39R)	10908	32.24	21.02	16.92	80.5	125	0.4	2.5	2.5	2.8
N524	Inc. N424M(g) (Hs1)	8790	26.19	21.23	16.73	78.9	118	0.9	3.3	3.3	3.3
Z510	Inc. Z210 (8S Polish, rzzrz)	9796	26.80	22.52	18.23	80.9	136	5.1	4.3	4.3	4.3
Y467-21	RZM Y267-21	9849	29.42	21.88	16.77	76.7	130	0.4	1.5	1.5	1.5
R443-14	RZM R243-14	11281	34.46	21.23	16.40	77.3	136	0.5	2.5	2.5	2.8

TEST 506. EVALUATION UNDER RHIZOMANIA OF PMR/SBCN RESISTANT LINES AND PROGENIES FOR PERFORMANCE & PM,
SALINAS, CA, 2006

(cont.)

Variety	Description	Acre Yield		Beets	Tons	Sucrose %	Soluble Solids %	RJAP %	Beets/ 100'	No.	Powdery Mildew		Foliar		Seg
		Sugar	Lbs								Mean	Score	Color	Score	
Mean		10525.7	31.31			16.76	21.46	78.1	134.7		1.1	2.4		2.5	
ISD (.05)		1660.5	4.71			0.80	0.89	3.0	21.4		1.0	0.9		1.0	
C.V. (%)		11.3	10.77			3.41	2.96	2.7	11.4		63.9	27.3		28.2	
F value		10.2**	8.89**			6.89**	8.58**	2.6**	1.2NS		20.6**	6.7**		5.6**	

Powdery Mildew: Powdery mildew developed late and mildly. Scored on a scale of 0 to 9 (severe). Test 506 did not have PM control, but tests up wind did and there appeared to be fuming/drift across this test that reduced onset and severity. Pm appeared to have maintained its efficacy.

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

Progeny Lines: The majority of lines evaluated in this test are increases of either full-sib or S1 (selfed) progeny lines selected from prior year's tests for one trait or another; e.g., powdery mildew resistance (Pm), rhizomania resistance, cyst nematode resistance (NR) or tolerance (NT), yield, % sugar, etc.

See tests 1106, 1206, B406, and B506 for hybrid performance of these lines.

TEST 3106. EVALUATION OF LINES & HYBRIDS UNDER RHIZOMANIA AND CERCOSPORA LEAF SPOT, SALINAS, CA, 2006

64 entries x 6 reps, RCB
1-row plots, 11 ft. long

Planted: May 5, 2006

Harvested: November 20, 2006

Inoc. Cb: July 18 & August 8,

2006

Variety	Description	Acre Yield		Sucrose		Soluble Beets/		DI	%R		Foliar		CLS
		Sugar	Beets	Sucrose	Solids	100'	(0-3)		(0-4)	Color	Seg		
		Lbs	Tons	%	%	No.	%		%	Score	Score		
<u>Score</u>													
<u>Checks</u>													
HH142	Holly Hyb, 3/10/06	13951	40.00	17.46	20.47	135	3.3	73.2	90.0	1.7	1.2	1.5	
Angelina	Betaseed, 3/20/06	13268	38.22	17.38	20.27	123	3.1	85.1	96.4	1.3	1.3	4.2	
Roberta	Betaseed, 3/20/06	4909	17.34	13.99	17.37	109	5.5	7.2	10.0	4.0	3.8	3.8	
Beta 4430R	Betaseed, 3/28/06	12826	36.76	17.47	19.63	133	2.9	90.1	93.5	2.2	1.7	5.1	
CR411H50	C790-15CMS x CR311	12854	37.31	17.23	20.18	138	3.3	76.5	88.3	1.3	1.3	2.1	
ACH555	CLSR ck, 8107307, 3/8/02	7127	19.32	18.43	21.82	138	4.9	22.1	28.0	4.3	4.5	2.2	
HM-E17	CR ck, 4/05 Syngenta	9431	27.30	17.24	20.38	139	5.2	16.6	20.8	4.0	4.3	2.5	
Monohikari	CR ck, 1/21/03	8090	23.04	17.61	20.12	133	4.5	29.4	37.0	2.7	3.2	2.6	
<u>Multigerm lines & populations</u>													
4931	RZM 3931aa x A (C931)	11624	33.25	17.50	20.78	121	3.3	74.5	86.7	2.0	1.8	1.8	
CR411	RZM CR311aa x A (CR11)	11641	35.56	16.49	20.12	109	3.2	80.6	89.3	1.7	1.7	1.7	
5944	popn-944(C)aa x A	12892	35.80	18.09	21.98	105	3.2	78.0	96.0	1.7	1.5	2.0	
5933	popn-933(C)aa x A	12529	35.94	17.40	20.78	111	3.6	64.9	77.2	1.7	1.7	1.8	
EL-SP7322-0	Inc. SP22-0	6047	20.74	14.66	17.62	111	5.2	21.7	21.7	4.7	4.8	1.7	
Y577	IRZM-8 Y277, Y377	12721	38.14	16.66	19.80	126	3.3	72.9	87.8	1.3	1.3	2.0	
R521	IRZM-8 R021, R321	11129	32.69	17.02	20.42	129	3.1	83.3	93.2	1.2	1.5	2.0	
R540	IRZM-8 R940, R840, R740	12982	38.68	16.76	19.98	124	3.4	73.2	85.8	1.7	1.7	1.9	
R541/2	IRZM-8 R641, R642 (C79-10, -11)	10377	32.48	15.96	19.48	121	3.4	74.4	85.5	2.0	1.7	2.1	
R522	IRZM-8 R522, (C51)	10460	34.11	15.38	19.12	126	3.4	73.3	87.6	1.7	1.7	3.3	
Y595	Inc. Y95(C)	12716	37.91	16.81	20.13	121	3.3	78.0	91.3	1.8	1.8	2.2	
P531CT	PMR-RZM P431CT, CP09CT	11448	33.33	17.19	20.53	123	3.6	62.8	84.3	1.8	2.0	2.3	
Y591	IRZM-8 Y391, CY91	12680	36.59	17.31	20.57	127	3.4	74.9	85.0	1.0	1.0	1.2	
Z510	Inc. Z210 (8S Polish)	7769	20.25	18.83	22.22	112	5.2	12.3	12.3	3.8	3.7	5.3	

(cont.)

Variety	Description	Acre Yield		Soluble Beets/		DI	%R (0-3)		%R (0-4)	Foliar Foliar		CLS	
		Sugar	Beets	Sucrose	100'		%	%		Color	Seg		
		Lbs	Tons	%	No.		%	%		Score	Score		
Multigerm lines & populations (cont.)													
05-FC1036	RZM 04-FC1028,1037,1038aa x A	12676	36.70	17.26	20.72	3.4	126	72.4	82.2	2.0	2.2	1.8	
		10723	29.64	18.21	21.48	3.8	124	57.1	68.7	2.0	2.3	3.2	
05-FC1022	RZM-CR-% 20031022												
05-FC1018	RZM-CR-% 20031018	9964	28.79	17.36	20.95	3.9	124	53.0	66.0	2.2	2.2	1.8	
05-FC1019	RZM-CR-% 20031019	11734	34.95	16.82	20.33	3.9	126	52.8	71.2	1.7	2.2	2.4	
05-FC1030-15 (Sp)	03-FC1030-15aa x A	10557	29.53	17.86	21.48	3.9	121	51.7	69.3	2.7	2.3	2.3	
05-FC1030-16 (Sp)	03-FC1030-16aa x A	10370	31.05	16.79	19.88	4.7	109	33.0	33.0	2.8	2.7	2.7	
05-FC1023 (Iso)M Inc.	20021023 (A,aa)M	10674	31.39	17.02	20.58	3.5	120	67.7	85.2	2.0	2.0	1.8	
		CR509-1-312	Inc. CR301-1-312 (A,aa)	7503	21.17	17.74	22.13	121	87.4	99.0	1.3	1.2	1.6
		CR510-2-305	Inc. CR310-2-305 (A,aa)	10391	30.55	16.98	20.65	120	69.9	95.4	2.2	2.8	1.7
		CR511-7-302	Inc. CR311-7-303,-304 (A,aa)	7185	22.26	16.13	20.33	124	41.8	66.3	1.3	1.8	1.0
CR511-88	RZM CR311-88 (CR11-88)	13043	39.98	16.38	18.73	3.0	114	86.2	96.3	1.7	1.5	1.3	
		CR311-6	Inc. CR111-6 (A,aa)	11715	34.98	16.74	20.43	114	79.7	91.9	1.5	1.7	1.0
		CR412-5	Inc. CR212-5-# (C)	10953	32.68	16.78	20.47	120	68.4	90.3	1.2	1.3	1.2
		CR412-211	Inc. CR212-5-211	10101	30.04	16.75	20.43	118	67.9	93.8	1.3	1.2	1.3
4933-14 (Sp)	2933-14aa x A (CR933-14)	11000	30.27	18.12	21.57	3.4	108	75.6	89.7	1.2	1.2	1.0	
		CR410-231	Inc. CR210-14-2-231	8715	27.12	16.04	20.72	117	77.3	94.7	1.2	1.0	0.8
		4951-210	Inc. 2951-210 (CR951-10)	9031	27.01	16.75	20.93	106	69.9	79.6	1.3	1.7	1.1
Monogerm lines & populations													
5849m	Inc. 4849-# (C)mm	12346	36.13	17.13	20.42	3.3	120	77.0	89.8	1.8	2.2	1.7	
03-FC1014-22	Inc. 01-FC1014-22 (A,aa)	8929	25.59	17.43	21.27	3.9	121	48.5	63.7	2.0	2.0	2.3	
03-FC123-31	Inc. 01-FC123-31 (A,aa)	10329	30.47	17.11	20.17	3.5	135	69.2	79.2	3.0	3.0	3.6	
4850M	Inc. 2252-2MmAA	10033	27.81	18.07	21.70	3.3	130	77.0	89.2	3.0	3.8	4.3	
EL-SP7322-0	Inc. SP22-0	6700	22.16	15.08	17.85	5.2	112	14.8	19.9	4.5	4.8	1.9	

(cont.)

Variety	Description	Acre Yield		Soluble Beets/ 100'		DI	%R		(0-4)	Foliar		CLS
		Sugar	Beets	Sucrose	Solids		%R	Color		Seg		
		Lbs	Tons	%	%		%	Score		Score		
Score												
Hybrids												
Roberta	Betaseed	7022	22.76	15.63	17.60	130	4.7	29.0	30.0	3.3	3.5	4.0
HM-E17	CR check, Syngenta	8356	24.71	16.95	19.65	124	5.2	17.5	20.9	4.3	4.0	2.6
Monohikari	CR check, Seedex	9216	27.97	16.50	18.90	126	4.4	36.1	39.8	3.0	3.0	3.5
Beta 4430R	Betaseed	12296	35.76	17.18	19.52	136	2.8	94.7	95.8	2.0	2.2	5.0
4951-210H50	C790-15CMS x 2951-210	12520	35.86	17.48	20.92	144	3.4	71.3	92.5	1.0	1.0	1.3
CR509-1-312H50	C790-15CMS x CR309-1-312	11437	32.20	17.73	21.28	129	3.2	79.5	94.7	1.2	1.2	1.9
CR310-2-305H50	C790-15CMS x CR310-2-305	13145	38.59	17.01	20.02	130	3.3	76.8	91.3	1.3	1.7	1.8
CR511-7-302H50	C790-15CMS x CR311-7-303,-304	12118	35.15	17.22	20.50	129	3.3	75.4	93.0	1.5	1.2	1.1
CR511-88H50	C790-15CMS x CR311-88	11647	35.82	16.27	18.97	132	3.4	70.7	82.7	1.5	1.3	2.3
4933-14H50	C790-15CMS x 2933-14	13226	38.55	17.11	20.15	118	3.3	77.6	92.5	1.3	1.2	1.7
CR412-211H50	C790-15CMS x CR212-5-211	11727	33.78	17.35	20.38	135	3.2	82.5	94.4	1.2	1.0	2.3
CR412-5H50	C790-15CMS x CR212-5-# (C)	11935	34.80	17.17	20.28	133	3.2	84.6	96.1	1.3	1.3	1.4
05-FC1030-15H50	C790-15CMS x 03-FC1030-15	10785	32.04	16.83	19.82	123	3.7	61.3	70.5	2.2	2.2	3.5
05-FC1030-16H50	C790-15CMS x 03-FC1030-16	8952	27.02	16.51	19.25	130	4.4	38.1	44.9	2.8	2.8	3.9
05-FC1036H50	C790-15CMS x RZM 04-FC1028,1037,1038	11353	33.62	16.86	19.98	126	3.7	64.2	71.4	2.2	2.2	2.8
05-FC1022H50	C790-15CMS x RZM-CR-# 20031022	10432	29.63	17.61	20.68	132	3.5	71.3	80.3	2.2	1.8	3.2
05-FC1018H50	C790-15CMS x RZM-CR-# 20031018	10796	31.19	17.31	20.17	141	3.9	55.8	65.2	2.5	2.3	2.7

(cont.)

Variety	Description	Acre Yield		Soluble Beets/		%R		%R		Foliar Foliar	
		Beets		100'		(0-3)		(0-4)		Color	
		Lbs	Tons	%	No.	%	%	%	Score	Seg	Score
<u>Score</u>											
<u>Hybrids (cont.)</u>											
05-FC1019H50	C790-15CMS x RZM-CR-% 20031019										
	10646	32.60	16.31	19.23	133	3.9	54.9	65.1	2.3	2.5	2.4
5933H50	C790-15CMS x popn-933 (C)	12932	38.49	16.83	117	3.2	81.6	92.8	1.7	1.3	2.3
5944H50	C790-15CMS x popn-944 (C)	12986	37.07	17.52	129	3.4	74.6	82.4	2.0	1.3	2.2
Mean		10744.9	31.60	16.98	20.24	124.0	3.7	62.8	74.4	2.1	2.3
LSD (.05)		1920.8	5.56	0.83	0.71	19.2	0.5	18.6	17.1	0.6	0.6
C.V. (%)		15.7	15.49	4.30	3.10	13.6	11.2	26.1	20.3	25.2	27.7
F value		8.8**	8.17**	7.78**	15.87**	1.8**	15.5**	10.8**	16.9**	18.7**	17.6**
											25.0**

NOTES:

Test had moderate rhizomania and Cercospora leaf spot. 0.5% of plants developed root rot due to Sclerotium rolfsii and a few with Erwinia root rot from adjacent inoculated Erwinia test. Powdery mildew was controlled until late in the season. Otherwise there appeared to be little other disease pressure. Plots were hand harvested. Plots were partially topped, lifted, laid out on the soil surface, and roots individually scored for rhizomania, where 1 = normal root to 9 = very severe rhizomania or dead. Few roots were scored > 7 and < 2. The beets were then topped, bagged, washed, weighed by plot, and run thru the sugar lab. Brei was measured for soluble solids and filtrate for % sugar.

Rhizomania: DI = Disease Index = average score of each plant within the variety; % Resistant(0-3) = total roots in classes 0+1+2+3/total roots scored. %Resistant(0-4) = roots in classes 0-4/total roots scored. Because test was mild, it was observed that many of the roots in the susceptible checks were scored as 4 or less but in the resistant checks, some resistant roots were also scored as 4's or higher. I.e., there did not appear to be a discrete separation between resistant and susceptible roots based on the action of the Rz1 allele.

(cont.)

Variety	Description	Acre Yield		Soluble Beets/		%R		%R		Foliar Foliar	
		Beets		Sucrose		DI		(0-3)		Color	
		Lbs	Tons	%	No.	%	%	%	%	Score	Score
Score											

NOTES (cont.):

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

Cercospora Leaf Spot. Leaf spot was scored on a scale of 0 to 9, where 9 = complete defoliation. Development of leaf spot was slow, but uniform across test and varietal differences appeared to separate fairly discretely. Leaf spot was scored twice and the mean of the ratings used. In terms of performance, rhizomania was more important than Cercospora.

Roberta is rrrz. Beta 4430R is Rz1. Angelina is Rz1Rz2. CR311 & CR411 = CR11. 4931 = C931. R540 = C79-#s Rz2. P531CT = CP09CT. Y591 = CY91 released in 2007. Z510 = composite of 2n Polish high & sugar accessions, rrrz. 05-FC #s = Salinas Rz1 x FC CLS, Rhizoctonia by Lee Panella. CR511-88 = CR11-88 released in 2006 (see test 3206). Experimental hybrids named H50 use C790-15CMS as mm tester. C790-15 is rrrz.

TEST 3206. CERCOSPORA EVALUATION OF S_n PROGENIES FROM CR11-88 UNDER RHIZOMANIA, SALINAS, CA, 2006

72 entries* x 4 reps, sequential
1-row plots, 11 ft. long

Planted: May 5, 2006

Harvested: November 20 & 21, 2006

Inoc. Cb: July 18, August 8, 2006

Variety	Description	Acre Yield		Soluble Beets/ 100'		%R (0-3)		%R (0-4)		Foliar Color		Foliar Seg		CLS
		Sugar	Beets	Sucrose	Solids	DI	(0-3)	(0-4)	Color	Seg				
		Lbs	Tons	%	%	No.	%	%	Score	Score				
Checks														
EL-SP7322-O	Inc. SP7322-0	5977	19.94	14.85	17.52	132	5.4	11.2	13.7	4.8	4.3	1.9		
HM-E17	4/05, Syngenta	8948	26.32	16.73	19.83	127	5.9	7.5	10.4	4.5	4.5	2.8		
Roberta	3/20/06	5847	19.25	14.70	17.77	118	5.1	16.5	16.5	2.5	2.8	3.9		
Beta 4430R	3/28/06	12769	38.35	16.70	19.30	139	2.9	90.6	93.8	1.8	1.5	5.5		
HH142	3/10/06	13618	37.98	17.98	20.88	134	3.4	77.8	90.3	1.0	1.3	1.9		
Monohikari	1/21/03	8969	25.20	17.65	19.80	130	5.1	10.8	18.8	3.5	3.3	3.6		
CR411	RZM CR311aa x A (CR11)	11949	35.11	17.00	20.08	120	3.3	77.1	86.7	1.5	1.3	1.8		
5933	popn-933(C)aa x A	13601	38.42	17.83	20.98	98	3.4	73.0	84.4	1.3	1.3	1.8		
5944	popn-944(C)aa x A	13392	36.40	18.42	22.20	102	3.1	85.3	93.4	1.8	1.8	2.4		
05-FC1036	RZM 04-FC1028,1037,1038aa x A	13328	38.13	17.50	20.58	130	3.3	73.1	88.9	2.0	2.3	2.3		
05-FC1030-15	03-FC1030-15aa x A	9575	26.34	18.10	21.50	109	3.9	50.4	69.6	2.0	1.8	2.3		
05-FC1030-16	03-FC1030-16aa x A	9008	27.14	16.73	19.92	105	5.2	18.8	22.9	3.3	2.8	4.1		
05-FC1022	RZM-ER-8 20031022	12947	38.11	17.13	20.70	107	3.5	71.5	84.6	1.8	2.0	3.3		
CR509-1-312	Inc. CR301-1-312 (A,aa)	7776	21.71	17.95	21.95	114	3.2	82.5	97.9	1.3	1.3	2.1		
CR510-2-305	Inc. CR310-2-305 (A,aa)	10726	30.64	17.50	21.08	114	3.5	64.8	85.4	2.8	3.5	1.8		
CR511-7-302	Inc. CR311-7-303,-304 (A,aa)	7531	22.66	16.63	20.40	102	3.9	42.3	72.3	1.8	1.8	1.1		
CR511-88, CR11-88	RZM CR311-88 (A,aa)	12782	37.84	16.95	19.80	116	3.3	75.5	91.1	1.5	1.3	1.3		
Beta 4430R	3/28/06	11412	33.93	16.83	19.50	130	2.9	86.7	93.5	2.3	1.8	5.4		
Sn Progenies from CR11-88														
CR511-88-501	CR311-88⊗	10163	32.30	15.77	18.42	111	3.6	59.1	82.7	1.5	1.8	1.3		
-502		10272	32.44	15.82	18.88	107	3.2	84.6	96.1	1.5	1.5	1.8		
-503		9562	30.84	15.60	18.50	118	3.6	59.6	80.0	2.8	2.3	1.8		
-504		10602	36.45	14.57	17.08	123	3.1	86.6	94.1	1.8	2.3	2.3		
-505		13609	39.89	17.13	20.27	109	2.9	95.3	95.3	1.5	1.3	1.4		
-506		9656	32.24	14.95	18.33	107	3.6	58.8	81.7	2.5	2.5	1.8		

(cont.)

Variety	Description	Acre Yield		Soluble Beets/		%R		%R		Foliar		CLS
		Sugar	Beets	Sucrose	Solids	100'	DI	(0-3)	(0-4)	Color	Seg	
		Lbs	Tons	%	%	No.	%	%	%	Score	Score	
Sn Progenies from CR11-88 (cont.)												
CR511-88-507 CR311-88⊗												
-508		12131	38.88	15.63	18.67	109	3.1	85.7	100.0	1.5	1.3	2.6
-509		12502	37.08	16.98	19.48	86	3.3	82.6	87.5	1.8	2.5	1.3
-510		8063	23.56	17.10	20.55	109	3.4	68.7	86.4	1.3	1.0	1.0
-511		12938	43.12	15.02	17.88	116	3.0	93.6	100.0	1.3	2.0	1.6
-512		9881	31.24	15.82	18.33	77	3.1	85.0	95.0	1.5	1.8	1.8
		9591	34.87	13.77	17.15	109	3.2	84.6	86.4	1.8	2.3	1.0
-513		9503	28.17	16.77	19.70	107	3.4	69.6	88.6	1.5	1.5	1.3
-514		12022	36.05	16.65	19.52	102	2.9	90.0	96.2	1.8	2.3	1.5
-515		11928	35.89	16.63	19.85	118	3.2	83.2	98.2	1.0	1.0	0.9
-516		10882	37.14	14.60	17.83	118	3.3	75.5	98.1	1.3	2.3	1.1
-517		11200	34.99	16.02	19.10	120	3.2	76.9	98.4	1.0	1.0	1.3
-518		10679	34.99	15.35	19.10	107	2.8	100.0	100.0	1.3	1.5	1.3
-519		11527	34.18	16.92	19.92	130	3.2	84.6	96.8	1.3	1.0	1.1
-520		11120	34.64	16.17	18.92	118	3.3	76.1	96.5	1.8	2.3	0.9
-521		11250	33.63	16.78	19.98	123	3.1	87.3	89.2	1.5	1.5	1.3
-522		11992	36.64	16.35	19.20	111	3.0	91.0	100.0	1.8	1.3	1.4
-523		9113	27.36	16.65	19.23	125	3.4	66.5	89.4	2.0	1.5	1.4
-524		12675	40.91	15.50	18.50	109	3.1	83.6	94.4	2.0	1.8	1.9
-525		10468	31.32	16.73	19.85	114	3.0	92.1	100.0	1.0	1.0	1.3
-526		11736	35.42	16.55	19.85	105	3.1	86.5	97.9	1.0	1.0	1.1
-527		11848	36.21	16.33	19.77	91	3.0	89.4	95.0	1.5	1.0	1.9
-528		11683	35.63	16.40	19.58	105	3.8	53.6	70.8	1.8	1.8	1.8
-529		6514	19.71	16.52	20.73	102	3.7	59.5	70.3	2.8	2.3	2.1
-530		13289	41.06	16.20	19.52	114	3.2	82.5	98.1	1.0	1.3	1.5
-531		10014	31.14	16.25	19.60	120	2.9	91.4	98.3	1.5	1.5	2.1
-532		14154	43.62	16.17	18.90	102	3.4	71.4	88.2	1.8	1.8	1.3
-533						0						

(cont.)

Variety	Description	Acre Yield		Soluble Beets/		%R		%R		Foliar Foliar		CLS
		Sugar	Beets	Sucrose	100'	DI	(0-3)	(0-4)	Color	Seg		
		Lbs	Tons	%	%	%	%	%	Score	Score		
Sn Progenies from CR11-88 (cont.)												
CR511-88 -534	CR311-88⊗	12809	42.75	15.00	18.08	107	3.1	86.6	95.6	1.0	1.3	0.6
-535		13012	38.82	16.77	19.73	102	3.4	76.9	84.0	1.3	1.5	1.3
-536		12619	36.35	17.33	20.58	102	3.2	86.9	91.3	1.3	1.5	1.9
-537		8560	27.34	15.88	19.23	123	3.6	63.2	76.0	2.0	1.8	1.4
-538		10386	33.73	15.48	18.73	95	3.1	88.5	96.9	1.8	1.5	1.4
-539		10760	32.82	16.40	19.60	93	3.2	76.5	87.1	1.3	1.8	1.4
-540		11233	36.07	15.60	18.67	114	3.3	77.1	85.4	1.8	1.8	1.5
-541		12086	38.53	15.65	18.48	123	3.3	79.2	92.3	1.3	1.5	1.1
-542		9912	30.47	16.27	19.38	105	3.5	70.6	82.6	1.5	1.3	1.0
-543		10072	31.34	16.10	19.30	116	3.3	80.1	90.5	1.0	1.0	1.5
-544		12657	38.17	16.60	19.90	102	3.2	75.8	91.3	1.3	1.3	1.3
-545		13790	41.47	16.63	19.70	125	3.2	84.2	93.8	1.5	1.3	1.0
-546		11714	34.78	16.85	20.23	120	3.0	90.5	97.9	1.0	1.0	1.1
-547		10506	31.54	16.67	19.10	116	3.5	62.3	82.9	1.8	1.3	1.6
-548		10662	34.20	15.55	18.63	109	3.0	94.4	100.0	2.3	1.8	3.3
-549		11658	33.59	17.40	20.63	107	3.1	84.8	98.3	1.8	1.5	2.3
-550		11375	35.41	16.15	18.77	98	3.6	69.7	76.5	3.3	2.5	1.8
-551		11450	37.51	15.25	18.92	116	3.4	75.2	85.6	2.0	1.8	1.4
-552		10583	34.82	15.30	18.25	123	3.0	91.2	94.8	1.8	1.8	1.9
-553		12186	37.55	16.23	19.20	120	3.2	74.6	96.0	1.3	1.5	2.3
-554		11244	37.32	14.98	17.75	91	3.5	66.6	82.1	1.0	1.0	0.9
Mean		11014.1	33.80	16.32	19.42	112.0	3.4	73.6	85.1	1.8	1.7	1.8
LSD (.05)		2172.4	6.85	1.05	1.01	26.2	0.5	21.4	16.4	0.8	0.8	0.7
C.V. (%)		14.2	14.54	4.60	3.72	16.8	9.6	20.9	13.8	31.5	31.0	26.9
F value		5.6**	5.18**	6.17**	8.54**	1.6*	13.0**	7.0**	12.2**	7.3**	6.8**	14.9**

TEST 3206. CERCOSPORA EVALUATION OF S_n PROGENIES FROM CR11-88 UNDER RHIZOMANIA, SALINAS, CA, 2006

(cont.)

Variety	Description	Acre Yield		Soluble Beets/		%R		%R		Foliar Foliar		CLS
		Beets		100'		(0-3)		(0-4)		Color Seg		
		Sugar		Solids		DI		%		Score		
		Lbs	Tons	%	No.	%	%	Score	Score			

Notes: CR11-88 was released in 2006 as a MM, Sf, A:aa line with moderate resistance to cercospora leaf spot and Rz1 resistance to rhizomania. In prior progeny line tests it had shown high sugar yield performance but only fair % sugar and was not as leaf spot resistant as some of its sister half-sib lines. CR11-88 is the increase of one half-sib family from CR11. From CR11-88, individual plants were selfed. These selfed progeny families were grown in Test 3206 to determine if genetic variability remained for improvement of % sugar and resistance to Cercospora. Test 3206 shows that the S1 progenies are either Rz1Rz1 or segregate 3Rz1_rz1. There appears to be limited opportunity to select among the S1s for improvement in sucrose concentration and resistance to Cercospora. C11-88 and the Sn progenies are very attractive in terms of canopy color, uniformity, and vigor. Roots were large, smooth, and nicely shaped. A few of the individual progenies such as CR511-88-505 will be increased and reevaluated to see if improved.

Rhizomania: DI = Disease Index = average score of each plant within the variety; % Resistant(0-3) = total roots in classes 0+1+2+3/total roots scored. %Resistant(0-4) = roots in classes 0-4/total roots scored.

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

Cercospora Leaf Spot. Leaf spot was scored on a scale of 0 to 9, where 9 = complete defoliation. Development of leaf spot was slow, but uniform across test and varietal differences appeared to separate fairly discretely. Leaf spot was scored twice and the mean of the ratings used. In terms of performance, rhizomania was more important than Cercospora.

16 entries x 6 reps, sequential
1-row plots, 11 ft. long

Planted: May 15, 2006
Harvested: November 6, 2006

Variety	Description	Acre Yield		Soluble		Beets/ 100'	DI	%R		%R		Foliar Foliar	
		Sugar Lbs	Beets Tons	Sucrose	Solids			(0-3)	(0-4)	Color	Seg		
												%	%
C37 Background													
05-C37	Inc. 04-C37; rzrz	3657	13.37	13.67	17.32	201	5.4	6.2	11.0	3.8	3.7	2.5	
R540	IRZM-% R940;...C79-#s	8301	26.61	15.55	18.85	185	4.6	31.1	39.0	2.5	2.2	1.7	
R525	IRZM-% R324;C79-2,-3(WB41,42)	7835	25.03	15.77	19.17	177	4.1	41.1	60.2	2.5	2.2	1.8	
R437	RZM-% R637,R337;C79-9(WB151)	7860	24.82	15.82	20.00	191	3.5	71.1	81.0	2.5	2.3	1.7	
Differential Checks													
Beta4430R	Resist.ck.; Rz1	5206	18.28	14.23	17.43	200	5.3	4.2	7.1	3.3	3.2	4.7	
BetaG017R	Resist.ck.; Rz2	11425	35.55	15.97	19.03	194	3.8	58.5	68.3	2.2	1.8	3.2	
Angelina	Resist.ck.; Rz1+Rz2	12050	36.35	16.45	19.53	203	3.9	58.7	65.2	1.7	1.3	2.5	
Roberta	Susc. Ck.; rzrz	5321	18.61	14.17	17.45	197	5.6	3.2	4.8	3.7	3.7	4.2	
Breeding Lines and Populations													
R521	IRZM-% R321,R021(C51,C26,C27)	7726	25.67	14.92	18.13	200	4.6	27.1	34.8	2.5	2.5	2.7	
R539	Inc. R039,(C39R) (quant)rzrz	10242	34.34	14.83	18.32	186	3.6	65.6	76.1	1.7	1.5	1.3	
Y577	IRZM-% Y277,Y375 (Bvm gp)	7443	23.41	15.87	19.13	201	4.8	23.0	29.1	2.5	2.2	1.8	
R524-302	Inc. R324-302,-306	6933	22.20	15.72	19.37	200	4.9	22.9	31.5	3.0	2.8	2.2	
R541/2	IRZM-% R641,R642 (WB169,258)	6591	22.17	14.75	18.05	214	4.6	30.8	40.1	2.3	2.5	1.8	
R537-302	Inc. R337-302	6791	21.08	16.03	19.73	182	5.0	24.5	30.0	3.2	3.0	3.0	
R525-301	Inc. R325-301,-302	6418	20.07	16.00	19.78	200	4.6	32.4	40.7	2.5	2.7	2.2	
C28	Inc. C28 Rz1?	3818	14.27	13.23	16.28	185	5.5	5.6	17.3	3.3	3.3	2.5	
Mean		7351.1	23.87	15.19	18.60	194.8	4.6	31.6	39.8	2.7	2.6	2.5	
LSD (.05)		1537.0	4.54	1.12	1.23	27.4	0.5	16.7	16.4	0.8	0.8	1.1	
C.V. (%)		18.2	16.55	6.41	5.76	12.2	9.4	45.8	35.8	27.1	28.6	36.9	
F value		19.1**	18.05**	5.76**	6.02**	1.0NS	14.9**	14.1**	17.5**	4.6**	5.5**	6.0**	

(cont.)

Variety	Description	Acre Yield		Soluble Beets/		%R		Foliar Foliar	
		Sugar	Beets	Sucrose	100'	DI	(0-3)	(0-4)	Color Seg
		Lbs	Tons	%	No.	%	%	%	Score Score
									CLS
									Score
									Score

Notes:

Tests 4206 & 4306 were grown in a field area that was originally inoculated with IV-BNYVV in 2003 and rhizomania tests were grown in 2004, 2005, and 2006. These tests were severe.

Rhizomania: DI = Disease Index = average score of each plant within the variety; % Resistant(0-3) = total roots in classes 0+1+2+3/total roots scored. %Resistant(0-4) = roots in classes 0-4/total roots scored. It was observed that many of the roots in the susceptible checks were scored as 4 or less but in the resistant checks, some resistant roots were also scored as 4's or higher. I.e., there did not appear to be a discrete separation between resistant and susceptible roots based on the action of the Rz1 and Rz2 alleles.

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

Cercospora: Natural infection with Cercospora occurred late in the summer and became moderate on some entries by harvest. Foliar leaf spot symptoms were scored on a scale of 0 to 9, where 9 = 100% of leaf area diseased.

48 entries x 4 reps, sequential
1-row plots, 11 ft. long

Planted: May 15, 2006
Harvested: November 6-7, 2006

Variety	Description	Acre Yield		Soluble		Beets/ 100'	DI	%R		Foliar		CLS
		Sugar	Beets	Sucrose	Solids			(0-3)	(0-4)	Color	Seg	
		Lbs	Tons	%	%			%	%	Score	Score	
Hybrid checks (Differential checks)												
Robertta	Susc. check, rzrz	4021	15.55	12.90	15.80	189	6.1	4.2	8.5	2.8	2.8	3.8
Angelina	Resist. check, Rz1+Rz2	14407	45.41	15.93	18.35	216	3.7	63.5	73.2	1.0	1.0	4.0
G017R	Resist. Check Rz2	11682	37.98	15.45	18.30	184	3.5	71.7	81.3	1.3	1.3	4.3
Beta 4430R	Resist. Check Rz1	4980	17.20	14.22	16.73	200	5.4	7.3	14.3	3.3	3.3	4.0
Lines with Quantitative resistance												
R539	Inc. R039, (C39R), (Q,rzrz)	12147	41.59	14.68	18.33	198	3.5	67.6	85.7	1.3	1.3	1.5
R539H5	C833-5CMS x R039, Rz1xQ	6487	21.64	15.10	18.30	186	5.5	12.3	22.6	2.3	2.3	2.0
US H11	Susc. check, rzrz	3118	12.73	12.38	15.45	209	6.0	2.8	12.0	3.0	2.8	2.3
Lines with C78/3 germplasm												
R578(Iso)	RZM R378 _{Iso} , (C37/3) Rz1	6708	21.81	15.18	18.48	202	5.3	16.3	24.2	1.8	1.8	2.0
P529	PMR-RZM P429, (CP05)	6645	23.23	14.35	17.45	193	5.8	9.0	13.6	2.3	2.0	2.8
P530	PMR-RZM P430, (CP06)	6351	21.75	14.60	17.50	216	4.8	35.4	44.0	2.0	1.5	2.5
P507/8	PMR-RZM P407/8, (CP07)	5534	19.10	14.50	17.70	218	6.0	7.0	9.5	2.8	3.0	3.3
P518-6	PMR-RZM P418-6, (CP08)	4895	16.44	14.95	18.27	202	5.8	9.2	15.5	1.8	1.5	2.3
P531CT(Iso)	PMR-RZM P431CT, (CP09CT)	5638	18.92	14.68	18.17	182	5.1	21.3	30.9	3.0	2.8	4.0
Y591	IRZM-8 Y391, (CY91)	6538	20.47	15.90	18.77	200	4.9	24.0	38.9	2.0	2.0	1.5
Y595	Y95(C), C1,Syn1 Fss Rz1+	6026	20.85	14.38	17.77	175	4.8	32.8	41.8	2.0	2.0	1.8
Z510	Inc. Z210 (% sugar Polish)	4485	14.00	15.68	19.23	200	5.8	5.7	14.2	3.3	2.8	3.0
Lines with C37 germplasm												
P527	PMR-RZM P427, (CP03)	7505	26.73	14.05	17.02	227	4.6	29.7	46.4	2.0	1.8	2.5
P528	PMR-RZM P428, (CP04)	3878	14.30	13.50	16.63	198	5.7	6.7	17.0	2.8	2.8	2.8
05-C37	Inc. 04-C37 rzrz	4095	14.32	14.23	17.63	209	5.9	6.1	13.3	3.3	3.0	3.5
C28	C28, Syngenta 90060149-0 Rz1? From PI206407	3145	12.84	12.30	15.73	202	5.6	11.6	24.1	3.5	3.3	3.0

TEST 4406. HARTNELL FIELD EVALUATION OF GERMPASM FOR REACTION TO IV-BNYVV, SALINAS, CA, 2006

(cont.)

Variety	Description	Acre Yield		Soluble		Beets/ 100'	DI	%R		%R		Foliar		CLS
		Sugar	Beets	Sucrose	Solids			(0-3)	(0-4)	Color	Seg			
		Lbs	Tons	%	%			%	%	Score	Score			
Lines with C37 germplasm (cont.)														
R340	RZM-ER-# R140, (C79-#s)	7701	25.14	15.27	18.75	198	4.6	36.2	44.6	1.5	1.3	2.0	2.0	
R540	IRZM-# R940, (C79-#s)	9066	29.60	15.32	18.40	214	4.3	46.2	56.3	1.5	1.5	2.0	2.0	
R424/5	RZM-# R824,RZM R324/5, (C79-2,-3; WB41,WB42)													
		6562	21.01	15.57	18.98	225	4.0	48.4	60.8	2.3	2.3	2.8	2.8	
R424	RZM-# R724,R324, (C79-2,WB41)	5537	17.72	15.53	18.88	209	4.5	33.4	49.2	2.5	2.0	2.3	2.3	
R425	RZM-# R725,R325, (C79-3,WB42)	6276	20.58	15.27	19.32	202	4.4	47.5	53.1	2.0	2.3	1.3	1.3	
R525	IRZM-# R324,R325,R337	6456	21.64	15.00	18.10	220	3.9	52.9	67.6	3.0	2.3	2.5	2.5	
R437	RZM-# R637,R337, (C79-9,WB151)													
		8396	26.73	15.70	19.27	227	3.4	73.4	86.1	2.5	2.5	2.8	2.8	
R541/2	IRZM-# R641,R642, (C79-10,-11; WB169,WB258)													
		5163	17.29	14.95	18.10	230	4.8	24.9	35.1	2.5	2.3	1.5	1.5	
R521	IRZM-# R021,R321, (C26 x C27)	6625	21.96	15.10	18.10	223	4.5	37.8	49.2	2.3	2.3	2.0	2.0	
R522	IRZM-# R522, (C51)	6035	20.16	14.98	18.25	227	4.5	37.8	53.7	2.5	2.3	3.5	3.5	
Y577	IRZM-# Y277, Y375 (Bvm gp)	6876	21.75	15.80	18.92	211	4.8	29.3	35.7	2.3	1.8	2.5	2.5	
4921	RZM-ER-#2921 (A,aa) , (Bvm gp)	7112	23.02	15.32	18.02	207	4.7	25.5	41.1	2.3	1.5	1.8	1.8	
R524-2/3	Inc. R324-213,-215,-222,-223	5340	18.46	14.42	17.90	214	4.5	36.2	48.7	2.3	1.8	2.5	2.5	
R524-302	Inc. R324-302, -306	5061	17.12	14.77	18.02	193	4.7	30.4	43.6	2.8	2.0	4.0	4.0	
R525-301	Inc. R325-301, -302	4284	14.32	14.68	18.33	230	4.7	33.0	45.2	2.0	1.5	2.8	2.8	
R537-302	Inc. R337-302	6671	20.79	15.98	19.25	195	4.7	40.1	44.4	2.3	2.0	2.3	2.3	
MM,S ^f ,Aa populations														
EL-SP7322-0	Inc. SP22-0, 4/05, rzzz	3797	15.25	11.85	15.23	205	5.6	11.1	16.4	3.8	3.5	1.3	1.3	
05-FC1036	RZM 04-FC1028,1037,1038aa x A, CA x (CO x EL)LSR													
		7989	25.89	15.32	18.05	211	5.0	24.1	32.7	3.3	2.8	1.8	1.8	
05-FC1022	RZM-CR-# 20031022	3936	14.48	13.47	16.95	173	5.4	10.1	18.5	3.0	2.3	2.3	2.3	
5933	popn-933(C)aa x A, (CA x CO)	5995	21.11	14.20	17.33	193	5.2	14.3	21.0	2.8	2.3	2.0	2.0	

(cont.)

Variety	Description	Acre Yield		Soluble		Beets/ 100'	DI	%R		%R		Foliar		CLS
		Sugar	Beets	Sucrose	Solids			(0-3)	(0-4)	Color	Seg			
		Lbs	Tons	%	%			%	%	Score	Score			
MM, S ^f , Aa populations (cont.)														
5944	popn-944(C)aa xA, C1, Syn1 S1	6670	22.60	14.75	17.92	186	5.4	11.4	16.6	2.8	2.5	2.5	2.5	
4931	RZM 3931aa x A, (C931) Rz1	5464	18.72	14.60	17.25	200	5.0	18.0	26.9	3.0	2.8	2.5	2.5	
CR411	RZM CR311aa x A, (CR11)Rz1	5370	19.10	14.02	17.23	191	5.7	14.1	17.7	3.3	3.0	2.3	2.3	
N412(Sp)	N312, N212-#(C)aa x A, (CN12)	5578	18.99	14.65	18.02	189	6.0	5.6	10.0	3.0	2.5	2.5	2.5	
Beta vulgaris subsp. maritima (composite crosses)														
R520	IRZM R720, Bvm composite	2526	10.08	12.50	18.13	223	3.9	58.5	71.2	2.0	2.0	1.8	1.8	
R523	IRZM R423, Bvm composite	3439	12.31	13.98	19.20	243	3.9	58.7	68.8	2.0	1.8	2.0	2.0	
R523B	IRZM R423B, Bvm composite	1993	8.60	11.57	18.67	216	3.4	74.2	86.5	1.5	1.3	1.8	1.8	
36K5308	Betaseed, 3-20-06	5380	21.32	12.65	15.15	227	6.0	4.8	7.2	3.0	3.0	3.8	3.8	
Mean		6032.9	20.47	14.50	17.86	206.0	4.9	28.8	38.3	2.4	2.2	2.5	2.5	
LSD (.05)		1748.3	5.44	1.49	1.42	30.3	0.7	17.5	19.7	0.9	1.0	1.1	1.1	
C.V. (%)		20.7	19.01	7.36	5.70	10.5	9.7	43.5	36.8	26.3	30.8	31.9	31.9	
F value		13.8**	13.30**	4.28**	4.32**	2.1**	10.9**	11.1**	10.8**	4.0**	3.3**	3.9*	3.9*	

Notes:

Test 4406 was grown in an area contiguous with 4206 and 4306 but was inoculated with IV-BNYVV in 2004 and rhizomania tests were grown in 2005. Rhizomania appeared to be moderately severe and fairly uniform.

Rhizomania. DI = Disease Index = average score of each plant within the variety; % Resistant(0-3) = total roots in classes 0+1+2+3/total roots scored. %Resistant(0-4) = roots in classes 0-4/total roots scored. It was observed that many of the roots in the susceptible checks were scored as 4 or less but in the resistant checks, some resistant roots were also scored as 4's or higher. I.e., there did not appear to be a discrete separation between resistant and susceptible roots based on the action of the Rz1 and Rz2 alleles.

TEST 4406. HARTNELL FIELD EVALUATION OF GERMPASM FOR REACTION TO IV-BNYVV, SALINAS, CA, 2006

(cont.)

Variety	Description	Acre Yield		Soluble Beets/		DI	%R		%R		Foliar Foliar	
		Sugar	Beets	Sucrose	Solids		(0-3)	(0-4)	Color	Seg	CLS	
		Lbs	Tons	%	%		%	%	Score	Score	Score	

Notes: (cont.)

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

Cercospora: Cercospora leaf spot resulted from natural infection and was more severe in 4406 than in 4206 having spread from test 4606. Plots were scored at harvest on a scale of 0 to 9, where 9 = 100% of the leaf area covered or dead.

24 entries x 4 reps, RCB
1-row plots, 11 ft. long

Planted: May 15, 2006
Harvested: November 7, 2006

Variety	Description	Acre Yield		Soluble		Beets/		DI	%R		%R		Foliar		CLS
		Sugar	Beets	Sucrose	Solids	100'	No.		%	%	(0-3)	(0-4)	Color	Seg	
		Lbs	Tons	%	%			%					Score	Score	Score
<u>Differential Checks</u>															
G017R	Resistant check, Rz2	7577	28.63	13.00	16.00	200		3.5	74.9	78.7			1.5	2.0	5.8
Angelina	Resist. check, Rz1+Rz2	7536	28.58	13.23	16.15	200		3.6	68.0	70.4			1.5	2.5	4.3
Beta 4430	Resist. Check Rz1	7862	31.83	12.20	15.43	209		3.8	67.6	72.0			1.3	2.0	5.8
Robertta	Susc. ck, 9/19/05 rzrz	7474	27.93	13.35	16.50	193		3.6	73.4	74.5			1.3	1.5	3.8
<u>C37 Background</u>															
05-C37	Inc. 04-C37 rzrz	3387	14.22	11.93	15.28	200		4.7	33.4	41.3			2.5	2.5	2.5
R540	IRZM-# R940,..., (C79-#s)	8594	29.60	14.52	17.05	184		3.9	55.3	61.4			1.5	1.8	1.8
R525	IRZM-# R325,R324,..., (C79-2,-3)	5010	19.21	13.07	17.52	184		3.7	64.0	71.8			2.0	2.8	2.5
R437	RZM-# R637,R337, (C79-9,WB151)	7196	24.19	14.88	18.60	180		3.3	81.2	85.6			1.8	2.0	1.8
<u>Progeny lines</u>															
R524-302	Inc. R324-302,-306	3905	15.28	12.90	15.85	191		4.3	43.7	51.8			2.0	2.5	2.5
R525-301	Inc. R325-301,-302	4683	17.15	13.48	17.33	191		4.2	49.1	57.6			2.3	2.0	1.8
R524-2/3	Inc. R324-213,-215,-222,-223	4745	17.19	13.60	16.50	198		4.1	51.0	54.7			2.0	2.3	2.3
R537-302	Inc. R337-302	6116	22.49	13.45	17.33	173		4.8	41.3	46.4			1.5	2.0	2.3
Y575-305	Inc. Y375-305	3759	14.96	12.45	15.82	202		4.9	28.1	30.3			2.0	2.0	1.8
Y575-311	Inc. Y375-311	4191	16.44	12.77	15.38	218		5.7	10.0	13.6			2.0	2.5	2.8
Y590-40 (Iso)	RZM Y390-40	5757	21.11	13.65	17.20	216		5.9	13.3	14.6			1.3	1.8	1.8
Y595	Y95 (C)	6675	24.82	13.38	16.43	180		4.5	39.6	40.9			1.5	2.0	1.8
<u>monogerm lines & populations</u>															
4842 (Iso)	RZM-# 2842, (C842) Rz1	3820	16.76	11.43	13.55	211		4.2	44.2	50.8			1.5	2.3	2.5
4859 (Iso)M	Inc. 4849-# (C) Rz1	5043	21.54	11.63	14.60	200		4.4	42.0	49.0			2.0	2.0	2.5
4848	RZM-# 2848 (A,aa) Rz?	5384	21.64	12.43	15.15	202		4.7	31.6	33.9			1.8	2.5	3.5
5848-1m	RZM 2848-1mm Rz?	4916	19.52	12.63	15.48	180		3.3	85.0	92.6			2.5	2.5	2.5
5812M	Inc. 3912-2,-5,-6,-42 Rz2	5941	23.45	12.55	15.27	202		3.5	70.2	72.9			1.8	1.8	3.0
5812H5	C833-5CMS x " Rz1+Rz2	5927	21.75	13.63	16.95	195		4.5	33.8	37.0			1.8	1.8	2.3
5819M	Inc. 3819-26,-27,-28 Rz?	4739	21.49	11.02	13.63	177		3.6	62.2	70.3			1.5	2.0	3.5
5819H5	C833-5CMS x " Rz1+Rz?	4417	17.40	12.73	15.02	189		4.5	44.3	46.3			1.5	2.3	3.5

(cont.)

Variety	Description	Acre Yield		Soluble		Beets/		%R		%R		Foliar Foliar	
		Beets		Sucrose		100'		(0-3)		(0-4)		Color	
		Lbs	Tons	%	%	No.	%	%	%	%	%	Score	Score
Mean		5610.6	21.55	12.91	16.00	194.8	4.2	50.3	54.9	1.8	2.1	2.8	
LSD (.05)		1893.2	5.87	1.67	1.68	31.5	0.6	19.6	19.0	0.7	0.9	1.3	
C.V. (%)		23.9	19.32	9.14	7.46	11.5	10.2	27.6	24.5	29.5	30.5	32.3	
F value		4.9**	5.86**	2.34**	4.17**	1.2NS	10.4**	8.5**	9.6**	2.0*	1.0NS	6.2**	

NOTES: Test area for 4606 was inoculated in 2005 and one inoculation crop grown. This is the first year for tests in this area. Rhizomania appeared to be mild and highly variable.

Rhizomania. DI = Disease Index = average score of each plant within the variety; % Resistant(0-3) = total roots in classes 0+1+2+3/total roots scored. %Resistant(0-4) = roots in classes 0-4/total roots scored. It was observed that many of the roots in the susceptible checks were scored as 4 or less but in the resistant checks, some resistant roots were also scored as 4's or higher. I.e., there did not appear to be a discrete separation between resistant and susceptible roots based on the action of the Rz1 and Rz2 alleles.

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

Cercospora: Cercospora leaf spot resulted from natural infection and was more severe in 4406 than in 4206 having spread from test 4606. Plots were scored at harvest on a scale of 0 to 9, where 9 = 100% of the leaf area covered or dead.

24 entries x 4 reps, sequential
1-row plots, 11 ft. long

Planted: May 15, 2006

Harvested: November 13, 2006

Variety	Description	Acre Yield		Soluble Beets/		%R		Foliar Foliar		CLS
		Sugar	Beets	Sucrose	100'	DI	(0-3)	(0-4)	Color	
		Lbs	Tons	%	No.	%	%	%	Score	Score
C37 Background										
R525	IRZM-8 R324, (C79-2, -3) (Rz2)	4410	18.99	11.32	15.13	164	3.3	79.3	88.6	1.0 1.5 1.8
R437	RZM-8 R627, R337, (C79-9; WB151)	7391	27.51	13.10	16.50	195	3.5	71.3	78.4	1.5 1.5 1.8
05-C37	Inc. 04-C37 (xrzr)	1931	9.34	10.35	14.05	182	5.1	15.5	20.1	3.0 2.3 2.0
R540	IRZM-8 R940 (C79-#s) (Rz2)	7293	26.20	13.95	17.15	177	4.1	47.5	54.1	2.0 2.0 2.0
R521	IRZM-8 R321, R021, (C26 x C27) 6836	24.82	24.82	13.60	16.55	177	3.9	55.0	61.2	1.5 1.8 2.0
Fargo entries										
04N0090	L53/PI546420//L19	2707	10.26	12.95	16.13	173	4.1	44.4	56.3	3.5 3.8 2.5
04N0091	L53/PI546420//L19	3137	13.21	11.35	14.20	193	5.1	18.4	21.6	2.8 3.0 1.8
01N0056	3747/Bm (Denmark)	2550	10.84	11.77	15.80	89	5.3	19.2	19.2	2.3 2.5 2.3
04N0106	3747/Bm (Belgium)	3866	17.02	10.93	14.25	75	5.0	26.3	28.8	1.5 2.0 1.5
04N0107	3747/Bm (Ireland)	3097	14.57	10.15	14.43	25	5.4	16.7	16.7	1.8 1.8 2.5
03N0082	R376-43/PI540689 (Belgium)	4711	19.94	11.63	14.73	180	5.4	12.6	15.8	1.8 1.8 2.8
04N0093	R376-43/PI540682 (Denmark)	3002	13.65	11.23	14.35	50	5.4	12.5	12.5	1.8 2.0 1.8
04N0095	R376-43/PI540593 (France)	4324	19.51	10.88	14.48	111	5.8	1.9	4.0	2.8 2.5 3.8
04N0096	R376-43/PI540579 (France)	5057	20.77	12.15	15.80	134	5.7	7.2	9.1	2.3 2.3 2.8
04N0097	R376-43/PI518418 (Ireland)	1711	11.82	7.43	10.14	132	5.6	11.2	19.3	2.5 2.5 2.8
04N0098	R376-43/PI540582 (Denmark)	4209	17.45	12.13	15.52	123	5.7	7.4	9.0	2.3 2.0 2.8
04N0100	R376-43/PI540578 (France)	3017	12.17	12.20	15.33	86	6.0	8.1	10.4	2.0 2.5 2.0
04N0101	R376-43/PI540659 (France)	5030	22.07	11.25	14.40	141	5.4	8.7	11.7	1.8 2.0 2.8
05N0155	R376-43/PI540678 (Denmark)	3858	16.68	11.45	15.20	141	5.5	9.7	12.2	1.8 1.8 2.3
04N0068	F1016/961009H2 (Root Maggot)	4872	18.39	13.23	16.52	184	5.4	8.5	9.7	3.0 3.3 2.0
EL06- 2→ 9	Composite C869 x WB879	3857	16.79	11.35	13.80	182	5.1	14.9	21.5	1.8 1.8 2.5
EL06-10→13	Composite C869 x WB185	3779	14.57	13.20	17.33	164	4.9	24.1	27.2	2.0 1.8 2.5
EL06-14→27	Composite SP6822-0 x WB879	5092	19.10	13.25	16.52	189	4.9	24.3	25.7	2.8 3.0 1.8
EL-SP7322-0	SP22-0, 4/05	2852	12.73	10.98	14.93	193	5.0	23.2	27.4	3.5 3.8 1.8

(cont.)

Variety	Description	Acre Yield		Soluble		%R		Foliar Foliar	
		Sugar	Beets	Sucrose	Beets/	DI	%R	Color	Seg
		Lbs	Tons	%	100'	%	(0-3)	Score	Score
Mean		4108.0	17.02	11.741	15.13	144.1	5.0	23.7	27.5
LSD (.05)		2032.3	6.67	2.49	2.39	51.7	0.7	22.3	21.8
C.V. (%)		35.1	27.79	15.00	11.20	25.4	10.3	66.7	56.1
F value		4.5**	4.43**	2.52**	3.06**	7.1**	7.7**	6.9**	8.8**
								2.8**	2.2**
									1.6NS

NOTES: Rhizomania was mild and variable. Test area was inoculated with infested soil in 2005 and one inoculation crop grown. DI, % Resistant, and sugar yield give trends and possibilities more than discrete reaction data. Stands were also variable. Roots were often sprangled and difficult to harvest and rate for disease. It may be useful to consider reevaluating several of the lines, including EL06-14-27, 04N0098, 04N0096, 03N0082, 040106, et al. (See tests 206 and 306 for performance and reaction under normal BNYVV).

Rhizomania. DI = Disease Index = average score of each plant within the variety; % Resistant(0-3) = total roots in classes 0+1+2+3/total roots scored. %Resistant(0-4) = roots in classes 0-4/total roots scored. It was observed that many of the roots in the susceptible checks were scored as 4 or less but in the resistant checks, some resistant roots were also scored as 4's or higher. I.e., there did not appear to be a discrete separation between resistant and susceptible roots based on the action of the Rz1 and Rz2 alleles.

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania. By November harvest, foliar scores were not as different as observed in late summer.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

Cercospora: Cercospora leaf spot resulted from natural infection and was more severe in 4406-4606 than in 4206 having spread from test 4606. Plots were scored at harvest on a scale of 0 to 9, where 9 = 100% of the leaf area covered or dead. In adjacent test 4606, the most susceptible entries were scored 5-6.

TEST 806. EVALUATION OF MONOGERM POPULATIONS AND LINES UNDER RHIZOMANIA, SALINAS, CA, 2006

48 entries x 4 reps., sequential
1-row plots, 11 ft. long

Planted: May 5, 2006
Harvested: October 13, 2006

Variety	Description	Acre Yield		Sucrose %	Soluble Solids %	RJAP %	Beets/ 100'	Powdery Mildew		Foliar Color	Foliar Seg
		Sugar	Beets					Mean	Score		
		Lbs	Tons								
Checks											
04-C790-15m	Inc. 00-C790-15 (rzrz)	7439	24.99	14.82	19.13	77.5	143	0.3	3.5	3.8	
04-C790-15H0m	99-C790-68CMS x Inc. 00-C790-15 (rzrz)	7687	25.19	15.32	18.92	80.9	139	1.0	4.0	3.8	
2833-5HO (Sp)	1833-5HO x RZM,T-O 1833-5-#(C)	8929	25.71	17.25	21.77	79.2	127	0.8	2.0	1.5	
2833-5 (Sp)	RZM,T-O 1833-5-#(C)mmaa x A	9437	28.21	16.73	21.40	78.2	116	0.5	2.0	1.5	
2833-5NB	NB-RZM-8 0833-5 (Sp) (A,aa)	9818	28.21	17.40	22.33	78.0	132	0.3	2.0	2.3	
4850	Inc. 2252-2MmAA	10169	29.13	17.50	22.13	79.1	134	0.0	3.0	2.8	
4851	Inc. 2252-5MmAA	10935	32.44	16.85	21.35	78.9	132	0.5	2.3	1.8	
3849m	RZM 2251-2255 (C)mmaa x A	11095	34.05	16.30	20.88	78.1	125	0.8	1.3	0.8	
Curly top resistant, monogerm, rzrz inbreds											
05-C562HO	97-C562HO x 97-C562	4314	15.01	14.43	18.67	77.3	134	2.5	4.3	4.5	
05-C562	Inc. 97-C562, (C562)	2132	7.25	14.98	19.27	77.5	134	1.0	4.3	4.8	
05-C718	Inc. 97-C718, (C718)	4568	16.02	14.10	18.60	75.7	136	1.3	4.3	4.3	
05-C718HO	97-718HO x 97-C718	3856	13.22	14.52	18.47	78.7	118	1.5	4.0	4.5	
05-C546	Inc. 97-C546, (C546)	3060	11.08	13.80	18.58	74.3	136	0.3	4.5	4.5	
05-C762-17	Inc. 0762-17, (C762-17)	5451	19.34	14.02	18.40	76.2	139	0.3	3.8	3.8	
Monogerm, S ^f , Aa populations											
5849m	Inc. 4849-#(C)mm (A,aa)	10776	33.65	16.00	20.35	78.6	130	0.5	2.0	1.5	
5842 (C842)	RZM 4842mmaa x A(CTR,mm,O-T)	9638	31.76	15.20	19.92	76.3	134	1.8	2.3	2.0	
4842(Iso)m	RZM-8 2842 (A,aa)	7899	24.78	15.92	20.48	77.8	132	1.5	2.3	3.0	
3842	RZM 2842 (C)mmaa x A	8529	27.00	15.75	20.25	77.8	139	2.0	2.0	2.3	
3869	1869 (C)mmaa x A (C869)	11053	35.87	15.40	19.40	79.4	148	2.5	1.5	1.8	
EL-C869	C869 Salem (WCBSCo)040020,4/05	10392	33.13	15.65	19.60	79.9	132	0.5	1.5	2.0	
5845	RZM 845 (C1,C2)mmaa x A	10434	31.84	16.42	20.92	78.5	123	1.8	2.3	2.3	
Monogerm, Rz2											
5812M	Inc. 3812-2,-5,-6,-42 (A,aa)mm	8599	27.83	15.42	19.88	77.6	116	1.5	2.8	2.5	

(cont.)

Variety	Description	Acre Yield		Soluble Solids	RJAP	Beets/ 100'	Powdery Mildew		Foliar Color		
		Sugar	Beets				Mean	Score	Color	Seg	
		Lbs	Tons				%	%			
Monogerm, S ^f , Aa populations, Rz2 (cont.)											
5812H5	2833-5HO x Inc. 3812-2,-5,-6,-42 (A,aa)mm, F1 (Rz1Rz1cms x Rz2Rz2)	11769	34.86	16.90	79.8	123	0.5	2.0	1.5		
5819H5	2833-5HO x " "	10783	32.84	16.42	77.9	132	1.3	1.5	1.3		
5819m	Inc. 3819-26,-27,-28 (A,aa)mm	6746	22.77	14.85	79.0	130	0.5	2.8	3.3		
5848-1m	RZM 2848-1mm	7502	23.58	15.92	78.0	132	3.8	3.5	3.8		
5848-1H0	RZM 2848-1H5 x RZM 2848-1mm	9909	30.22	16.40	79.0	141	3.0	3.0	2.8		
Monogerm, CTR x %S, Rz1											
5849(Iso)m	Inc. 4849-# (C)mm	9480	29.22	16.23	78.2	116	0.5	1.5	1.5		
5843-10HO	4843HO x 3843-10 (A,aa)	9706	30.22	16.05	77.4	134	0.8	2.5	3.0		
5843-10CT	Inc. 3843-10 (A,aa)mm	8536	26.40	16.17	78.7	143	0.5	2.5	3.0		
N569mHs1	Inc. N469-# (C)g, N469(g)mm	8198	26.40	15.52	76.1	132	0.5	2.3	1.8		
4850M	Inc. 2252-2MmAa (A,aa)	10696	31.23	17.13	77.5	127	0.0	2.8	2.5		
FC monogerm lines and populations											
05-FC1023H5	2833-5HONB x FC20021023	11836	35.06	16.88	78.5	127	0.8	1.8	2.0		
05-FC1023M	FC20021023aa x A	10354	31.84	16.25	75.3	132	2.5	2.5	3.0		
05-FC1023M	Inc. FC20021023 (A,aa)M	9518	30.43	15.65	75.1	134	1.3	2.5	2.8		
05-FC1023H50	C790-15CMS x FC20021023	9937	31.92	15.55	78.9	132	0.8	2.3	2.5		
05-FC1030-15	RZM 03-FC1030-15 (A,aa)M	10045	30.83	16.33	76.3	136	0.3	3.5	3.8		
05-FC1030-16	RZM 03-FC1030-16 (A,aa)M	9606	30.23	15.82	79.0	134	1.5	3.3	3.3		
03-FC1014-22	Inc. 01-FC1014-22 (A,aa)	7869	24.18	16.33	76.1	130	1.5	2.3	2.5		
03-FC123-31	Inc. 01-FC123-31 (A,aa)	10166	30.83	16.50	81.0	150	2.8	3.0	2.8		
20051007HOMS	Rhizoc. 03-FC1014-22 (FC201 sib)	9642	30.02	16.08	74.9	136	0.8	2.3	2.3		
20051007HOPF	Rhizoc. 03-FC1014-22 (FC201 sib)	6915	21.16	16.38	76.2	132	0.3	3.3	3.3		
20051007H01-X	C833H5CMS x 01-FC1014-22	9896	29.22	16.95	77.3	139	0.8	1.8	2.5		

(cont.)

Variety	Description	Acre Yield		Soluble Solids	Beets/ 100'	Powdery Foliar		Seg	
		Sugar	Beets			RJAP	Mildew		Color
		Lbs	Tons			%	No.		Mean
Retest of monogerm lines as F1 hybrids (mmRz1Rz1cms x CTR, mm, O-type)									
4842-226H5	2833-5HOB x 2842-226 (T-O)mm	9893	28.41	17.38	76.5	120	1.0	1.8	2.0
4842-256H5	2833-5HOB x 2842-256 (T-O)mm	9845	29.62	16.63	79.5	118	2.0	1.5	1.8
4842-262H5	2833-5HOB x 2842-262 (T-O)mm	9488	28.21	16.77	78.8	123	1.8	1.0	1.8
4837-6-203H5	2833-5HOB x 2837-6-203 (T-O)mm								
4836-13H5	2833-5HOB x RZM, T-O 2836-13-# (C)mm	11115	33.65	16.52	79.4	111	2.5	1.3	1.3
		13259	38.28	17.30	78.7	127	1.8	2.3	2.3
Mean		8935.8	27.65	16.02	77.9	131.0	1.2	2.5	2.6
LSD (.05)		1975.1	6.01	0.9	2.6	21.0	1.3	0.9	1.0
C.V. (%)		15.8	15.55	4.2	2.4	11.5	78.6	24.3	26.3
F value		11.1**	9.27**	7.6**	2.7**	1.2NS	3.7**	8.6**	8.2**

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

TEST 606. MONOGERM S₁ PROGENY TEST FROM POPN-849 FOR %SUGAR & SUGAR YIELD UNDER RHIZOMANIA, SALINAS, CA, 2006

128 entries x 3 reps., sequential
1-row plots, 11 ft. long

Planted: May 5, 2006
Harvested: Nov. 15-17, 2006

Variety	Description	Acre Yield		Beets		Sucrose %	Soluble Solids		RJAP %	Beets/ 100'	Powdery Foliar Mildew		Foliar Color		Seg
		Sugar Lbs	Tons	%	%		No.	Mean			Score	Mean	Score		
Checks															
2833-5 (Sp)	RZM,T-O 1833-5-# (C)mmaa x A	10148	28.43	17.93	21.40	83.8	124	0.7	1.7	0.7	1.7	1.7	1.7	1.7	1.7
EL-C869	C869 Salem (WCBSCO) 040020, 4/5	12375	37.20	16.60	19.33	85.8	148	1.7	1.7	1.7	1.7	1.7	1.7	2.0	2.0
4842 (Iso)	RZM-# 2842 (A,aa), C842	9886	29.48	16.80	20.33	82.7	139	2.0	2.0	2.0	2.0	2.0	2.0	1.3	1.3
3849m	RZM 2251-2255 (C)mmaa x A	12562	34.09	18.43	20.70	89.0	136	0.7	1.3	0.7	1.3	1.3	1.3	1.7	1.7
5849m	Inc. 4849-# (C)mm (A,aa)	11795	34.94	16.87	20.30	83.1	152	0.7	1.3	0.7	1.3	1.3	1.3	1.7	1.7
4851	Inc. 2252-5MmAA	11439	30.98	18.47	22.03	83.8	142	0.0	2.3	0.0	2.3	2.3	2.3	2.3	2.3
4850	Inc. 2252-2MmAA	10241	27.46	18.63	22.37	83.3	130	0.0	3.0	0.0	3.0	3.0	3.0	2.3	2.3
2833-5NB	NB-RZM-# 0833-5 (A,aa), C833-5	10122	28.43	17.83	21.57	82.7	133	0.0	1.7	0.0	1.7	1.7	1.7	1.7	1.7
4850	Inc. 2252-2MmAA	12075	31.54	19.17	22.67	84.6	127	0.3	3.0	0.3	3.0	3.0	3.0	2.7	2.7
4851	Inc. 2252-5MmAA	11933	33.52	17.80	21.47	82.9	130	0.0	2.0	0.0	2.0	2.0	2.0	2.0	2.0
S ₁ 's from 4850mm⊗, F ₃ (CZ25-9Mmaa x C833-5), (11 S ₁ progenies)															
5850-#s	range	9220-	24.19-	16.20-	19.48-	77.3-	103-	0.0-	2.0-	0.0-	2.0-	1.7-	1.7-	1.7-	1.7-
		11551	30.34	20.03	23.00	88.3	130	0.3	3.7	0.3	3.7	3.7	3.7	3.7	3.7
mean		9946	27.20	18.31	21.92	8.36	116	0.0	3.0	0.0	3.0	3.0	3.0	2.7	2.7
S ₁ 's from 4849mm⊗, F ₃ (%SMmaa x mm), (100 S ₁ progenies)															
5849-#s	range	5477-	15.14-	14.33-	17.70-	74.4-	64-	0.0-	1.3-	0.0-	1.3-	1.0-	1.0-	1.0-	1.0-
		12271	36.07	20.20	23.83	88.4	152	4.0	4.7	4.0	4.7	4.7	4.7	4.7	4.7
mean		9308.7	26.99	17.29	20.83	83.1	120	0.8	2.8	0.8	2.8	2.8	2.8	2.5	2.5
Mean															
LSD (.05)		9564.0	27.42	17.48	21.01	83.2	121.1	0.7	2.8	0.7	2.8	2.8	2.8	2.5	2.5
C.V. (%)		2181.4	6.07	1.15	1.13	3.8	28.5	1.3	1.1	1.3	1.1	1.1	1.1	1.0	1.0
F value		14.2	13.76	4.09	3.33	2.8	14.7	113.5	24.7	113.5	24.7	24.7	24.7	24.4	24.4
		3.9**	4.25**	6.31**	9.75**	3.0**	2.5**	3.6**	5.1**	3.6**	5.1**	5.1**	5.1**	5.4**	5.4**

(cont.)

Variety	Acre Yield		Description	Soluble		Beets/		Powdery Foliar	
	Beets			100'		Foliar			
	Sugar	Sucrose		RJAP	Mildew	Color	Seg		
	Lbs	Tons		%	Mean	Score	Score		

Notes: Part of test was harvested by machine under very muddy conditions. Two days later, the remainder of the test was harvested by hand.

In a curly top test at Kimberly, ID run and evaluated by Anne Gillen, for each set of S₁s, the low and high disease score, respectively, was: 5849-#s ranged from 2.4 to 6.8 (mean = 4.7, std dev = 1.4); 5850-#s ranged from 3.0 to 5.9 (mean = 4.7, std dev = 1.7); and 5851-#s ranged from 3.4 to 5.8 (mean = 4.6, std dev = 1.2).

In greenhouse type-0 testing, S₁s from 4850 were mostly non-type-0. S₁s from 4851 were mostly type-0. S₁s from 4849 were mostly non-type-0 or segregated for type-0.

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

TEST 2006. EVALUATION OF HYBRIDS WITH PROGENY LINE POLLINATORS UNDER RHIZOMANIA, SALINAS, CA, 2006

48 entries x 8 reps., RCB(e)
1-row plots, 22 ft. long

Planted: May 4, 2006
Harvested: October 2-3, 2006

Variety	Description	Acre Yield		Sucrose %	Soluble Solids %	Beets/ 100'	RJAP %	Foliar	
		Sugar	Beets					Color ¹	Foliar
		Lbs	Tons					Score	Seq ² Score
Checks									
Beta 4430R	Betaseed, 8-21-03/	10913	33.62	16.24	19.61	136	82.8	1.4	1.6
Phoenix	Holly Hybrids, 9-12-03/	8537	27.89	15.27	18.81	123	81.2	1.3	1.5
HH142	Holly Hybrids, 3/10/06	10146	32.30	15.66	19.41	124	80.7	1.4	1.1
Beta 4309R	Betaseed, 9/05	11990	36.04	16.63	20.41	140	81.5	1.3	1.1
S ₁ progeny from R278H23 = CZ25-9aa x C78/3									
R578H23-308H50	C790-15CMS x R378H23-308	9719	30.60	15.90	19.90	127	79.9	2.1	2.3
R578H23-312H50	C790-15CMS x R378H23-312	10101	31.18	16.19	20.10	133	80.5	2.3	2.6
R578H23-320H50	C790-15CMS x R378H23-320	10133	30.89	16.40	20.55	136	79.8	2.5	2.9
R578H23-325H50	C790-15CMS x R378H23-325	10345	31.91	16.23	20.55	125	78.9	2.3	2.6
S ₁ progeny from R278H40 = C930-35aa x C78/3									
R578H40-306H50	C790-15CMS x R378H40-306	9812	29.86	16.42	20.80	130	79.0	2.3	2.1
R578H40-312H50	C709-15CMS x R378H40-312	11043	33.04	16.69	20.99	132	79.5	1.9	2.3
R578H40-324H50	C790-15CMS x R378H40-324	10811	32.80	16.45	20.64	136	79.7	2.0	2.6
R578H50	C790-15CMS x R378, (C78/3)	10068	32.10	15.69	19.96	123	78.6	2.1	2.4
S ₁ progeny from Y291H23 = CZ25-9aa x Y191									
Y591H23-311H50	C790-15CMS x Y391H23-311	9479	28.43	16.65	20.44	131	81.5	2.5	3.0
Y591H23-313H50	C790-15CMS x Y391H23-313	10695	31.18	17.15	21.54	132	79.7	1.5	1.6
Y591H23-314H50	C790-15CMS x Y391H23-314	11868	35.90	16.52	21.02	132	78.6	1.8	1.5
Y591H23-322H50	C790-15CMS x Y391-H23-322	9287	28.89	16.05	20.25	137	79.3	1.8	2.1
S ₁ progeny from Y291H41 = C941aa x Y191									
Y591H41-301H50	C790-15CMS x Y391H41-301	10180	31.29	16.27	20.55	128	79.2	1.3	1.6
Checks									
Y595H50	C790-15CMS x RZM Y95 (C)	10279	32.28	15.93	20.02	137	79.5	1.6	2.0
5944H50	C790-15CMS x 944 (C)	10359	31.06	16.69	21.06	122	79.2	1.9	2.1
5930-35H50	C790-15CMS x 2930-35, (C930-35)	10874	32.60	16.67	21.15	127	78.8	1.4	1.6

(cont.)

Variety	Description	Acre Yield		Sucrose %	Soluble Solids %	RJAP %	Beets/ 100'	Foliar Color ¹ Score	Foliar Seq ² Score
		Sugar	Beets						
		Lbs	Tons						
<u>S₁ progeny from 2943-9 = CZ25-9aa x 943</u>									
5943-9-6H50	C790-15CMS x 3943-9-6	10471	31.41	16.65	21.04	79.2	122	1.8	2.1
5943-9-7H50	C790-15CMS x 3943-9-7	11544	35.45	16.29	20.69	78.8	129	1.1	1.5
<u>S₁ progeny from 2943-19 = C930-19aa x 943</u>									
5943-19-312H50	C790-15CMS x 3943-19-312	11070	33.99	16.29	20.54	79.3	137	1.1	1.3
<u>S₁ progeny from 2943-35 = C930aa x 943</u>									
5943-35-301H50	C790-15CMS x 3943-35-302	10617	31.36	16.92	21.24	79.7	128	1.1	1.3
5943-35-318H50	C790-15CMS x 3943-35-318	10668	32.22	16.58	20.60	80.5	132	2.3	2.9
<u>S₁ progeny from 2930-19 = C930-19</u>									
5930-19-312H50	C790-15CMS x 3930-19-312	11537	34.73	16.61	20.81	79.8	133	1.3	1.4
5930-19-325H50	C790-15CMS x 3930-19-325	11284	35.58	15.84	19.71	80.4	136	1.1	1.0
<u>S₁ progeny from 2930-35 = C930-35</u>									
5930-35-312H50	C790-15CMS x 3930-35-312	10238	29.74	17.20	21.91	78.5	128	1.8	2.3
<u>S₁ progeny from Z225-9 = CZ25-9</u>									
Z525-9-307H50	C790-15CMS x Z325-9-307	10067	30.31	16.60	20.92	79.4	126	2.0	2.1
Z525-9-308H50	C790-15CMS x Z325-9-308	11241	34.04	16.52	20.73	79.8	126	1.9	2.4
<u>S₁ progeny from 2936-10</u>									
5936-10-310H50	C790-15CMS x 3936-10-310	12147	37.14	16.35	20.34	80.4	140	1.0	1.0
<u>S₁ progeny from 2936-16</u>									
5936-16-313H50	C790-15CMS x 3936-16-313	11087	31.89	17.38	21.76	79.8	137	1.4	1.8
<u>S₁ progeny from CR009-1 & CR10-2, CR11-7, & CR11-88</u>									
CR509-1-312H50	C790-15CMS x CR309-1-312	10089	31.37	16.08	20.76	77.4	132	1.0	1.0
CR510-2-305H50	C790-15CMS x CR310-2-305	11006	35.35	15.63	20.10	77.8	132	1.4	1.6

TEST 2006. EVALUATION OF HYBRIDS WITH PROGENY LINE POLLINATORS UNDER RHIZOMANIA, SALINAS, CA, 2006

(cont.)

Variety	Description	Acre Yield		Sucrose %	Soluble Solids %	RJAP %	Beets/ 100'	Foliar Color ¹	Foliar Seq ²
		Sugar	Beets						
		Lbs	Tons						
S ₁ progeny from CR009-1 & CR10-2, CR11-7, & CR11-88 (cont.)									
CR511-7-302H50	C790-15CMS x CR311-7-303, -304	10782	33.77	15.97	20.25	78.9	134	1.3	1.0
CR511-88H50	C790-15CMS x CR311-88, (CR11-88)	10772	33.81	15.91	19.88	80.1	128	1.8	1.9
Experimental hybrids and retests									
5933H50	C7990-15CMSx 933 (C)	10487	32.46	16.16	20.20	80.0	126	1.4	1.6
05-FC1036H50	C790-15CMS x RZM 04-FC1028, 37, 38	9853	31.97	15.41	19.23	80.2	138	2.3	2.6
05-FC1030-15H50	C790-15CMS x 03-FC1030-15	9627	29.96	16.08	20.25	79.4	128	2.1	2.6
05-FC1030-16H50	C790-15CMS x 03-FC1030-16	9869	30.94	15.95	19.77	80.7	130	2.5	2.8
05-FC1022H50	C790-15CMS x RZM-ER-8 20031022	9386	28.93	16.17	20.56	78.7	128	1.9	2.1
05-FC1018H50	C790-15CMS x RZM-CR-8 20031018	9592	30.12	15.89	19.95	79.6	135	2.8	3.1
05-FC1019H50	C790-15CMS x RZM-CR-8 20031019	10604	34.94	15.15	19.06	79.5	140	2.1	2.5
Y590-40H50	C790-15CMS x Y390-40	11041	33.51	16.46	20.54	80.2	130	1.1	1.3
RR480-6H50	C790-15CMS x R280-6	10819	33.60	16.08	20.02	80.3	126	1.1	1.3
4952-205H50	C790-15CMS x 2952-205, (CZ25 x Y90)	11237	34.00	16.54	20.55	80.5	130	1.9	1.8
4954-210H50	C790-15CMS x 2954-210, (C941 x Y90)	11007	32.64	16.86	21.25	79.4	129	1.4	1.3
4953-209H50	C790-15CMS x 2953-209, (C931 x Y90)	10386	31.67	16.39	20.67	79.3	135	1.8	2.0
Mean		10524.3	32.31	16.3	20.4	79.7	131.0	1.7	1.9
LSD (.05)		850.8	2.4	0.5	0.6	1.5	10.9	0.5	0.6
C.V. (%)		8.2	7.6	3.2	3.0	2.0	8.4	26.9	30.4
F value		5.8**	6.0**	6.6**	8.9**	2.5**	1.6NS	8.5**	8.7**

C970-15CMS = mm, rzzz. See test 906 for performance of pollinators per se.

¹Foliar color due to rhizomania. 1 = all normal green; 2 = +25% yellowish; 3 = +50% yellowish; 4 = +75% yellowish; 5 = 100% yellowish.

²Foliar segregation pattern for rhizomania. 1 = all green; 2 = +25% yellowish (1-25%); 3 = 50:50 green: yellowish; 4 = +75% yellowish (75-99%); 5 = all yellowish.

TEST 1706. EVALUATION OF HYBRIDS WITH R₂2 AND OTHER UNDER RHIZOMANIA CONDITIONS, SALINAS, CA, 2006

24 entries x 8 reps., RCB(e)
1-row plots, 22 ft. long

Planted: May 4, 2006
Harvested: September 28, 2006

Variety	Description	Acre Yield		Sucrose %	Soluble Solids %	RJAP %	Beets/ 100'	Foliar	
		Sugar	Beets					Color ¹	Foliar
		Lbs	Tons					Score	Seq ²
<u>Checks</u>									
Phoenix	Holly Hybrids, 3-10-06	11354	40.52	14.06	17.96	78.2	126	1.1	1.8
HXR3	Holly Hybrids, 3-24-06	12080	41.21	14.59	18.84	77.4	131	1.3	1.6
<u>Differential Checks</u>									
Beta 4430R	Betaseed, 3-28-06 Rz1	12617	41.15	15.34	19.70	77.9	148	1.4	1.5
Beta G017R	Betaseed, 3-28-06 Rz2	12504	39.84	15.70	19.99	78.5	130	1.1	1.6
Roberta	Betaseed, 3-20-06 rzrz	6381	26.43	12.04	15.96	75.4	127	4.3	4.5
Angelina	Betaseed, 3-20-06 Rz1+Rz2	13310	42.78	15.54	19.94	77.8	128	1.1	1.1
<u>Company Hybrids</u>									
HXR1	Holly Hybrids, 3-24-06	11835	35.18	16.83	20.81	80.8	146	1.1	1.6
HXR2	Holly Hybrids, 3-24-06	12503	37.14	16.83	21.09	79.8	136	1.1	2.0
36K5308	Betaseed, 3-20-06	12469	40.55	15.30	19.41	78.8	136	1.4	1.4
<u>Experimental hybrids</u>									
Y591H50	C790-15CMS x IRZM- $\frac{1}{2}$ Y391	10880	35.67	15.26	18.95	80.6	134	1.8	2.3
R578H5	C833-5CMS x R378, (C78/3)	11806	37.28	15.86	20.06	79.1	126	1.1	1.4
Y577H5	C833-5CMS x IRZM Y277, Y375	11739	36.86	15.90	20.07	79.2	120	1.0	1.5
Y595H5	C833-5CMS x RZM Y95 (C)	11816	38.55	15.38	20.00	76.9	128	1.0	1.4
P531CTH5	C833-5CMS x P431CT, (CP09CT)	12168	37.76	16.01	20.31	78.8	128	1.1	1.5
R522H5	C833-5CMS x IRZM R522 (Sp)	10850	34.56	15.70	19.94	78.7	110	1.0	1.6
R521H5	C833-5CMS x IRZM- $\frac{1}{2}$ R321,R021	12249	39.26	15.60	19.98	78.1	125	1.0	1.5
R539H5	C833-5CMS x R039, (C39R)	11877	38.58	15.41	19.51	79.0	122	1.5	1.8
R525H5	C833-5CMS x IRZM- $\frac{1}{2}$ R325,...	11243	36.25	15.61	20.23	77.1	115	1.3	1.4
R540H5	C833-5CMS x IRZM- $\frac{1}{2}$ R940,...	11382	37.19	15.27	19.80	77.0	132	1.4	1.5
R541/2H5	C833-5CMS x IRZM R641,R642	9901	32.63	15.21	19.73	77.1	126	1.1	1.6

TEST 1706. EVALUATION OF HYBRIDS WITH R₂2 AND OTHER UNDER RHIZOMANIA CONDITIONS, SALINAS, CA, 2006

(cont.)

Variety	Description	Acre Yield		Sucrose		Soluble Solids		RJAP		Beets/ 100'		Foliar Foliar	
		Sugar	Beets	%		%		%		No.		Color ¹	Seq ²
		Lbs	Tons									Score	Score
<u>Experimental hybrids (cont.)</u>													
R524-302H5	C833-5CMS x R324-302, -306	11633	36.46		15.95		20.36		78.3		119	1.1	1.6
R525-301H5	C833-5CMS x R525-301, -302	11191	35.12		15.90		20.40		77.9		123	1.4	1.5
R524-2/3H5	C833-5CMS x R324-213, -215, -222, -223												
		11489	36.99		15.56		20.15		77.2		113	1.1	1.3
R537-302H5	C833-5CMS x R337-302	11601	35.13		16.50		21.00		78.6		130	1.0	1.5
Mean		11536.7	37.21		15.47		19.76		78.3		127.5	1.3	1.7
LSD (.05)		1553.3	4.36		0.85		0.56		3.5		12.0	0.4	0.5
C.V. (%)		13.7	11.90		5.57		2.87		4.5		9.6	27.9	30.6
F value		5.5**	4.63**		9.70**		27.65**		1.0NS		4.3**	24.7**	12.5**

NOTES: Normal BNYVV at Spence Field. Moderate rhizomania. See tests 4206 thru 4506 for performance under IV-BNYVV at Hartnell Field. C790-15CMS = mm,rzrz. C833-5CMS = mm,Rz1Rz1.

¹Foliar color due to rhizomania. 1 = all normal green; 2 = +25% yellowish; 3 = +50% yellowish; 4 = +75% yellowish; 5 = 100% yellowish.

²Foliar segregation pattern for rhizomania. 1 = all green; 2 = +25% yellowish (1-25%); 3 = 50:50 green: yellowish; 4 = +75% yellowish (75-99%); 5 = all yellowish.

TEST 2106. RHIZOMANIA EVALUATION OF HYBRIDS OF SOURCES OF RESISTANCE, SALINAS, CA, 2006

Planted: May 4, 2006
Harvested: October 16, 2006

12 entries x 8 reps., RCB
1-row plots, 22 ft. long

Variety	RZM Resist	Description	Acre Yield		Sucrose %	Soluble Solids %	RJAP %	Beets/ 100' No.	Foliar Color ¹		Foliar Rot %
			Sugar Lbs	Beets Tons					Seq ² Score	Seq ² Score	
USH11	zzrz	susc. check	8977	30.12	14.88	18.70	79.6	126	3.6	3.8	0.6
R540H5	R ₂ 1,C79-#1's	C833-5CMS x IRZM-% R940,...	12115	36.08	16.80	21.42	78.4	124	1.3	1.3	0.0
R525H5	R ₂ 1,C79-2,-3; WB41,42	C833-5CMS x IRZM-% R325,R324,...	12711	37.85	16.80	21.61	77.7	114	1.5	1.3	0.0
R541/2H5	R ₂ 2,C79-10,11; WB169,258	C833-5CMS x IRZM-% R641,R642	11710	35.51	16.51	20.95	78.8	116	1.1	1.0	0.0
<u>Differential Checks</u>											
Beta G017R	R ₂ 2	Betaseed, 3/28/06	14002	39.08	17.90	21.91	81.7	123	1.4	1.5	0.4
Beta 4430R	R ₂ 1	Betaseed, 3/28/06	14267	41.35	17.24	20.96	82.2	138	2.4	1.6	0.5
Robertia	zzrz	Betaseed, 3/20/06	9684	32.23	14.95	18.34	81.5	135	4.1	4.1	1.2
Angelina	R ₂ 1,R ₂ 2	Betaseed, 3/20/06	13602	38.55	17.64	21.75	81.1	128	1.4	1.3	0.0
<u>Experimental Hybrids</u>											
R521H5	R ₂ 1, B7m	C833-5CMS x IRZM-% R321	12871	38.59	16.67	21.34	78.1	127	1.4	1.1	2.4
R539H5	R ₂ 1, Q	C833-5CMS x R039	12057	35.54	16.98	21.21	80.0	109	1.4	1.3	0.0
Y577H5	R ₂ 1, B7m	C833-5CMS x IRZM Y277	12047	35.45	17.01	21.71	78.4	116	1.4	1.1	0.0
R537-302H5	R ₂ 1, C79-9; WB151	C833-5CMS x R337-302	13121	37.30	17.60	22.41	78.5	127	1.5	1.8	0.0
Mean			12263.8	36.47	16.75	21.03	79.7	123.6	1.9	1.8	0.4
ISD (.05)			1150.9	3.17	0.53	0.57	1.8	14.9	0.6	0.5	1.6
C.V. (%)			9.4	8.72	3.20	2.74	2.2	12.1	30.6	26.5	373.7
F value			15.2**	7.43**	25.43**	37.27**	6.4**	2.6**	24.3**	40.9**	1.7NS

Notes: Normal BNYVV at Spence Field. Moderate rhizomania. See tests 4206 thru 4506 for performance under IV=BNYVV.

See tests 1606, et al. for Foliar color and Foliar segregation explanations.

TEST 1806. EVALUATION OF TOPCROSS & POPULATION HYBRIDS UNDER RHIZOMANIA CONDITIONS, SALINAS, CA, 2006

24 entries x 8 reps., RCB(e)
1-row plots, 22 ft. long

Planted: May 4, 2006

Harvested: September 28, 2006

Variety	Description	Acre Yield		Sucrose %	Soluble Solids %	RJAP %	Beets/ 100'	Foliar Color ¹	Foliar Seq ²
		Sugar	Beets						
		Lbs	Tons						
<u>Checks</u>									
Beta 4430R	Betaseed, 8-21-05	12201	38.46	15.79	19.15	82.4	128	1	2
Phoenix	Holly Hybrids, 3-10-06	10310	35.36	14.64	18.33	79.9	131	2	2
<u>Topcross hybrid checks</u>									
R578H50	C790-15CMS x R378, (C78/3)	10407	34.85	14.90	18.90	78.6	130	3	2
R578H5	C833-5CMS x R378, (C78/3)	11504	36.49	15.75	20.11	78.3	119	1	2
<u>Topcross hybrids</u>									
R578H33	4842-226H5 x R378	10826	35.64	15.18	19.89	76.3	126	2	2
R578H34	4842-256H5 x R378	11273	36.26	15.57	19.46	80.0	131	2	2
R578H35	4842-262H5 x R378	11114	35.37	15.68	19.86	78.9	127	1	1
R578H36	4836-13H5 x R378	11219	36.30	15.51	20.06	77.3	115	2	2
<u>Population hybrids</u>									
R578H37	4837-6-203H5 x R378	10980	35.16	15.56	19.40	80.2	118	2	2
R578H51	4851H5 x R378	11056	35.09	15.76	20.39	77.3	120	1	2
R578H52	4850H5 x R378	11293	35.15	16.05	20.09	79.9	118	2	2
R578H99	N469HO (g) x R378	9511	31.43	15.13	19.49	77.7	123	1	2
<u>Population hybrids</u>									
R578H42	3842HO (C842CMS) x R378	10552	36.55	14.45	19.25	75.1	131	2	2
R578H70	3869HO (C869CMS) x R378	10804	35.82	15.07	18.83	80.1	127	2	2
R578H91	4891HO (C890-1CMS) x R378	11571	36.43	15.88	20.11	78.9	122	2	2
5933H5	C833-5CMS x 933 (C)	11982	37.73	15.88	19.94	79.6	128	1	2
<u>Population hybrids</u>									
5944H50	C790-15CMS x 944 (C)	10547	34.53	15.35	19.66	78.1	122	2	2
5944H5	C833-5CMS x 944 (C)	11389	35.94	15.89	20.36	78.0	128	1	1
5944H49	4849mmmaa x 944 (C)	10186	32.27	15.77	20.04	78.7	129	2	2
5944H51	4851H5 x 944 (C)	12032	36.38	16.54	20.81	79.5	120	2	2
<u>Population hybrids</u>									
5944H52	4850H5 x 944 (C)	12007	37.32	16.06	20.84	77.1	122	2	2
05-FC1036H5	C833-5CMS x 04-FC1028, 1037, 1038	11507	37.21	15.48	20.05	77.2	123	2	2

(cont.)

Variety	Description		Acre Yield		Sucrose	Soluble Solids	RJAP	Beets/ 100'	Foliar Color ¹	Foliar Seq ²
	Sugar	Beets	Tons							
	Lbs			%	%	No.	Score	Score		
Population hybrids (cont.)										
05-FC1030-15H5	C833-5CMS x 03-FC1030-15		12296	37.11	16.57	20.77	79.8	116	2	2
05-FC1030-16H5	C833-5CMS x 03-FC1030-16		11859	36.38	16.25	20.34	79.9	122	2	2
Mean	11184.5	35.80			15.61	19.84	78.7	123.8	1.6	1.8
LSD (.05)	1223.4	3.51			0.76	0.59	3.1	10.6	0.5	0.6
C.V. (%)	11.1	9.94			4.95	3.01	4.1	8.7	32.9	32.2
F value	2.6NS	1.52NS			3.79**	9.31**	1.9*	1.7*	2.7**	1.9*

C790-15CMS = mm, rzrz. C833-5CMS = mm, Rz1Rz1. 944 (C) = Cycle1, Syn1 S1 progeny aa x A.

H5 = C833-5CMS x T-O.

¹Foliar color due to rhizomania. 1 = all normal green; 2 = +25% yellowish; 3 = +50% yellowish; 4 = +75% yellowish; 5 = 100% yellowish.

²Foliar segregation pattern for rhizomania. 1 = all green; 2 = +25% yellowish (1-25%); 3 = 50:50 green: yellowish; 4 = +75% yellowish (75-99%); 5 = all yellowish.

TEST 1306. EVALUATION OF C78/3 HYBRIDS SELECTED FOR HIGH %SUGAR, SALINAS, CA, 2006

12 entries x 8 reps., RCB
1-row plots, 22 ft. long

Planted: May 4, 2006
Harvested: October 16, 2006

Variety	Description	Acre Yield		Sucrose %	Soluble Solids %	RJAP %	Beets/ 100'	Foliar Foliar	
		Sugar	Beets					Color	Seg
		Lbs	Tons					Score	Score
<u>Checks</u>									
Beta 4430R	Betaseed	13667	40.31	17.00	20.79	81.8	144	2.5	2.9
Roberta	Betaseed, pelleted	7729	26.26	14.60	18.17	80.3	130	4.5	4.8
<u>Check for Experimental Hybrids</u>									
R578H50	C790-15CMS x R378 (C78/3)	11207	33.86	16.55	20.65	80.1	130	2.6	2.9
<u>Hybrids with selections from CZ25-9</u>									
Z525-9-308H50	C790-15CMS x Z325-9-308	12817	37.29	17.21	21.41	80.4	139	2.3	2.5
<u>Hybrids with selection from C930-35</u>									
5930-35-312H50	C790-15CMS x 3930-35-312	11781	32.65	18.05	22.74	79.4	138	2.5	2.9
<u>Hybrids with selection from C930-19</u>									
5930-19-312H50	C790-15CMS x 3930-19-312	13048	38.53	16.93	20.98	80.7	132	1.4	1.4
<u>Hybrids with selections from CZ25-9 x C78/3</u>									
R578H23-312H50	C790-15CMS x R378H23-312	11530	34.06	16.90	21.05	80.3	136	3.3	3.8
R578H23-325H50	C790-15CMS x R378H23-325	11904	35.07	16.96	21.33	79.6	132	2.5	2.8
<u>Hybrids with selections from C930-35 x C78/3</u>									
R578H40-306H50	C790-15CMS x R378H40-306	11355	33.51	16.95	21.26	79.7	135	3.3	3.3
R578H40-312H50	C790-15CMS x R378H40-312	12649	36.54	17.31	21.61	80.1	136	2.1	2.5
<u>Hybrids with selections from MM&S x MM&S</u>									
5943-9-7H50	C790-15CMS x 3943-9-7	13123	38.83	16.91	21.25	79.6	132	1.6	1.8
5943-35-318H50	C790-15CMS x 3943-35-318	12719	37.31	17.04	20.99	81.3	131	3.4	3.9
Mean		11960.9	35.35	16.87	21.02	80.3	134.6	2.7	2.9
LSD (.05)		1196.2	3.55	0.53	0.73	1.6	10.2	0.6	0.7
C.V. (%)		10.1	10.08	3.17	3.51	2.0	7.6	23.7	22.7
F value		13.2**	8.77**	17.84**	15.97**	1.6NS	1.4NS	14.4**	15.2**

(cont.)

Variety	Description	Acre Yield		Sucrose	Soluble Solids	RJAP	Beets/ 100'	Foliar Foliar	
		Sugar	Beets					Color	Seg
		Lbs	Tons	%	%	%	No.	Score	Score

C790-15CMS = mm, r2rz.

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

TEST 2206. EVALUATION OF Y91 HYBRIDS SELECTED FOR HIGH %SUGAR, SALINAS, CA, 2006

12 entries x 8 reps., RCB
1-row plots, 22 ft. long

Planted: May 4, 2006
Harvested: October 16, 2006

Variety	Description	Acre Yield		Soluble		Beets/		Foliar		Root
		Sugar	Beets	Sucrose	Solids	100'	Color	Seg	Rot	
		Lbs	Tons	%	%	No.	Score	Score	%	
Checks										
Roberta	Betaseed, pelleted	5160	19.45	13.09	16.16	80.9	127	3.9	4.4	3.4
Beta 4430R	Betaseed	11322	35.35	16.01	19.55	81.9	134	1.8	2.6	0.4
Experimental Hybrid Checks										
Y591H50	C790-15CMS x IRZM-% Y391	9990	31.30	15.93	19.79	80.5	120	1.8	1.9	5.2
Z525-9-307H50	C790-15CMS x Z325-9-307	10972	32.65	16.81	21.25	79.1	124	2.3	2.5	0.4
Hybrids with selections from Mmaa x Y91										
Y591H41-301H50	C790-15CMS x Y391H41-301	11104	32.92	16.83	20.86	80.7	116	1.3	1.5	0.5
Y591H23-311H50	C790-15CMS x Y391H23-311	8979	27.25	16.44	20.94	78.5	128	2.8	3.3	0.0
Y591H23-313H50	C790-15CMS x Y391H23-313	9916	28.76	17.25	21.67	79.6	120	1.4	1.9	1.4
Y591H23-314H50	C790-15CMS x Y391H23-314	10769	32.46	16.60	20.90	79.4	126	1.5	1.8	2.2
Y591H23-322H50	C790-15CMS x Y391H23-322	8957	26.90	16.65	20.59	80.9	123	2.6	2.9	4.7
Experimental hybrids										
Y590-40H50	C790-15CMS x Y390-40	9873	29.87	16.55	21.00	78.8	119	1.8	2.0	0.9
Y595H50	C790-15CMS x Y95 (C)	9706	29.91	16.34	20.25	80.7	119	1.9	2.3	1.4
5944H50	C790-15CMS x popn-944 (C)	10199	30.48	16.71	21.01	79.6	120	2.1	2.5	0.4
Mean										
LSD (.05)		9745.4	29.77	16.27	20.33	80.1	123.0	2.1	2.5	1.8
C.V. (%)		1720.5	5.11	0.56	0.64	1.6	12.9	0.6	0.7	4.3
F value		17.7	17.24	3.47	3.16	2.0	10.5	29.8	27.3	244.4
		7.2**	5.01**	28.38**	40.42**	3.3**	1.2NS	11.3**	11.2**	1.4NS

(cont.)

Variety	Description	Acre Yield		Soluble Solids	RJAP	Beets/ 100'	Foliar		Foliar Root		
		Sugar	Beets				Color	Seg Rot			
		Lbs	Tons				%	No.	Score	Score	%

C790-15CMS = mm, rrrz.

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

TEST 1706-2. HYBRIDS WITH RESISTANCE FROM C28 AND OTHERS, SALINAS, CA, 2006

6 entries x 8 reps., RCB
1-row plots, 22 ft. long

Planted: May 4, 2006
Harvested: October 06, 2006

Variety	Description	Acre Yield		Sucrose %	Soluble Solids %	RJAP %	Beets/ 100'	Foliar Foliar	
		Sugar Lbs	Beets Tons					Color ¹ Score	Seq ² Score
Roberta	susc. check, pelleted, 2-25-04	6056	20.90	14.44	17.86	80.9	128	4.3	4.8
Angelina	resist. check, pelleted, 3-20-06	11900	36.09	16.50	20.23	81.6	138	1.5	1.6
05006010	Syngenta C28 hybrid, 4-28-06	10038	31.36	16.00	19.91	80.4	140	2.8	3.1
04061095	Syngenta C28 hybrid, 4-28-06	9368	28.08	16.66	20.84	80.0	127	2.0	2.1
R540H5	C833-5CMS x IRZM-% R940,...	9633	29.93	16.08	20.45	78.6	120	1.4	1.5
Beta 4430R	Resistant check, 3-28-06	11119	33.13	16.77	20.49	81.9	149	2.9	2.8
Mean		9685.8	29.92	16.08	19.96	80.6	133.8	2.5	2.7
LSD (.05)		887.3	2.44	0.71	0.83	2.0	13.8	0.5	0.6
C.V. (%)		9.0	8.02	4.37	4.07	2.5	10.1	21.2	20.7
F value		42.6**	37.57**	12.00**	13.97**	2.9*	4.9**	34.0**	39.0**

NOTES: Normal ENYV at Spence Field. Machine harvested, so not scored for rhizomania. Moderately severe rhizomania.

¹Foliar color due to rhizomania. 1 = all normal green; 2 = +25% yellowish; 3 = +50% yellowish; 4 = +75% yellowish; 5 = 100% yellowish.

²Foliar segregation pattern for rhizomania. 1 = all green; 2 = +25% yellowish (1-25%); 3 = 50:50 green: yellowish; 4 = +75% yellowish (75-99%); 5 = all yellowish.

TEST 1206. PERFORMANCE OF HYBRIDS WITH RESISTANCE TO SBCN/RHIZOMANIA, SALINAS, CA, 2006

48 entries x 8 reps., RCB(e)
1-row plots, 22 ft. long

Planted: May 4, 2006
Harvested: October 11-12, 2006

Variety	Description	Acre Yield		Sucrose %	Soluble Solids %	RJAP %	Beets/ 100'	Foliar	
		Sugar	Beets					Color ¹	Seq ²
		Lbs	Tons					Score	Score
<u>Checks</u>									
Phoenix	Holly Hybrids, 3-10-06	10615	34.26	15.48	19.01	81.4	136	1.3	2.3
Beta 4430R	Betaseed, 8-21-05	11448	35.24	16.26	19.70	82.6	135	1.8	2.4
Beta G017R	Betaseed	12010	35.97	16.73	20.67	80.9	135	1.3	1.8
HH142	Holly Hybrids, 3-10-06	10370	32.08	16.16	20.00	80.8	133	1.0	1.8
P531CTH50	C790-15CMS x P431CT, (CP09CT)	11496	34.08	16.85	20.59	81.9	132	2.6	3.4
Y591H50	C79-15CMS x IRZM-% Y391	10447	32.18	16.24	20.31	80.0	141	2.5	3.0
R578H50	C790-15CMS x R378, (C78/3)	11233	34.25	16.38	20.48	80.0	136	2.5	3.0
1927-4H5	C833-5CMS x RZM 9927-4, (C927-4)	11012	34.00	16.20	20.66	78.4	120	1.4	1.6
<u>Hybrids with progenies from R22,C50,C51 germplasm</u>									
5927-202H50	C790-15CMS x 4927-202, (CN927-202) (NR)	11538	34.82	16.55	20.81	79.5	135	1.1	1.6
5927-4-302H5	C833-5CMS x 3927-4-302 (NR)	10998	32.27	17.05	21.40	79.7	110	1.0	1.6
5927-4-303H5	C833-5CMS x 3927-4-303 (NR)	11163	33.90	16.45	20.74	79.3	116	1.4	1.9
5927-4-307H5	C833-5CMS x 3927-4-307 (NS)	10921	33.74	16.17	20.42	79.2	94	1.1	1.6
5927-4-308H5	C833-5CMS x 3927-4-308 (NR)	11813	36.23	16.31	20.54	79.4	121	1.0	1.3
5927-4-309H5	C833-5CMS x 3927-4-309 (NS)	11469	34.05	16.84	21.48	78.4	116	1.1	1.4
5921-306H5	C833-5CMS x 3921-306, (CN921-306) (NR)	11587	34.13	16.98	21.66	78.4	129	1.0	1.1
5926-11-3-22H5	C833-5CMS x 4926-11-3-22, (CN926-11-3-22) (NR)	10089	29.94	16.89	21.31	79.2	107	1.0	1.6
R522H5	C833-5CMS x IRZM R522 (sp) , (C51,R22)	10544	32.97	15.99	20.55	77.8	111	1.3	2.0
Y577H5	C833-5CMS x IRZM Y277,Y375	11163	32.56	17.17	21.32	80.6	123	1.5	1.8
Y575-305H50	C790-15CMS x Y375-305 (NT)	11385	35.09	16.23	20.27	80.0	135	1.3	2.1

(cont.)

Variety	Description	Acre Yield		Beets/ 100'	Soluble Solids	RJAP	Beets/ 100'	Foliar	Foliar
		Sugar Lbs	Beets Tons						
Hybrids with progenies from R22,C50,C51 germplasm (cont.)									
Y575-311H50	C790-15CMS x Y375-311(NT)	10353	32.08		20.06	80.5	140	2.8	3.1
R521H5	C833-5CMS x IRZM-8 R321,R021	11488	35.61		20.09	80.4	137	1.4	1.6
Hybrids with progenies with WB242 and other Bvm germplasm									
N572-233H5	C833-5CMS x N472-233(NR)	11419	34.64		21.20	77.9	140	1.1	1.9
N512-11H5	C833-5CMS x N412-11(NR)	11497	34.15		21.44	78.6	120	1.6	1.9
N512-13H5	C833-5CMS x N412-13(NS)	11290	34.13		20.75	79.8	126	1.1	1.4
P529-305H50	C790-15CMS x P329-305	12129	36.78		20.67	79.8	136	1.4	1.8
P507-303H50	C790-15CMS x P307-303(NT)	10325	31.73		20.31	80.1	138	2.5	2.9
P507-304H50	C790-15CMS x P307-304(NS)	10043	32.08		19.67	79.5	129	3.4	3.9
P507-306H50	C790-15CMS x P307-306(NT)	11161	34.12		20.34	80.5	136	1.6	1.9
P507-308H50	C790-15CMS x P307-308(NT)	11545	35.47		20.23	80.5	134	1.6	2.4
P507-311H50	C790-15CMS x P307-311(NT)	10933	33.89		20.41	78.9	135	2.1	2.8
Hybrids that segregate for Hs-1 from B.procumbens									
R578H94	N465-9HO(g) x R378, (C78/3)	11144	35.18		20.13	78.7	130	1.5	2.0
R578H99	N469HO(g) x R378, (C78/3)	9525	29.54		20.41	79.0	128	1.4	2.0
Hybrids from commercial companies with NR									
Betaseed									
2VK0305	Betaseed, 9-16-05/3-20-06	12037	38.68		19.45	80.0	131	1.4	1.5
OVK6280	Betaseed, 9-16-05/3-20-06	6641	23.24		17.58	80.6	136	4.0	4.4
3EN5112	Betaseed, 3-20-06	12284	38.75		19.95	79.6	134	1.4	1.5
2EN5066	Betaseed, 9-16-05/3-20-06	9201	32.08		17.59	81.7	141	3.4	3.8
5AP0701	Betaseed, 3-20-06	14068	39.07		21.99	81.8	144	1.0	1.0
5AP0703	Betaseed, 3-20-06	13576	36.87		22.41	82.2	134	1.1	1.3
Syngenta									
Hil-2	Syngenta, 9/05	10690	36.14		18.31	80.5	138	1.8	2.6
Hil-3	Syngenta, 9/05	6464	24.92		16.10	80.0	141	4.0	4.6
Hil-4	Syngenta, 9/05	11609	34.73		20.73	80.6	139	1.0	1.1
Hil-5	Syngenta, 9/05	10225	31.41		19.89	81.8	128	1.1	1.0

TEST 1206. PERFORMANCE OF HYBRIDS WITH RESISTANCE TO SBCN/RHIZOMANIA, SALINAS, CA, 2006
(cont.)

Variety	Description	Acre Yield		Beets 100'	Soluble		RJAP	Beets/ 100'		Foliar Foliar	
		Sugar	Beets		Sucrose	Solids		Color	Seg		
		Lbs	Tons		%	%		No.	Score	Score	
Holly											
HXN4	Holly Hybrids, 3-06	10109	31.36	16.05	19.74	81.3	130	1.8	2.3		
HXN5	Holly Hybrids, 3-06	10302	32.27	15.96	19.13	83.5	131	3.0	3.6		
Checks											
Roberta	Betaseed, 2-25-04, pelleted	7808	27.69	14.09	17.59	80.1	134	4.0	4.4		
Angelina	Betaseed(KWS), 9-19-05, pelleted	14107	41.63	16.92	21.01	80.5	144	1.0	1.9		
P531CTH5	C833-5CMS x P431CT, (CP09CT)	11943	36.15	16.55	21.20	78.1	121	1.1	1.5		
Y595H5	C833-5CMS x Y95(C)	11846	36.43	16.24	20.55	79.0	128	1.4	1.5		
Mean		10980.5	33.80	16.19	20.23	80.1	130.2	1.7	2.2		
LSD (.05)		920.2	2.63	0.60	0.60	1.9	10.6	0.5	0.6		
C.V. (%)		8.5	7.89	3.75	3.00	2.4	8.3	30.0	26.9		
F value		18.9**	11.91**	18.76**	31.34**	3.3**	7.3**	22.6**	20.4**		

Rhizomania: Performance of commercial checks suggested that a little Rz1 resistance breaking BNYVV may have been present.

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

Nematodes. NR = Nematode resistant or segregates for NR based on field and/or greenhouse tests. NS = nematode susceptible. NT = nematode tolerant based on Brawley field tests. Soil samples for representative varieties were taken for sugarbeet cyst nematode counts at thinning and harvest, but counts have not yet been made. Low counts are expected for this test. Effects of rhizomania more important than SBCN.

C833-5CMS = mm, Rz1Rz1. C790-15CMS = mm, rzrz.

TEST 1106. HYBRIDS WITH SBCN RESISTANCE FROM VARIOUS SOURCES, SALINAS, CA, 2006

12 entries x 8 reps., RCB
1-row plots, 22 ft. long

Planted: May 4, 2006
Harvested: October 6, 2006

Variety	Description	Acre yield		Sucrose %	Soluble Solids %	RJAP %	Beets/ 100'	Foliar Foliar	
		Sugar	Beets					Color ¹	Seq ²
		Lbs	Tons					Score	Score
<u>Checks</u>									
Roberta	Susceptible check, pelleted	6331	23.53	13.44	16.86	79.7	138	5	5
Beta 4430R	Betaseed, 3-20-06	11925	35.47	16.88	20.58	82.0	147	2	2
<u>Resistance from R22,C50,C51</u>									
5927-202H50	C790-15CMS x CN927-202 (NR)	11841	36.30	16.31	20.36	80.1	141	1	1
5926-11-3-22H5	C833-5CMS x CN926-11-3-22 (NR)	10671	31.68	16.84	21.00	80.2	130	1	1
5921-306H5	C833-5CMS x CN921-306 (NR)	11826	35.57	16.64	21.35	77.9	134	1	1
Y575-311H50	C790-15CMS x Y375-311 (NT)	9132	30.01	15.20	19.24	79.0	137	3	3
<u>Resistance from WB242 & CN12</u>									
N512-11H5	C833-5CMS x N412-11 (NR)	11233	33.70	16.69	21.33	78.2	127	1	1
N512-13H5	C833-5CMS x N412-13 (NS)	11082	34.29	16.15	20.20	80.0	147	1	1
P507-306H50	C790-15CMS x P307-306 (NT)	10687	33.56	15.91	20.04	79.4	135	1	2
<u>Resistance from CN72</u>									
N572-233H5	C833-5CMS x N472-233 (NR)	10162	31.57	16.06	20.34	79.1	132	1	1
<u>Commercial checks</u>									
2VK0305	Betaseed, 3-20-05	11369	36.33	15.64	19.33	81.0	141	2	2
3EN5112	Betaseed, 3-20-06	11454	34.94	16.39	20.30	80.7	143	2	2
Mean		10642.7	33.08	16.01	20.08	79.8	137.6	1.7	1.8
LSD (.05)		1083.9	3.19	0.56	0.69	1.7	11.5	0.5	0.5
C.V. (%)		10.2	9.68	3.49	3.47	2.1	8.4	28.5	25.6
F value		16.8**	10.17**	23.16**	24.09**	3.8**	2.4*	39.1**	44.1**

See test 1206 for descriptions. Soil cores for SBCN counts have not yet been analyzed, but popns were low. NR = cyst nematode resistant; NS = nematode tolerant; and NS = nematode susceptible.

¹Foliar color due to rhizomania. 1 = all normal green; 2 = +25% yellowish; 3 = +50% yellowish; 4 = +75% yellowish; 5 = 100% yellowish.

²Foliar segregation pattern for rhizomania. 1 = all green; 2 = +25% yellowish (1-25%); 3 = 50:50 green: yellowish; 4 = +75% yellowish (75-99%); 5 = all yellowish.

16 entries x 6 reps, sequential
1-row plots, 11 ft. long

Planted: May 15, 2006
Harvested: November 6, 2006

Variety	Description	Acre Yield		Soluble Beets/ 100'		DI	%R (0-3)		%R (0-4)	Foliar Foliar		CLS
		Sugar	Beets Tons	Sucrose	Solids		No.	% %		Color	Seg	
US H11	Susc. check, 10/4/02	4061	16.38	12.27	15.23	203	6.0	3.2	5.5	3.0	3.3	2.5
R540H5	C833-5CMS x IRZM-% R940, ...	6186	20.77	14.88	18.72	182	5.4	15.5	19.0	2.7	3.2	1.8
R525H5	C833-5CMS x IRZM-% R324, ...	5865	19.24	15.20	18.30	164	4.9	22.0	25.7	2.3	2.5	2.0
Beta 4309R	Betaseed, 3/28/06	10833	36.67	14.82	17.70	211	4.4	39.3	44.5	1.3	1.8	4.5
Differential Checks												
Beta 4430R	Resist. ck, 3/28/06	5655	20.72	13.48	16.27	211	5.5	7.0	7.8	2.3	2.7	3.8
Beta G017R	Resist. ck, 3/28/06	11490	38.76	14.82	17.88	182	3.8	57.4	69.6	2.0	2.0	3.8
Angelina	Resist. ck, pelleted, 3/20/06	11450	36.83	15.57	18.47	189	4.0	56.0	61.9	1.7	1.7	3.7
Roberta	Resist. ck, pelleted, 2/25/04	2861	12.51	11.28	15.85	176	6.1	2.3	4.4	3.5	3.7	3.7
Experimental Hybrids												
R521H5	C833-5CMS x IRZM-% R321, R021	3840	14.57	13.10	15.95	197	6.1	1.0	2.6	3.0	3.3	2.7
R539H5	C833-5CMS x R039	8338	28.16	14.80	18.05	173	5.4	5.9	13.8	2.2	2.5	1.7
Y577H5	C833-5CMS x IRZM Y277, Y375	5813	18.88	15.18	18.00	183	5.2	19.2	24.8	3.0	3.3	2.7
R524-302H5	C833-5CMS x R324-302, -306	4412	15.32	13.90	17.67	176	6.2	2.1	5.2	2.7	3.3	2.7
R524-301H5	C833-5CMS x R325-301, -302	4240	14.29	14.78	18.10	191	6.0	3.5	4.3	2.5	2.7	1.8
R524-2/3H5	C833-5CMS x R324-213, -215, -222, -223	6072	20.21	15.05	18.07	180	5.1	15.1	22.6	2.0	2.3	2.2
R5327-302H5	C833-5CMS x R337-302	4593	15.66	14.55	18.18	180	5.9	3.4	8.6	2.8	3.5	3.2
05006010	C28 hybrid	4561	17.21	13.00	15.98	200	5.5	10.4	13.4	3.0	3.3	3.2
Mean		6267.0	21.64	14.17	17.40	187.3	5.4	16.5	20.9	2.5	2.8	2.9
LSD (.05)		1720.2	5.44	1.26	0.94	24.5	0.6	16.0	18.5	0.8	0.9	1.0
C.V. (%)		23.9	21.87	7.74	4.71	11.4	10.3	84.8	77.1	28.2	26.6	29.2
F value		20.7**	20.00**	7.35**	11.27**	2.5*	11.2**	10.7**	10.0**	3.9**	4.3**	6.3**

(cont.)

Variety	Description	Acre Yield		Soluble Beets/		%R		%R		Foliar Foliar		CLS
		Sugar	Beets	Sucrose	Solids	100'	DI	(0-3)	(0-4)	Color	Seg	
		Lbs	Tons	%	%	No.	%	%	%	Score	Score	

Notes:

C833-5CMS is likely Rz1Rz1. Tests 4206 & 4306 were grown in a field area that was originally inoculated with IV-BNYVV in 2003 and rhizomania tests were grown in 2004, 2005, and 2006. These tests were severe. See tests 4206 and 4406 for other descriptions and notes.

Rhizomania: DI = Disease Index = average score of each plant within the variety; % Resistant(0-3) = total roots in classes 0+1+2+3/total roots scored. %Resistant(0-4) = roots in classes 0-4/total roots scored. It was observed that many of the roots in the susceptible checks were scored as 4 or less but in the resistant checks, some resistant roots were also scored as 4's or higher. I.e., there did not appear to be a discrete separation between resistant and susceptible roots based on the action of the Rz1 and Rz2 alleles.

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

Cercospora: Natural infection with Cercospora occurred late in the summer and became moderate on some entries by harvest. Foliar leaf spot symptoms were scored on a scale of 0 to 9, where 9 = 100% of leaf area diseased.

24 entries x 4 reps, sequential
1-row plots, 11 ft. long

Planted: May 15, 2006
Harvested: November 7, 2006

Variety	Description	Acre Yield		Soluble		Beets/ 100'	DI	%R		%R		Foliar		CLS
		Sugar	Beets	Sucrose	Solids			%	%	(0-3)	(0-4)	Color	Seg	
		Lbs	Tons	%	%	No.	%	%	%	%	Score	Score	Score	
Differential Checks														
Angelina	Resist.ck, Rz1+Rz2	8478	30.77	13.82	16.40	184	3.9	68.5	69.9	1.3	1.3	3.3		
Roberta	Susc.ck, rzz	2678	13.75	9.73	12.05	155	6.1	2.3	2.3	2.3	2.0	3.8		
Beta 4430	Resist. check, Rz1	4043	18.12	11.07	13.52	175	5.1	19.5	25.6	1.8	2.3	4.5		
G017R	Resist. check, Rz2	10186	35.96	14.25	17.33	168	3.7	66.0	73.9	1.8	1.3	4.0		
Company Hybrids														
36K5308	Betaseed,	6066	27.14	11.15	14.25	168	5.1	25.7	28.7	1.5	1.5	3.3		
HXR1	Holly Hybrids,	7175	26.42	13.50	16.77	180	4.1	53.1	57.3	1.3	1.5	4.5		
HXR2	Holly Hybrids,	9037	29.57	15.18	17.70	186	3.9	63.5	67.6	2.3	1.8	6.0		
HXR3	Holly Hybrids,	4610	18.25	12.57	15.02	191	5.9	1.5	2.9	2.8	2.3	2.5		
Experimental hybrids														
USH11	Susc. check	4200	19.31	10.68	13.65	173	5.8	4.8	4.8	2.0	1.8	2.3		
R539H5	C833-5CMS x R039	7487	28.24	13.02	15.98	186	5.3	16.3	18.7	1.0	1.0	1.8		
R578H5	C833-5CMS x R378	6340	21.01	15.02	17.70	161	5.4	14.1	17.9	1.8	1.5	1.8		
Y577H5	C833-5CMS x IRZM Y277, Y375	6051	21.33	14.20	17.60	170	5.2	14.8	14.8	1.8	2.3	2.0		
Y595H5	C833-5CMS x Y95 (C)	4792	17.21	13.93	16.65	152	5.5	10.9	12.4	2.3	2.5	2.0		
Y591H50	C790-15CMS x IRZM-% Y391	6407	23.76	13.30	15.60	195	4.7	21.9	32.0	1.3	1.5	2.5		
R540H5	C833-5CMS x IRZM-% R940	6265	20.69	15.13	18.22	182	4.6	36.5	39.5	2.3	2.3	2.5		
R525H5	C833-5CMS x IRZM-% R324,...	5173	18.03	14.32	17.35	170	5.0	24.2	29.7	1.5	1.5	1.5		
R524-302H5	C833-5CMS x R324-302, -306	3911	15.26	12.32	15.35	166	5.4	15.8	17.5	2.3	1.8	2.8		
R525-301H5	C833-5CMS x R325-301, -302	3912	14.53	13.43	16.15	193	5.3	23.5	29.2	2.0	1.5	2.3		
R524-2/3H5	C833-5CMS x R324-213, -215, -222, -223	6173	21.01	14.60	17.70	159	5.1	18.0	27.3	1.3	1.3	1.8		
R537-302H5	C833-5CMS x R337-302	5472	18.46	14.75	17.83	173	5.4	11.4	15.9	2.3	2.3	2.5		
R541/2H5	C833-5CMS x IRZM-% R641, R642	5138	19.52	13.07	15.95	173	5.4	12.0	17.6	1.8	1.8	1.5		
R521H5	C833-5CMS x IRZM-% R321, R021	6351	24.61	12.98	15.85	195	5.2	16.7	20.2	1.5	1.3	1.8		
05006010	C28 hybrid	3710	16.92	10.75	13.65	175	5.5	8.6	11.6	2.0	2.0	2.3		
04061095	C28 hybrid	5728	21.43	13.38	15.98	191	5.3	7.5	14.3	1.5	1.8	1.8		

(cont.)

Variety	Description	Acre Yield		Soluble		Beets/		%R		%R		Foliar Foliar	
		Beets		Sucrose		100'		(0-3)		(0-4)		Color	
		Lbs	Tons	%	%	No.	%	%	%	%	%	Score	Score
Mean		5807.6	21.72	13.17	16.01	175.9	5.1	23.2	27.2	1.8	1.7	2.7	2.7
LSD (.05)		2319.1	7.60	1.80	1.98	26.6	0.8	20.9	22.2	1.0	0.9	1.3	1.3
C.V. (%)		28.3	24.80	9.70	8.78	10.7	10.8	63.8	57.8	38.7	38.1	33.1	33.1
F value		4.7**	4.29**	5.77**	5.42**	1.8*	5.3**	7.2**	6.9**	1.6NS	1.6NS	6.6**	6.6**

NOTES: Test area for 4506 thru 4706 was inoculated in 2005 and an inoculation crop grown. This is the first year for tests in this area. Rhizomania appeared to be milder and more variable than in areas for tests 4206 thru 4406.

C833-5CMS is probably Rz1Rz1. See test 4206, 4306, and 4406 for descriptions of the pollinator lines.

Rhizomania. DI = Disease Index = average score of each plant within the variety; % Resistant(0-3) = total roots in classes 0+1+2+3/total roots scored. %Resistant(0-4) = roots in classes 0-4/total roots scored. It was observed that many of the roots in the susceptible checks were scored as 4 or less but in the resistant checks, some resistant roots were also scored as 4's or higher. I.e., there did not appear to be a discrete separation between resistant and susceptible roots based on the action of the Rz1 and Rz2 alleles.

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowishness, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowishness, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

Cercospora: Cercospora leaf spot resulted from natural infection and was more severe in 4406 than in 4206 having spread from test 4606. Plots were scored at harvest on a scale of 0 to 9, where 9 = 100% of the leaf area covered or dead.

72 entries (58 company + 14 USDA) x 8 reps, RCB

Planted: May 4, 2006

Harvested: Oct. 24 & 27 and Nov. 15, 2006

1-row plots, 22 ft. long

Variety	Description	Acre Yield		Beets		Sucrose		Soluble Solids		Stand Count		DI	%R		%R	Foliar		PM
		Sugar Lbs	Tons	%	%	%	%	No.	No.	%	%		Color	Seg		Score	Score	
Checks																		
Beta G017R	resist ck, 3-28-06	13225	36.67	18.04	21.79	28	29	3.1	85.2	92.6	1.9	2.0	1.1					
Roberta	susc. ck, 3-20-06	8371	26.66	15.61	18.85	29	27	4.6	34.4	36.2	4.0	4.1	1.4					
Beta 4430R	Betaseed, 3-28-06	14371	40.17	17.86	21.34	31	31	2.7	94.0	96.8	2.0	1.9	0.8					
Angelina	Betaseed, 3-20-06	14017	38.53	18.19	22.04	29	30	2.9	91.6	97.1	1.3	1.1	4.3					
HXR1	Holly Hyb, 3-24-06	12570	33.26	18.91	22.41	29	27	2.9	90.7	98.5	2.6	2.5	3.4					
HXR2	Holly Hyb, 3-24-06	13398	35.33	18.97	22.63	30	29	3.1	84.5	98.6	2.8	3.0	1.5					
HXR3	Holly Hyb, 3-24-06	14689	42.72	17.22	20.62	29	29	3.1	85.9	91.2	1.1	1.3	0.8					
USH11	susc. ck, 10-14-02	8222	25.94	15.83	19.29	28	28	4.5	35.4	40.6	3.4	3.5	7.5					
CBGA Coded RZM																		
Rhz - 1	RAPTOR	12075	37.13	16.23	19.54	29	28	3.0	86.5	94.0	2.1	2.1	2.8					
- 2	5YK0512	15915	44.20	17.99	21.27	30	29	3.1	78.5	92.7	1.6	1.6	0.9					
- 3	CRYSTAL R656	12871	38.06	16.88	20.26	30	29	3.4	69.1	82.1	1.9	1.6	0.4					
- 4	5YK0511	17456	47.65	18.32	21.66	30	29	2.8	92.7	97.9	2.0	1.6	0.5					
- 5	4YK0504	15179	41.09	18.48	22.05	30	29	3.1	82.2	96.3	1.4	1.4	0.4					
- 6	04HX428	13640	38.37	17.79	21.72	30	29	2.9	91.4	97.9	1.6	1.3	1.8					
- 7	04HX427	15033	43.17	17.43	20.81	28	29	3.0	87.2	93.0	1.9	2.0	0.8					
- 8	6YK9011	13045	34.92	18.67	22.29	30	30	2.9	89.4	96.2	1.3	1.6	1.4					
- 9	BETA 8520N	13377	39.25	17.04	20.42	29	28	3.1	83.3	95.8	1.8	1.9	3.3					
-10	05HX527	12903	35.58	18.12	21.32	31	31	2.7	92.9	96.4	2.4	2.3	2.6					
-11	05HX529	14260	41.53	17.17	20.68	29	29	2.8	95.2	97.4	1.6	1.3	0.5					
-12	CRYSTAL R549	14931	41.53	17.96	21.22	30	29	2.9	91.1	97.1	1.0	1.0	0.5					
-13	4YK0505	15466	42.59	18.13	21.48	32	32	3.0	86.3	94.3	2.0	2.3	0.1					
-14	CRYSTAL R510	13923	38.81	17.98	21.59	29	26	3.3	76.4	88.4	1.5	1.4	0.9					

(cont.)

Variety	Description	Acre Yield		Soluble Stand Harv		%R (0-3)		%R (0-4)		Foliar Color		Foliar Seg	
		Sugar	Beets	Sucrose	Solids	Count	DI	%	%	Color	Seg	Score	Score
		Lbs	Tons	%	%	No.	No.	%	%	Score	Score	Score	Score
CBGA Coded RZM (cont.)													
Rhz -15	5YK0514	15978	43.94	18.18	21.58	32	2.7	98.4	100.0	1.4	1.0	0.3	
-16	BETA 4776R	14946	43.01	17.38	20.83	31	2.8	94.8	98.7	1.6	1.8	0.4	
-17	VIPER	14888	42.51	17.51	20.77	27	2.9	90.7	95.5	1.5	1.3	0.8	
-18	04HX425	13400	36.66	18.26	22.13	29	3.0	89.4	94.7	1.6	1.6	1.6	
-19	6YK9013	14198	38.11	18.63	22.32	30	2.8	93.5	98.7	1.5	1.6	0.1	
-20	5YK0517	13411	36.80	18.19	21.87	31	3.0	88.9	97.9	1.1	1.1	2.3	
-21	05HX516	13406	36.77	18.22	21.84	30	2.8	92.7	99.2	2.1	2.6	3.0	
-22	1J5155	15498	44.27	17.49	20.71	30	3.3	75.2	88.7	1.8	1.8	0.5	
-23	6YK9012	11564	34.62	16.74	20.46	27	3.1	86.4	95.9	2.4	2.3	3.4	
-24	03HX314	14761	41.83	17.64	21.00	28	3.1	87.6	93.2	1.8	1.9	0.6	
-25	05HX511	13660	37.14	18.39	22.36	27	3.0	89.5	93.9	1.5	1.9	2.9	
-26	5YK0513	13686	37.72	18.08	21.64	31	3.2	79.1	93.0	1.5	1.4	1.8	
-27	05HX513	14588	41.40	17.63	20.87	25	3.0	91.0	93.5	1.5	1.8	0.8	
-28	CRYSTAL R362	13986	39.30	17.82	21.11	29	3.0	89.4	95.0	1.8	1.8	1.0	
-29	5YK0904N	13444	38.76	17.35	20.91	28	2.9	89.2	97.8	1.8	2.0	2.9	
-30	05HX501	13723	40.00	17.17	20.23	28	3.2	79.1	88.1	2.1	1.8	2.9	
-31	BETA 4309R	14818	41.43	17.88	21.46	32	3.0	91.2	98.7	1.8	1.8	0.1	
-32	5YK0520	14237	37.29	19.09	22.61	31	3.0	90.0	98.0	1.4	1.4	1.6	

Checks

Roberta susc. ck, pelleted, 3-20-06

8260 25.96 15.69 18.81 27 27 4.9 27.1 30.7 4.4 4.3 1.9

USH11 susc. ck, 10-4-02

8649 27.80 15.54 19.10 29 28 4.5 32.1 36.0 3.8 3.8 6.9

CBGA Coded RZM (cont.)

Rhaz -33 4YK0501

14048 38.59 18.21 21.71 28 28 3.0 88.1 93.1 2.4 2.4 0.8

-34 4YK0503

14463 41.47 17.44 20.98 28 27 3.0 86.9 95.0 1.8 1.8 2.4

(cont.)

Variety	Description	Acre Yield		Beets		Sucrose		Soluble		Stand Harv		DI	%R		Foliar Color	Foliar Seg	PM
		Sugar Lbs	Tons	Beets	Tons	%	%	Solids	Count	No.	%		(0-3)	(0-4)			
CBGA Coded RZM (cont.)																	
Rhz -35	05HX504	14743	41.55	17.74	20.99	32	30	2.7	96.2	99.2	1.4	1.6	2.0				
-36	05HX526	13042	36.31	17.96	21.53	30	30	2.6	94.5	99.2	1.8	2.1	1.8				
-37	5YK0515	15334	40.47	18.94	22.98	31	31	2.7	95.8	100.0	1.8	1.8	0.5				
-38	CRYSTAL R441	15460	43.86	17.63	20.86	29	30	3.3	77.0	87.7	1.9	1.8	0.4				
-39	05HX528	10891	33.83	16.04	19.36	28	27	4.0	51.5	56.5	3.4	3.5	0.5				
-40	5YK0905	15495	42.60	18.15	22.14	30	29	2.9	92.8	98.1	1.0	1.5	1.3				
-41	05HX505	12424	36.94	16.83	20.48	28	27	3.5	70.6	76.5	2.0	2.1	1.8				
-42	05HX515	13732	37.12	18.51	22.40	27	26	2.9	92.4	95.5	1.6	1.9	3.5				
Checks																	
Roberta	susc. ck, pelleted, 3-20-06	9724	30.45	15.92	19.21	29	29	4.4	40.3	44.0	4.1	4.3	2.4				
Beta G017R	resist. ck, 3-28-06	13934	38.59	18.06	21.99	30	30	3.0	86.6	94.8	2.0	2.3	1.4				
Angelina	resist. ck, pelleted, 3-20-06	13915	38.40	18.12	21.70	29	30	2.8	94.8	99.2	1.3	1.5	4.5				
Beta 4430R	resist. ck, 3-28-06	13129	37.05	17.73	21.19	28	28	2.6	97.8	99.1	2.0	1.6	1.1				
CBGA Coded RZM (cont.)																	
Rhz -43	05HX519	13750	37.61	18.27	21.81	30	28	2.8	94.3	97.9	2.1	2.3	3.3				
-44	ALPINE	12952	40.49	16.00	19.36	29	28	2.9	90.1	95.5	2.0	2.3	2.8				
-45	5YK0510	14639	40.91	17.88	21.38	29	29	3.1	84.6	94.8	1.0	1.0	0.6				
-46	1GK0062	15382	43.67	17.61	21.07	31	30	2.7	97.4	98.6	1.4	1.9	0.6				
-47	5YK0522	15204	41.95	18.13	21.51	30	30	2.8	95.5	98.8	1.0	1.3	0.1				
-48	BETA 4430R	14784	41.13	17.97	21.59	30	30	2.6	97.4	98.7	1.6	1.6	0.8				
-49	4YK0502	14223	41.07	17.32	21.09	26	26	3.2	75.3	91.5	2.1	2.0	2.5				
-50	5YK0521	14510	40.68	17.84	21.12	30	28	2.9	95.3	98.8	1.0	1.0	0.9				
-51	5YK0906	7867	24.12	16.30	19.28	30	30	4.9	17.2	19.8	4.0	4.1	5.3				
-52	PHOENIX	13409	39.60	16.94	20.32	29	27	2.9	92.0	97.6	2.0	2.1	2.6				

(cont.)

Variety	Description	Acre Yield		Beets	Sucrose	Soluble Solids		Stand Harv		DI	%R (0-3)	%R (0-4)	Foliar		PM
		Sugar	Tons			%	No.	%	Color				Seg		
		Lbs					No.		Score				Score		
CBGA Coded RZM (cont.)															
Rhz -53	03HX308	13043	39.00	16.73	20.34	27	25	3.5	72.8	79.0	1.8	1.5	1.0		
-54	EAGLE	12533	37.00	16.93	20.54	28	25	2.9	90.1	96.4	2.0	2.1	3.1		
-55	HH-142	13481	38.79	17.35	21.38	26	26	2.9	90.5	97.4	1.3	1.3	1.5		
-56	04HX403	13369	37.97	17.58	20.83	25	24	2.8	89.3	98.4	1.3	1.3	2.8		
-57	5YK0516	15879	43.59	18.25	21.86	28	28	2.6	98.1	99.1	1.6	1.6	1.3		
-58	04HX404	14279	40.96	17.42	20.95	27	28	3.1	85.9	89.5	1.3	1.4	0.4		
Mean		13606.6	38.53	17.60	21.11	29.0	28.6	3.1	83.2	89.6	1.9	1.9	1.8		
LSD (.05)		1312.6	3.49	0.52	0.57	2.9	3.1	0.3	11.4	9.9	0.6	0.6	0.9		
C.V. (%)		9.8	9.23	3.02	2.72	10.0	11.2	10.9	14.0	11.2	32.5	28.7	52.8		
F value		16.1**	13.10**	19.89**	22.18**	2.3**	2.4**	18.8**	18.8**	25.7**	12.1**	15.6**	21.0**		

NOTES:

Test 1506 was run as two 4-replication tests separated by about 200 feet by other rhizomania tests. Each 4 rep section was harvested individually to accommodate the test size and number of samples. The 4 rep sections were separated in case there are large differences in intensity of rhizomania and not to hit a section of the field without rhizomania. In this case, the two sections are very similar and were combined. Test had moderate rhizomania. Otherwise there appeared to be little other disease pressure. Powdery mildew was controlled until very late in the season. Plots were partially topped, lifted, laid out on the soil surface, and roots individually scored for rhizomania, where 1 = normal root to 9 = very severe rhizomania or dead. Few roots were scored > 7 and < 2. The beets were then topped, bagged, washed, weighed by plot, and run thru the sugar lab. Brei was measured for soluble solids and filtrate for % sugar.

Rhizomania: DI = Disease Index = average score of each plant within the variety; % Resistant(0-3) = total roots in classes 0+1+2+3/total roots scored. %Resistant(0-4) = roots in classes 0-4/total roots scored. Because test was mild, it was observed that many of the roots in the susceptible checks were scored as 4 or less but in the resistant checks, some resistant roots were also scored as 4's or higher. I.e., there did not appear to be a discrete separation between resistant and susceptible roots based on the action of the Rz1 allele.

(cont..)

Variety	Description	Acre Yield		Soluble Stand Harv		%R		%R		Foliar	
		Sugar		Beets		Sucrose		Solids		Count	
		Lbs	Tons	%	No.	%	No.	%	No.	(0-3)	(0-4)
										Color	Seg
										Score	Score
										PM	

NOTES: (cont.)

Checks: Roberta is a widely grown hybrid in Europe. In the absence of rhizomania, it performs very well in California as well. Beta4430R is a popular variety in California with Rz1. BetaG017R is an experimental hybrid with Rz2 allele. Angelina is a European variety with high performance and has both Rz1 + Rz2 alleles. USH11 was widely grown in California 20 years ago, but is now relatively low performing and highly susceptible to rhizomania.

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

Coefficients of correlation (r) were calculated:

Disease Index (DI)	DI	%R(0-3)	%R(0-4)	Fol.Color	Fol. Seg	SY/A	RY/A	Harv.	
								%S	Count
%R (0-3)	-0.97**	-0.97**	-0.95**	0.63**	0.61**	-0.68**	-0.64**	-0.53**	-0.12**
%R (0-4)	-0.95**	0.96**	0.96**	-0.64**	-0.62**	0.68**	0.63**	0.54**	0.10*
Foliar Color	0.63**	0.96**	-0.67**	-0.67**	-0.67**	0.71**	0.66**	0.59**	0.09*
Foliar Segregation	0.61**	-0.64**	-0.67**	0.79**	0.79**	-0.58**	-0.53**	-0.45**	-0.05NS
Gross Sugar Yield (SY/A)	-0.68**	-0.62**	-0.67**	-0.58**	-0.61**	-0.61**	-0.57**	-0.45**	-0.04NS
Tons Roots/Acre (RY/A)	-0.64**	0.68**	0.71**	-0.53**	-0.61**	0.96**	0.96**	0.62**	0.18**
%S	-0.53**	0.63**	0.66**	-0.45**	-0.57**	0.96**	0.37**	0.37**	0.14**
Harvest Count	-0.12**	0.54**	0.59**	-0.05NS	-0.45**	0.62**	0.14**	0.19**	0.19**
		0.10*	0.09*		-0.04NS	0.18**	0.14**		

TEST 1406. MICHIGAN SUGAR, WESTERN SUGAR, SOUTHERN MINNESOTA BEET SUGAR CODED HYBRID EVALUATION UNDER RHIZOMANIA,
SALINAS, CA, 2006

72 entries (46 company + 26 USDA) x 8 reps, RCB
1-row plots, 22 ft. long

Planted: May 4, 2006
Harvested: October 23 & November 1, 2006

Variety	Description	Acre yield		Soluble Solids		Stand Count		DI	%R (0-3)		%R (0-4)		Foliar Color		Foliar Seg		PM
		Sugar Lbs	Beets Tons	%	%	No.	No.		%	%	Score	Score					
Checks																	
Angelina	Resist. check, pelleted, 3-20-06	14053	39.22	17.92	22.58	29	27	2.6	96.3	99.6	1.5	1.4	4.6				
Roberta	Susc. check, pelleted, 3-20-06	8833	28.01	15.71	19.54	30	31	4.2	42.2	49.3	4.4	4.1	2.1				
Beta 4430R	Resist. check	14070	39.25	17.95	22.09	32	32	2.5	96.9	98.8	1.9	2.0	1.0				
Beta G017R	Resist. check	13414	37.38	17.96	22.68	30	30	2.9	91.8	96.3	2.1	2.0	1.3				
HXR3	Holly Hybrids, 3-10-06	13235	37.97	17.44	21.45	29	29	2.9	91.5	97.8	1.5	1.6	1.0				
Alpine	Holly Hybrids, 3-10-06	13281	42.35	15.72	19.53	30	29	2.7	97.4	99.5	1.8	1.5	3.0				
R578H5	C833-5CMS x RZM R378	13909	38.90	17.90	22.74	29	30	2.7	97.9	100.0	1.0	1.5	1.8				
US H11	Susc. check	7956	25.07	15.88	19.99	30	29	4.2	43.0	48.9	4.0	4.5	7.3				
Western Sugar Entries																	
WS-1	HM 7172	12727	34.16	18.64	23.54	29	29	2.9	88.3	97.5	1.0	1.0	1.0				
WS-2	HM 1655	12964	35.72	18.16	22.74	27	28	3.2	74.2	89.8	1.4	1.3	1.6				
WS-3	Monohikari check	9971	29.07	17.11	20.95	31	30	4.1	43.5	51.8	3.6	3.6	5.0				
WS-4	HM 1338RZ	12806	33.44	19.14	24.02	30	29	3.0	89.0	94.5	1.1	1.3	1.4				
Monohikari	susc. check, Seedex	9060	26.07	17.31	21.29	29	28	4.5	34.6	41.6	3.4	3.6	5.6				
WS-5	HH Meridian	13461	39.38	17.13	21.20	30	30	2.7	97.2	98.8	2.1	2.0	2.8				
WS-6	Crystal C327	13657	37.10	18.41	22.99	30	31	2.9	91.3	99.6	2.3	2.1	1.4				
WS-7	Beta 8610R	13330	36.98	18.06	22.68	31	31	3.0	91.8	97.3	2.3	2.0	1.1				
WS-8	Crystal R322	13329	36.17	18.46	23.02	28	28	3.0	88.6	97.0	2.1	2.3	1.4				
Southern Minnesota Entries																	
SMSBC-601	rec'd 4-3-06	13302	34.44	19.33	23.98	29	29	2.8	96.1	100.0	1.8	1.6	0.6				
SMSBC-602	rec'd 4-3-06	13640	34.84	19.59	24.10	28	28	2.7	94.2	97.3	1.5	1.4	0.9				
SMSBC-603	rec'd 4-3-06	11408	29.32	19.45	24.14	26	25	3.0	90.9	96.9	1.9	1.5	2.4				

(cont.)

Variety	Description	Acre Yield		Beets		Sucrose		Soluble Solids		Stand Count		Harv		DI		%R		Foliar		PM
		Sugar	Lbs	Tons	%Beets	%Sucrose	%Solids	%Stand	Count	No.	No.	Count	%DI	%R (0-3)	%R (0-4)	Color	Seg			
																		Score	Score	
Southern Minnesota Entries (cont.)																				
SMBSC-604	rec'd 4-3-06	13210		35.00	18.88	23.32	28	27	2.9	92.2	98.7	1.5	1.4	1.0						
	rec'd 4-20-06	12291		34.28	17.95	22.03	29	30	2.8	92.0	95.5	2.0	1.9	1.6						
Monohikari	susc. check, Seedex, 1-21-03	8981		26.02	17.26	20.94	29	28	4.2	41.4	50.4	3.6	3.9	5.8						
Roberta	susc. check, pelleted, 3-20-06	8393		26.62	15.73	19.51	29	28	4.3	40.5	45.5	4.5	4.5	3.0						
Michigan Sugar entries																				
MS- 1	rec'd 4-7-06	14738		42.11	17.50	21.61	30	30	2.6	98.0	99.6	1.6	1.6	1.6						
MS- 2	rec'd 4-7-06	11724		30.79	19.03	23.70	29	28	3.5	65.1	79.0	3.0	3.0	2.9						
MS- 3	rec'd 4-7-06	13210		35.39	18.65	23.23	28	27	2.9	87.8	97.1	1.1	1.1	1.1						
MS- 4	rec'd 4-7-06	12951		35.09	18.48	22.99	32	32	3.1	87.4	95.5	1.9	1.8	2.8						
MS- 5	rec'd 4-7-06	13466		35.37	19.05	23.74	32	32	2.7	97.7	99.6	1.5	1.5	2.5						
MS- 6	rec'd 4-7-06	12233		31.87	19.18	23.50	31	30	2.9	91.5	96.8	2.5	2.0	2.4						
MS- 7	rec'd 4-7-06	11199		30.05	18.64	23.31	27	25	3.5	69.5	80.3	2.5	2.8	3.9						
MS- 8	rec'd 4-7-06	12768		34.21	18.66	23.12	32	31	3.1	84.2	97.3	1.6	1.5	2.9						
MS- 9	rec'd 4-7-06	11418		30.74	18.54	23.56	29	30	3.1	82.2	91.4	2.1	2.3	1.5						
MS-10	rec'd 4-7-06	13423		37.23	18.05	22.21	29	29	2.7	97.8	99.6	1.1	1.0	2.5						
MS-11	rec'd 4-7-06	11160		28.67	19.49	24.02	29	28	3.5	70.8	80.4	2.6	2.4	2.8						
MS-12	rec'd 4-7-06	13002		34.01	19.12	23.56	29	28	2.8	91.9	97.3	1.3	1.5	0.9						
MS-13	rec'd 4-7-06	11553		30.35	19.04	23.77	29	29	3.3	81.4	88.9	2.6	2.5	3.6						
MS-14	rec'd 4-7-06	13416		34.93	19.22	23.52	29	29	2.8	91.9	98.9	1.1	1.1	3.0						
MS-15	rec'd 4-7-06	13638		36.91	18.49	23.18	27	28	2.6	96.4	99.6	1.0	1.0	1.9						
MS-16	rec'd 4-7-06	13764		35.72	19.29	23.88	30	29	3.0	88.4	99.0	1.3	1.4	0.6						

TEST 1406. MICHIGAN SUGAR, WESTERN SUGAR, SOUTHERN MINNESOTA BEET SUGAR CODED HYBRID EVALUATION UNDER RHIZOMANIA,
SALINAS, CA, 2006

(cont.)

Variety	Description	Acre Yield		Beets		Sucrose		Soluble Solids		Stand Harv		%R (0-3)		%R (0-4)		Foliar Color		Foliar Seg	
		Sugar	Beets	Tons	%	%	%	%	No.	No.	%	%	%	%	Score	Score	Score	Score	
		Lbs																	
Michigan Sugar entries (cont.)																			
Beta 4430R	resist ck, 3-28-06	13589		37.78	18.01		22.16	32	32	2.5	98.9	99.6	2.4	2.5	1.4				
Angelina	resist ck, pelleted, 3-28-06	13280		36.32	18.27		22.76	28	28	2.8	97.4	99.6	1.9	1.8	5.3				
Beta G017R	resist ck, 3-28-06	13245		36.38	18.21		22.74	31	31	3.0	90.4	99.6	2.3	1.8	1.8				
Roberta	susc. ck, pelleted, 3-28-06	8685		27.20	15.97		19.81	29	30	3.9	55.7	59.2	4.5	4.3	3.4				
MS-17	rec'd 4-7-06	9116		26.12	17.46		21.78	30	29	4.5	33.9	42.7	4.8	4.8	5.9				
MS-18	rec'd 4-7-06	13303		36.62	18.17		22.16	30	30	2.8	97.8	99.6	2.3	2.5	0.9				
MS-19	rec'd 4-7-06	12088		32.44	18.65		23.39	28	28	3.1	84.6	92.0	1.8	1.5	2.0				
MS-20	rec'd 4-7-06	12755		32.81	19.42		23.90	28	27	3.4	71.1	84.6	2.9	3.1	2.8				
MS-21	rec'd 4-7-06	11904		30.48	19.54		24.06	30	30	3.0	89.3	97.4	2.0	2.1	2.0				
MS-22	rec'd 4-7-06	12159		32.12	18.94		23.49	29	29	2.9	92.4	97.8	1.6	1.6	1.8				
MS-23	rec'd 4-7-06	12581		33.89	18.57		23.23	28	32	3.1	83.1	93.9	1.4	1.4	1.6				
MS-24	rec'd 4-7-06	12562		33.14	18.96		23.91	30	29	2.8	93.6	99.2	1.6	1.6	1.4				
HM-17	Syngenta, 4/05	7963		23.87	16.74		21.06	10	11	4.5	30.1	36.5	4.0	4.0	4.3				
MS-25	rec'd 4-7-06	14462		38.88	18.61		23.33	29	30	2.8	92.8	100.0	1.0	1.1	1.1				
MS-26	rec'd 4-7-06	12705		33.63	18.91		23.70	30	30	3.0	86.9	96.5	1.5	1.5	1.4				
MS-27	rec'd 4-7-06	12525		33.28	18.84		23.70	29	29	2.7	95.2	98.2	1.8	1.5	1.4				
MS-28	rec'd 4-7-06	13392		36.30	18.44		23.18	29	29	2.7	96.4	98.0	1.1	1.1	1.8				
MS-29	rec'd 4-7-06	11857		32.38	18.33		22.87	28	29	3.3	78.2	89.5	2.3	2.0	1.8				
MS-30	rec'd 4-7-06	13032		34.89	18.71		23.63	29	28	2.9	92.2	98.1	1.5	1.4	1.1				
MS-31	rec'd 4-7-06	12580		33.76	18.64		22.99	29	29	2.8	94.8	97.8	1.6	1.4	1.9				
MS-32	rec'd 4-7-06	12519		33.79	18.53		22.63	30	30	2.8	96.3	98.8	1.0	1.3	2.9				
MS-33	rec'd 4-7-06	13979		39.62	17.69		21.72	32	32	2.7	95.2	98.9	2.8	2.6	0.8				

TEST 1406. MICHIGAN SUGAR, WESTERN SUGAR, SOUTHERN MINNESOTA BEET SUGAR CODED HYBRID EVALUATION UNDER RHIZOMANIA,
SALINAS, CA, 2006

(cont.)

Variety	Description	Acre Yield		Soluble Stand Harv		%R		%R		Foliar	
		Sugar	Beets	Sucrose	Solids	Count	DI	(0-3)	(0-4)	Color	Seg
Checks		Lbs	Tons	%	%	No.	%	%	%	Score	Score
HM-17	Syngenta	6790	20.28	16.74	21.14	9	4.8	15.9	30.1	4.4	4.3
USH11	susc. check	7645	24.35	15.74	19.54	30	4.6	27.7	33.0	4.3	4.5
USDA Exp. Hybrids											
5933H5	C833-5CMS x popn-933(C) 12540	35.24	17.79	22.47	28	28	2.9	90.6	97.1	1.1	1.1
5944H5	C833-5CMS x popn-944(C) 12156	33.41	18.19	23.06	27	27	2.9	93.3	98.1	2.0	1.8
05-FC1036H5	C833-5CMS x 04-FC1028,1037,1038										
	11975	33.32	17.98	22.79	29	29	2.9	92.2	97.8	1.3	1.3
Y577H5	C833-5CMS x IRZM-% Y277,Y375										
	12573	34.73	18.12	22.76	28	28	2.7	97.5	100.0	1.5	1.5
Y595H5	C833-5CMS x RZM Y95(C) 12391	34.51	17.95	22.83	28	28	2.8	95.6	99.5	1.4	1.5
R540H5	C833-5CMS x IRZM-% R940, ...										
	13180	37.26	17.69	22.56	27	27	2.8	97.3	98.6	1.5	1.6
R521H5	C833-5CMS x IRZM-% R321,R021										
	12671	35.83	17.69	22.36	27	27	2.8	94.7	99.5	1.4	1.6
R531CTH5	C833-5CMS x PMR-RZM P431CT										
	12215	34.29	17.82	22.52	27	27	2.7	95.7	100.0	1.4	1.3
Mean		12213.4	33.60	18.15	22.61	28.7	28.4	3.1	82.4	88.5	2.1
LSD (.05)		1100.5	3.16	0.50	0.57	2.6	3.0	0.3	11.0	9.8	0.6
C.V. (%)		9.2	9.57	2.83	2.56	9.1	10.6	10.2	13.6	11.3	28.8
F value		20.2**	14.90**	29.01**	35.70**	15.2**	10.9**	25.2**	28.1**	31.0**	22.2**
										20.7**	18.2**

NOTES:

Test 1406 was run as two 4-replication tests separated by about 200 feet by other rhizomania tests. Each 4 rep section was harvested individually to accommodate the test size and number of samples. The 4 rep sections were separated in case there are large differences in intensity of rhizomania and not to hit a section of the field without rhizomania. In this case, the two sections are very similar and were combined. Test had moderate rhizomania. Otherwise there appeared to be little other disease pressure. Powdery mildew was controlled until very late in the season. Plots were

TEST 1406. MICHIGAN SUGAR, WESTERN SUGAR, SOUTHERN MINNESOTA BEET SUGAR CODED HYBRID EVALUATION UNDER RHIZOMANIA,
SALINAS, CA, 2006
(cont.)

Variety	Description	Acre Yield		Beets Sucrose		Soluble Solids		Stand Harv		DI		%R		%R		Foliar		Foliar	
		Lbs	Tons	%	%	%	%	No.	No.	%	%	%	%	%	%	Score	Seg	Score	PM

NOTES: (cont.)

partially topped, lifted, laid out on the soil surface, and roots individually scored for rhizomania, where 1 = normal root to 9 = very severe rhizomania or dead. Few roots were scored > 7 and < 2. The beets were then topped, bagged, washed, weighed by plot, and run thru the sugar lab. Brei was measured for soluble solids and filtrate for % sugar.

Rhizomania: DI = Disease Index = average score of each plant within the variety; % Resistant(0-3) = total roots in classes 0+1+2+3/total roots scored. %Resistant(0-4) = roots in classes 0-4/total roots scored. Because test was mild, it was observed that many of the roots in the susceptible checks were scored as 4 or less but in the resistant checks, some resistant roots were also scored as 4's or higher. I.e., there did not appear to be a discrete separation between resistant and susceptible roots based on the action of the Rz1 allele.

Checks: Roberta is a widely grown hybrid in Europe. In the absence of rhizomania, it performs very well in California as well. Beta4430R is a popular variety in California with Rz1. BetaG017R is an experimental hybrid with Rz2 allele. Angelina is a European variety with high performance and has both Rz1 + Rz2 alleles. USH11 was widely grown in California 20 years ago, but is now relatively low performing and highly susceptible to rhizomania. Monohikari seed was obtained from Seedex. HM-17 (Syngenta) was obtained from Michigan Sugar Company several years ago, and after being used in these trials was found to have developed low seed viability under our storage conditions. Stands for HM-17 were low and yield was adjusted for missing feet.

Foliar Score. Before harvest, the canopy of each plot was scored for general color, where: 1 = dark green, 2 = green, 3 = light green or mixed green to yellowish, 4 = mostly yellowish, 5 = uniformly yellowish in the manner of susceptible varieties under rhizomania.

Foliar Segregation Score. Because the canopy or Foliar Score did not necessarily capture the plant to plant segregation or variability within a plot, i.e., the segregation for rhizomania, it was also attempted to score the plots for segregation for green vs yellowish, where 1 = all dark green, 2 = about 25% yellowish plants, 3 = 50% yellowish plants, 4 = 75% yellowish, and 5 = all yellowish. It appears that the scores for Foliar Color and Segregation are very much the same. One concern and problem for both of these rating methods is that we were wanting to evaluate the yellowing caused by rhizomania, but the plants also seemed to be segregating and variable for another yellowing/leaf chlorosis that more resembled Mg/Mn/Fe/Zn deficiency. I do not know what the relationship is between the light yellowing generally attributed to rhizomania and the "Mg" yellowing. It is also difficult with these scoring methods to separate the color due to natural canopy intensity of green and the effects of rhizomania.

TEST 1406. MICHIGAN SUGAR, WESTERN SUGAR, SOUTHERN MINNESOTA BEET SUGAR CODED HYBRID EVALUATION UNDER RHIZOMANIA,
SALINAS, CA, 2006
(cont.)

Variety	Description	Acre Yield		Soluble Stand Harv		%R (0-3)		%R (0-4)		Foliar Color		Foliar Seg	
		Sugar	Beets	Sucrose	Solids	Count	No.	Count	No.	Score	Score	Score	Score
		Lbs	Tons	%	%	No.	%	No.	%	Score	Score	Score	Score

Coefficients of correlation (r) were calculated:

	DI	%R(0-3)	%R(0-4)	Fol.Color	Fol. Seg	SY/A	RY/A	%S	Harv. Count
Disease Index (DI)									
%R (0-3)	-0.97**	-0.97**	-0.95**	0.71**	0.68**	-0.77**	-0.70**	-0.46**	-0.29**
%R (0-4)	-0.95**	0.97**	0.97**	-0.71**	-0.69**	0.78**	0.70**	0.48**	0.31**
Foliar Color	0.71**	0.97**	-0.73**	-0.73**	-0.72**	0.79**	0.69**	0.55**	0.30**
Foliar Segregation	0.68**	-0.69**	-0.72**	0.85**	0.85**	-0.67**	-0.58**	-0.45**	-0.19**
Gross Sugar Yield (SY/A)	-0.77**	0.78**	0.79**	-0.67**	-0.66**	-0.66**	-0.57**	-0.47**	-0.18**
Tons Roots/Acre (RY/A)	-0.70**	0.70**	0.69**	-0.58**	-0.66**	0.94**	0.94**	0.46**	0.32**
%S	-0.46**	0.48**	0.55**	-0.45**	-0.47**	0.46**	0.14**	0.14**	0.31**
Harvest Count	-0.29**	0.31**	0.30**	-0.19**	-0.18**	0.32**	0.31**	0.14**	0.14**

TEST B106. EVALUATION OF TOPCROSS HYBRIDS; HYBRIDS WITH Rz2 FOR RESISTANCE TO RHIZOMANIA,
IMPERIAL VALLEY, 2005-2006

24 entries x 8 reps., RCB (E)
1-row plots, 18 ft. long

Planted: September 22, 2005
Harvested: June 6, 2006

Variety	Description	Acre Yield		Beets/ 100'	Bolters %	Clean Beets %	NO3-N ppm
		Sugar lbs	Beets Tons				
<u>Checks</u>							
Beta G017R	Betaseed, 4-22-05	11511	39.84	155	3.1	98.2	273
Beta 4430R	Betaseed, 8-21-03	12561	44.09	159	0.0	99.0	386
<u>Experimental hybrids</u>							
5933H50	C790-15CMS x 933 (C)	10222	37.32	144	2.5	97.5	408
5933H5	C833-5CMS x 933 (C)	11112	40.59	137	0.5	98.1	320
Y595H5	C833-5CMS x RZM Y95 (C)	10217	37.88	140	4.0	98.3	366
P531CTH5	x P431CT, (CP09)	11316	41.10	149	8.6	98.1	293
R521H5	x IRZM-% R321	10664	41.52	145	3.2	97.9	329
R539H5	x R039, (C39R)	10732	40.46	139	5.1	98.1	367
<u>Topcross hybrids</u>							
5944H5	C833-5CMS x 944 (C)	11253	40.08	145	0.0	97.9	271
5944H49	4849mmaa x 944 (C)	10807	38.94	146	0.0	98.0	358
R578H5	C833-5CMS x R378, (C78/3)	10887	39.84	151	3.6	98.1	306
R578H33	4842-226H5 x R378, (C78/3)	10102	38.28	139	4.1	98.1	369
R578H34	4842-256H5 x R378	10500	39.85	154	2.7	98.5	379
R578H35	4842-262H5 x R378	11169	42.14	153	3.7	98.2	454
R578H36	4836-13H5 x R378	10239	38.29	139	5.4	98.0	348
R578H37	4837-6-203H5 x R378	10797	40.09	145	1.9	98.4	381
<u>Rz2 hybrids</u>							
R578H50	C790-15CMS x R378, (C78/3)	11436	42.32	152	9.1	97.8	413
R540H5	C833-5CMS x IRZM-% R940,R840,R740	11002	40.58	141	16.1	97.8	301
R525H5	x IRZM-% R325, ...	10119	38.03	118	5.5	97.8	356
R541/2H5	x IRZM-% R641,R642	9584	36.34	135	2.7	97.7	354

TEST B106. EVALUATION OF TOPCROSS HYBRIDS; HYBRIDS WITH Rz2 FOR RESISTANCE TO RHIZOMANIA,
IMPERIAL VALLEY, 2005-2006

(cont.)

Variety	Description	Acre yield		Beets/ 100'	Bolters %	Clean Beets %	NO3-N ppm
		Sugar	Beets				
		Lbs	Tons				
Rz2 hybrids (cont.)							
R524-302H5	x R324-302, -306	8997	34.08	13.22	134	0.0	339
R525-301H5	x R325-301, -302	10395	37.32	13.86	149	1.6	336
R524-2/3H5	x R324-213, -215, -223, -318						
		10201	37.30	13.70	122	1.2	363
R537-302H5	x R337-302	10395	36.14	14.34	149	0.9	312
Mean							
LSD (.05)		10675.7	39.27	13.61	143.3	3.6	349.2
C.V (%)		1223.1	4.08	0.65	14.4	4.4	68.8
F value		11.6	10.54	4.83	10.2	125.8	20.0
		2.7*	2.41NS	2.94**	3.5**	5.3**	3.2**

NOTES:

Test B106 was grown in Field J in the absence of BNYVV (rhizomania).

R521, R540, R525, R541/2, R524-302, R525-301, R524-2/3, and R537-302 are breeding lines with C37 background and resistance to rhizomania transferred from WB41, WB42, and/or WB151. These lines are being evaluated at Salinas under normal BNYVV and IV-BNYVV conditions and at Kimberly, ID (Gillen & Strausbaugh).

TEST B206. PERFORMANCE OF HYBRIDS CORRESPONDING TO ENTRIES IN SBCN/RHIZOMANIA TESTS,
IMPERIAL VALLEY, 2005-2006

48 entries x 8 reps., RCB(E)
1-row plots, 18 ft. long

Planted: September 22, 2005
Harvested: June 7, 2006

Variety	Description	Acre Yield		Beets/ 100'	Bolters	Clean Beets	NO3-N	
		Sugar	Beets					
		Lbs	Tons	%	No.	%	ppm	
Checks								
Phoenix	Holly Hybrids, 9-12-03	12686	48.91	13.01	161	1.5	98.2	370
Beta 4430R	Betaseed, 8-21-05	13134	45.28	14.48	158	0.9	98.9	298
Beta 4309R	Betaseed, 9/05	14374	50.29	14.26	158	19.2	96.7	361
Acclaim	Holly Hybrids, 3-15-05	11218	43.63	12.87	157	0.0	98.5	330
P531CTH50	C790-15CMS x P431CT, (CP09)	11592	42.21	13.76	165	27.0	97.2	315
Y591H50	C79-15CMS x IRZM-8 Y391	11913	43.92	13.56	163	7.8	97.3	305
R578H50	C790-15CMS x R378, (C78/3)	11126	40.65	13.70	159	14.8	97.8	309
1927-4H5	C833-5CMS x RZM 9927-4, (C927-4)	11628	41.45	14.02	158	15.2	96.6	243
Hybrids with progenies from R22, C50, C51 germplasm								
5927-202H50	C790-15CMS x 4927-202, (CN927-202)	11531	42.16	13.71	151	13.3	97.3	281
5927-4-302H5	C833-5CMS x 3927-4-302	11770	41.05	14.35	138	1.6	97.5	211
5927-4-303H5	C833-5CMS x 3927-4-303	11913	41.93	14.23	142	1.3	96.6	254
5927-4-307H5	C833-5CMS x 3927-4-307	11470	41.74	13.74	139	3.1	96.5	247
5927-4-308H5	C833-5CMS x 3927-4-308	11607	42.09	13.81	140	8.3	96.3	293
5927-4-309H5	C833-5CMS x 3927-4-309	11624	43.07	13.49	147	0.5	97.2	216
5921-306H5	C833-5CMS x 3921-306, (CN921-306)	11589	41.58	13.95	161	15.2	97.4	244
5926-11-3-22H5	C833-5CMS x 4926-11-3-22, (CN926-11-3-22)	10734	37.74	14.20	147	1.5	97.6	255
R522H5	C833-5CMS x IRZM R522 (Sp) , (C51,R22)	10011	37.53	13.32	131	20.4	97.0	335
Y577H5	C833-5CMS x IRZM Y277, Y375	11028	40.22	13.70	140	2.8	97.7	249
Y575-305H50	C790-15CMS x Y375-305	12091	44.84	13.48	149	0.9	97.4	366
Y575-311H50	C790-15CMS x Y375-311	11111	41.25	13.47	153	13.2	97.5	273
R521H5	C833-5CMS x IRZM-8 R321,R021	11194	41.59	13.44	147	4.5	96.2	288

TEST B206. PERFORMANCE OF HYBRIDS CORRESPONDING TO ENTRIES IN SBCN/RHIZOMANIA TESTS,
IMPERIAL VALLEY, 2005-2006

(cont.)

Variety	Description	Acre Yield		Beets/ 100'	Bolters %	Clean Beets %	NO3-N ppm
		Sugar Lbs	Beets Tons				
<u>Hybrids with progenies with WB242 and other Bvm germplasm</u>							
N572-233H5	C833-5CMS x N472-233	10573	40.41	13.07	158	7.5	97.6
N512-11H5	C833-5CMS x N412-11	11518	40.21	14.33	154	1.9	96.9
N512-13H5	C833-5CMS x N412-13	12216	46.26	13.27	156	0.3	97.4
P529-305H50	C790-15CMS x P329-305	12812	45.28	14.16	150	3.7	97.3
P507-303H50	C790-15CMS x P307-303	11811	41.91	14.09	149	3.1	97.7
P507-304H50	C790-15CMS x P307-304	12122	44.85	13.51	149	5.4	97.6
P507-306H50	C790-15CMS x P307-306	11480	41.67	13.83	158	2.1	97.0
P507-308H50	C790-15CMS x P307-308	12668	49.31	12.85	156	7.9	97.7
P507-311H50	C790-15CMS x P307-311	12429	46.74	13.28	153	2.1	97.0
<u>Hybrids that segregate for Hs-1 from B.procumbens</u>							
R578H94	N465-9HO(g) x R378, (C78/3)	11277	45.70	12.31	152	2.4	97.6
R578H99	N469HO(g) x R378, (C78/3)	10489	38.89	13.49	161	2.0	97.3
<u>Hybrids from commercial companies with NR</u>							
<u>Betaseed</u>							
2VK0305	Betaseed, 9-16-05	12235	42.74	14.34	167	4.4	97.3
OVK6280	Betaseed, 9-16-05	11995	45.82	13.07	151	9.0	97.5
2AP0852	Betaseed, 9-16-05	10399	41.49	12.57	156	11.2	96.3
2EN5066	Betaseed, 9-16-05	12960	46.18	14.03	177	5.1	98.7
<u>Syngenta</u>							
Hil-2	Syngenta, 9/05	9992	38.82	12.97	156	29.5	96.2
Hil-3	Syngenta, 9/05	10919	43.79	12.42	158	8.1	96.9
Hil-4	Syngenta, 9/05	12359	41.74	14.84	163	2.6	97.8
Hil-5	Syngenta, 9/05	13008	42.17	15.45	149	0.0	97.9
HXN1	Holly Hybrids, 4/05/05	11468	43.60	13.22	143	15.5	98.0
HXN2	Holly Hybrids, 4/05/05	10980	38.99	14.11	156	21.1	98.4

TEST B206. PERFORMANCE OF HYBRIDS CORRESPONDING TO ENTRIES IN SBCN/RHIZOMANIA TESTS,
IMPERIAL VALLEY, 2005-2006

(cont.)

Variety	Description	Acre Yield		Beets/ 100'	Bolters %	Clean	
		Sugar	Beets			Beets	NO3-N
		Lbs	Tons			%	ppm
Checks							
Roberta	Betaseed, 2-25-04	15141	54.17	13.98	0.0	98.2	289
US H11	Susc. check, 10-4-02	9019	37.64	11.98	0.0	97.3	436
Angelina	Betaseed (KWS), 9-19-05	12486	44.46	14.02	8.6	98.2	333
R578H5	C833-5CMS x R378, (C78/3)	12867	46.96	13.71	4.1	97.8	269
P531H5	C833-5CMS x P431CT, (CP09)	13054	47.04	13.87	11.5	98.2	284
Y595H5	C833-5CMS x Y95(C)	11404	41.66	13.68	7.4	98.1	276
Mean		11771.3	43.16	13.65	7.3	97.5	303.9
LSD (.05)		1533.7	5.39	0.72	6.8	1.1	67.7
C.V. (%)		13.2	12.67	5.32	95.4	1.2	22.6
F value		3.8**	3.12**	6.48**	2.1**	8.9**	6.9**

NOTES: See Tests B406 through B706 for performance under sugarbeet cyst nematode (SBCN) conditions. Tests in Field J at Brawley (B106-B306) tested negative for both SBCN and rhizomania. Tests in Field K were negative for rhizomania and positive for SBCN.

For all tests, one sample per plot was run for sugar analysis by Spreckels Sugar Company. Tests were grown at the Imperial Research Center, Brawley, California.

For B206, soil samples were taken on 2/15/06 from plots of Phoenix, Beta 4430R, 5927-202H50, 5926-11-3-22H5, 2AP0852, and Hil-2. No SBCN could be detected.

TEST B306. EVALUATION OF HYBRIDS WITH PROGENY LINE POLLINATORS, IMPERIAL VALLEY, 2005-2006

48 entries x 8 reps., RCB(E)
1-row plots, 18 ft. long

Planted: September 22, 2005
Harvested: June 8, 2006

Variety	Description	Acre Yield		Beets/ 100'	Bolters %	Clean Beets %	NO3-N ppm
		Sugar	Beets				
		Lbs	Tons				
<u>Checks</u>							
Beta 4430R	Betaseed, 8-21-03	11598	41.25	153	3.8	98.8	327
Phoenix	Holly Hybrids, 9-12-03	9945	38.17	147	4.7	98.4	378
Acclaim	Holly Hybrids, 3-15-05	10445	41.02	149	0.0	98.8	326
Beta 4309R	Betaseed, 9/05	12813	44.18	156	25.8	98.5	348
<u>S₁ progeny from R278H23 = CZ25-9aa x C78/3</u>							
R578H23-308H50	C790-15CMS x R378H23-308	11201	39.55	142	0.0	97.8	296
R578H23-312H50	C790-15CMS x R378H23-312	10156	35.62	146	0.5	96.7	330
R578H23-320H50	C790-15CMS x R378H23-320	10101	33.85	155	3.1	96.7	230
R578H23-325H50	C790-15CMS x R378H23-325	10992	39.29	152	1.8	96.9	277
<u>S₁ progeny from R278H40 = C930-35aa x C78/3</u>							
R578H40-306H50	C790-15CMS x R378H40-306	11362	39.57	151	3.6	96.9	291
R578H40-312H50	C709-15CMS x R378H40-312	10229	35.73	148	18.0	97.1	279
R578H40-324H50	C790-15CMS x R378H40-324	10774	37.42	149	5.8	97.1	267
R578H50	C790-15CMS x R378, (C78/3)	9969	36.41	146	11.1	97.7	295
<u>S₁ progeny from Y291H23 = CZ25-9aa x Y191</u>							
Y591H23-311H50	C790-15CMS x Y391H23-311	12276	41.37	164	3.0	97.0	207
Y591H23-313H50	C790-15CMS x Y391H23-313	11130	38.04	155	6.6	97.4	234
Y591H23-314H50	C790-15CMS x Y391H23-314	12927	46.09	142	1.3	97.3	298
Y591H23-322H50	C790-15CMS x Y391-H23-322	10088	35.27	144	3.8	97.2	215
<u>S₁ progeny from Y291H41 = C941aa x Y191</u>							
Y591H41-301H50	C790-15CMS x Y391H41-301	10179	35.33	156	7.4	97.3	236
<u>Checks</u>							
Y595H50	C790-15CMS x RZM Y95 (C)	10882	40.46	151	11.5	97.6	315
5944H50	C790-15CMS x 944 (C)	10608	38.79	156	2.7	97.3	313
5930-35H50	C790-15CMS x 2930-35, (C930-35)	11313	39.02	159	4.8	97.6	278

TEST B306. EVALUATION OF HYBRIDS WITH PROGENY LINE POLLINATORS, IMPERIAL VALLEY, 2005-2006

(cont.)

Variety	Description	Acre Yield		Beets/ 100'	Bolters %	Clean Beets %	NO3-N ppm
		Sugar	Beets				
		Lbs	Tons				
<u>S₁ progeny from 2943-9 = CZ25-9aa x 943</u>							
5943-9-6H50	C790-15CMS x 3943-9-6	11195	39.93	143	1.0	95.9	249
5943-9-7H50	C790-15CMS x 3943-9-7	10858	38.26	155	2.1	96.3	302
<u>S₁ progeny from 2943-19 = C930-19aa x 943</u>							
5943-19-312H50	C790-15CMS x 3943-19-312	11270	37.78	158	12.6	98.1	207
<u>S₁ progeny from 2943-35 = C930aa x 943</u>							
5943-35-301H50	C790-15CMS x 3943-35-302	11177	37.78	149	0.5	96.4	334
5943-35-318H50	C790-15CMS x 3943-35-318	11591	40.78	145	1.0	97.9	300
<u>S₁ progeny from 2930-19 = C930-19</u>							
5930-19-312H50	C790-15CMS x 3930-19-312	12278	41.16	154	0.9	96.8	211
5930-19-325H50	C790-15CMS x 3930-19-325	11492	41.62	145	1.5	96.6	242
<u>S₁ progeny from 2930-35 = C930-35</u>							
5930-35-312H50	C790-15CMS x 3930-35-312	11282	36.67	148	2.2	98.0	226
<u>S₁ progeny from Z225-9 = CZ25-9</u>							
Z525-9-307H50	C790-15CMS x Z325-9-307	12025	40.12	153	0.0	97.0	242
Z525-9-308H50	C790-15CMS x Z325-9-308	12239	42.03	145	0.0	97.0	245
<u>S₁ progeny from 2936-10</u>							
5936-10-310H50	C790-15CMS x 3936-10-310	10759	39.39	151	14.3	97.5	302
<u>S₁ progeny from 2936-16</u>							
5936-16-313H50	C790-15CMS x 3936-16-313	10778	35.68	149	2.8	98.1	181
<u>S₁ progeny from CR009-1 & CR10-2, CR11-7, & CR11-88</u>							
CR509-1-312H50	C790-15CMS x CR309-1-312	9983	36.82	145	5.2	96.8	344
CR510-2-305H50	C790-15CMS x CR310-2-305	9924	39.08	141	11.7	97.3	354
CR511-7-302H50	C790-15CMS x CR311-7-303,-304	11028	40.44	152	2.8	96.5	311
CR511-88H50	C790-15CMS x CR311-88, (CR11-88)	10704	40.14	153	6.8	97.9	336

TEST B306. EVALUATION OF HYBRIDS WITH PROGENY LINE POLLINATORS, IMPERIAL VALLEY, 2005-2006

(cont.)

Variety	Description	Acre Yield		Beets/ 100'	Bolters %	Clean Beets %	NO3-N ppm
		Sugar	Beets				
		Lbs	Tons	No.	%	%	
Experimental hybrids and retests							
P531CTH50	C790-15CMS x P431CT, (CP09)	10371	37.30	138	31.4	97.8	262
O5-FC1036H50	C790-15CMS x RZM 04-FC1028, 37, 38	9229	35.36	141	24.0	97.7	338
O5-FC1030-15H50	C790-15CMS x 03-FC1030-15	7850	33.11	144	40.4	97.8	285
O5-FC1030-16H50	C790-15CMS x 03-FC1030-16	8387	32.81	150	27.5	97.4	371
O5-FC1022H50	C790-15CMS x RZM-ER-% 20031022	10021	34.69	144	23.4	97.7	253
O5-FC1018H50	C790-15CMS x RZM-CR-% 20031018	8069	30.90	139	36.3	97.0	315
O5-FC1019H50	C790-15CMS x RZM-CR-% 20031019	8679	34.88	147	37.9	97.7	354
Y590-40H50	C790-15CMS x Y390-40	10577	38.65	156	1.8	97.5	241
R480-6H50	C790-15CMS x R280-6	11655	41.74	142	17.4	97.9	301
4952-202H50	C790-15CMS x 2952-202, (CZ25 x Y90)	13076	47.27	161	3.6	97.2	269
4954-204H50	C790-15CMS x 2954-204, (C941 x Y90)	11115	40.22	152	0.5	97.5	344
4953-209H50	C790-15CMS x 2953-209, (C931 x Y90)	11139	38.95	156	3.2	96.9	257
Mean		10786.2	38.54	149.5	9.0	97.4	285.6
LSD (.05)		1312.3	4.19	14.0	6.4	0.9	60.4
C.V. (%)		12.4	11.03	9.5	72.0	0.9	21.5
F value		5.9**	4.65**	6.40**	1.4NS23.4**	4.0**	5.0**

NOTES: Test B306 was grown in Field J under relative nondiseased conditions.

Most of the experimental hybrids in test B306 have pollinators that were selected from S₁ progenies produced from F₁ hybrids between self-fertile, aa lines and self-sterile lines. The self-fertile lines, (e.g. CZ25-9, C930-35) have R_{z1} and high %S from Polish germplasm. The self-sterile lines, (e.g. C78/3, Y191) have been under long term population improvement at Salinas. It was of interest to see if very early generation, S₁ progeny tests, could be used to identify favorable combinations of sugar yield, %S, disease resistance, etc.

The S₁ progenies were produced by selfing Aa F₁ plants. The progeny tests were run at Salinas under virus yellows, rhizomania, etc. conditions. The best S₁ progenies were selected, increased, and/or recombined (aa x A), and used as pollinators onto a common mm tester, C790-15CMS. This is a test of these experimental hybrids. Similar tests are being run at Salinas.

TEST B406. HYBRIDS WITH COMBINED RESISTANCE TO RHIZOMANIA & SBCN, IMPERIAL VALLEY, 2005-2006

24 entries x 8 reps., RCB(E)
1-row plots, 18 ft. long

Planted: September 22, 2005
Harvested: June 14, 2006

Variety	Resistance Rz NR1 NR2	Description	Acre Yield			Beets/ 100'	Root %	Clean Beets %	NO3-N ppm	Mean Appear Score
			Sugar Lbs	Relative SY(%)	Beets Tons					
Checks										
Beta 4430R	✓	Betaseed, 8/21/03	8550	65.1	26.54	170	0.0	98.2	199	3.8
Phoenix	✓	Holly Hybrids, 9/12/03	6910	54.5	22.71	181	4.0	97.8	274	4.1
Roberta		Betaseed, 2/25/04	8086	53.4	24.99	169	5.4	97.3	167	4.1
US H11		Susc. check, 10/4/02	4465	49.5	17.08	178	1.9	96.7	319	3.8
Hybrids with R22,C50,C51 germplasm										
P531CTH50	✓	x C790-15CMS	7136	61.6	23.82	188	0.3	95.8	195	2.5
1927-4H5	✓	x C833-5CMS								
		x P431CT, (CP09)	7136							
		x RZM 9927-4, (C927-4)	9032							
5927-4-302H5	✓	x C833-5CMS	8144	77.7	31.05	155	1.6	97.3	210	2.8
5927-4-303H5	✓	x C833-5CMS	10331	69.2	26.03	156	1.0	96.5	132	2.8
	✓	x C833-5CMS		86.7	35.38	161	3.1	97.6	169	2.1
5927-4-307H5	✓	x C833-5CMS	6586	57.4	23.20	138	5.6	96.1	213	3.5
5927-4-308H5	✓	x C833-5CMS	11057	95.3	37.93	154	0.0	97.2	198	2.1
5927-4-309H5	✓	x C833-5CMS	5975	51.4	19.53	166	3.8	95.8	110	3.5
Y575-305H50	✓	x C790-15CMS	9163	75.8	31.85	167	1.1	96.3	256	2.2
Hybrids with WB242 germplasm										
P507-303H50	✓	x C790-15CMS	9497	80.4	31.58	168	3.9	96.6	165	1.4
P507-304H50	✓	x C790-15CMS	6186	51.0	21.58	173	0.8	95.9	204	2.8
P507-308H50	✓	x C790-15CMS	8747	69.0	30.32	158	2.1	97.0	227	1.6
P507-311H50	✓	x C790-15CMS	9484	76.3	30.70	175	0.0	96.4	165	1.8
Hybrids that segregate for Hs-1 from B.procumbens										
R578H94	✓	x N465-9HO(g)	6962	61.7	25.71	161	0.0	96.9	239	2.8
R578H99	✓	x N469HO(g)	5725	54.6	19.84	174	2.3	96.7	183	3.6

TEST B406. HYBRIDS WITH COMBINED RESISTANCE TO RHIZOMANIA & SBCN, IMPERIAL VALLEY, 2005-2006

(cont.)

Variety	Resistance Rz NR1 NR2	Description	Acres Yield			Beets/ 100'			Clean	Mean		
			Sugar	Relative	Beets	Sucrose	100'	Rot				
											Lbs	SY(%)
Experimental hybrids												
Y577H5	✓	x C833-5CMS	7819	70.9	26.20	14.88	167	0.4	97.2	153	2.9	
R522H5	✓	x C833-5CMS	7926	79.2	27.05	14.62	150	0.5	95.5	171	2.8	
Hybrids from commercial companies												
2VK0305	✓	Betaseed, 9/16/05	10842	88.6	34.59	15.67	184	0.0	97.8	159	2.1	
2AP0852	✓	Betaseed, 9/16/05	7306	70.3	24.73	14.71	172	3.3	96.6	171	2.5	
Hil-4	✓	Syngenta, 9/05	8338	67.5	26.59	15.69	174	1.1	97.4	143	2.8	
HXN3	✓	Holly Hybrids, 4/05	9420		30.02	15.73	158	0.0	97.9	189	3.1	
Mean			8070.3		27.04	14.88	166.6	1.8	96.9	192.0	2.8	
LSD (.05)			1063.5		3.40	0.71	17.6	4.0	1.3	42.1	0.4	
C.V. (%)			13.4		12.76	4.85	10.7	231.3	1.4	22.2	15.7	
F value			18.9**		18.47**	9.20**	3.3**	1.5NS	2.5**	9.6**	23.9**	

NOTES: See Test B206 for non-SBCN conditions and B506 under SBCN conditions.

For B406, soil samples were taken on 2/15/06 and at harvest from plots of Beta 4430R, Phoenix, 2VK0305, and 2AP0852. For each variety across all reps, soil was composited before counting. For 2/15/06, counts for eggs + larvae/100g soil were 3655, 4611, 1768, and 728, respectively. At harvest (6/09/06), counts were 3706, 6000, 4567, and 3544, respectively.

Relative Sugar Yield (%) was calculated between the mean of the variety in Test B406 under SBCN conditions and Test B206 under nondiseased conditions.

TEST B506. HYBRIDS WITH COMBINED RESISTANCE TO SBCN & RHIZOMANIA FROM VARIOUS SOURCES, IMPERIAL VALLEY, 2005-2006

24 entries x 8 reps., RCB(E)
2-row plots, 18 ft. long

Planted: September 22, 2005
Harvested: June 14, 2006

Variety	Resistance Rz NR1 NR2	Description	Acre Yield			Beets/ 100'	Clean Beets	Root Rot	NO3-N ppm	Mean Appear Score
			Sugar Lbs	Relative SY(%)	Beets Tons					
Checks										
Phoenix	✓	Holly Hybrids, 9/12/03	7842	61.8	24.17	16.26	168	3.1	96.6	191
Beta 4430R	✓	Betaseed, 8/21/03	9178	69.9	27.11	17.04	175	0.0	97.8	114
Roberta		Betaseed, 2/25/04	9141	60.4	27.93	16.47	157	3.0	97.8	131
US H11		Susc. check, 10/4/02	5157	57.2	17.99	14.31	178	3.3	96.3	169
USDA experimental hybrids										
Resistance from R22,C50,C51										
5927-202H50	✓	✓ C790-15CMS x 4927-202, (CN927-202)	10061	87.3	33.45	15.11	178	0.8	96.9	132
5926-11-3-22H5	✓	✓ C833-5CMS x 4926-11-3-22, (CN926-11-3-22)	11152	103.9	35.09	15.88	149	0.0	97.1	90
5921-306H5	✓	✓ C833-5CMS x 3921-306, (CN921-306)	10155	87.6	32.68	15.53	167	0.4	97.0	89
Y575-311H50	✓	✓ C790-15CMS x Y375-311	9329	84.0	31.73	14.72	178	0.0	97.0	160
Resistance from WB242 & CN12 & CP07										
N512-11H5	✓	✓ C833-5CMS x N412-11	10208	88.6	32.99	15.46	156	0.9	96.4	95
N512-13H5	✓	✓ C833-5CMS x N412-13	6889	56.4	22.14	15.57	158	0.6	95.3	116
P507-306H50	✓	✓ C790-15CMS x P307-306	8411	73.3	26.82	15.66	165	0.5	95.9	80
Resistance from Bvm & CN72										
N572-233H5	✓	✓ C833-5CMS x N472-233	9192	86.9	30.87	14.88	165	0.2	97.4	164
Resistance from Commercial companies										
Betaseed										
2VK0305	✓	✓ 9/16/05	10885	89.0	35.38	15.38	175	0.0	97.8	125
0VK6280	✓	✓ 9/16/05	10805	90.1	36.44	14.81	160	1.7	97.3	159
2AP0852	✓	✓ 9/16/05	9213	88.6	31.27	14.74	173	2.8	96.2	113
2EN5066	✓	✓ 9/16/05	12174	93.9	38.59	15.80	181	0.2	98.4	223

(cont.)

Variety	Resistance Rz NR1 NR2	Description	Acre Yield		Beets/ 100'		Clean		Mean Appear Score
			Sugar Lbs	Relative SY (%)	Beets Tons	Sucrose %	No.	Rot %	ppm NO3-N
<u>Syngenta</u>									
Hil-2	✓	Syngenta, 9/05	8952	89.6	30.10	14.90	182	2.6	96.2 153
Hil-3	✓	Syngenta, 9/05	9153	83.8	32.07	14.25	165	5.7	96.7 147
Hil-4	✓	Syngenta, 9/05	10458	84.6	33.78	15.51	176	1.6	97.9 121
Hil-5	✓	Syngenta, 9/05	6823	52.5	18.05	18.89	164	0.8	97.0 77
<u>Holly Hybrids</u>									
HXN1	✓	Holly Hybrids, 4/05/05	9397	81.9	29.23	16.14	150	1.2	97.0 106
HXN2	✓	Holly Hybrids, 4/05/05	5794	52.8	18.84	15.48	167	0.2	97.6 121
<u>USDA Experimental hybrids</u>									
P531CTH50	✓	C790-15CMS x P431CT, (CP09)	6470	55.8	20.63	15.71	164	0.7	95.8 124
Y577H5	✓	C833-5CMS x IRZM Y277, Y375	7227	65.5	25.20	14.37	162	1.3	97.8 148
Mean			8919.5		28.86	15.54	167.2	1.3	97.0 131.1
LSD (.05)			994.5		2.97	0.82	11.2	2.6	1.0 49.8
C.V. (%)			11.3		10.43	5.38	6.8	199.4	1.0 38.6
F value			25.0**		31.94**	11.40**	5.6**	2.4**	4.8** 4.0** 33.6**

NOTES:

Rz = Holly (Rz1) or other sources of resistance to rhizomania.

NR1 = *B. procumbens* source of nematode resistance.

NR2 = Possible other sources of nematode resistance or tolerance.

See Test B206 for performance under relative nondiseased conditions.

Relative Sugar Yield (%) was calculated between the mean of the variety in Test B406 under SBCN conditions and Test B206 under nondiseased conditions.

(cont.)

SUGARBEET CYST NEMATODE SOIL COUNTS

Variety	Resistance <u>Rz NR1 NR2</u>	Description	Cysts Empty		Cysts Full/Viable		No. Eggs & Larvae	
			2/15/06	6/09/06	2/15/06	6/09/06	2/15/06	6/09/06
Phoenix	✓	Holly Hybrids, 9/12/03	216	234	41	61	4450	3290
Beta 4430R	✓	Betaseed, 8/21/03	232	172	35	59	4682	4261
5927-202H50	✓	C790-15CMS x 4927-202, (CN927-202)	244	156	33	32	2422	2015
5926-11-3-22H5	✓	C833-5CMS x 4926-11-3-22, (CN926-11-3-22)	230	157	32	46	1970	2010
N512-11H5	✓	C833-5CMS x N412-11	217	183	37	21	2934	741
N512-13H5	✓	C833-5CMS x N412-13	214	172	42	32	4763	1852
P507-306H50	✓	C790-15CMS x P307-306	230	146	30	41	3345	2220
N572-233H5	✓	C833-5CMS x N472-233	207	174	30	43	3345	2780
2VK0305	✓	9/16/05	175	173	24	35	1364	2199
2AP0852	✓	9/16/05	188	150	17	25	638	1153
Hil-2	✓	Syngenta, 9/05	206	100	20	17	406	669

11 varieties sampled on February 15, 2006 and again on June 9, 2006 at harvest.

NOTES: Counts for 100 grams soil. Soil cores taken to 12" deep, 8 cores/plot composited per plot, 3-4 inches from plants. Initial samples at planting not taken. In 2006, counts for individual plots were not made. For each variety, counts were made on soil composited over all reps. From the soil samples used to count cyst nematode, tests were run in the greenhouse to determine if there was BNYVV (rhizomania) in these trials. Based upon the ELISA results of the baited plants, Fields J and K at Brawley do not have rhizomania. BOLV was absent from all but 2 samples. Polymyxa betae occurred.

TEST B606. PERFORMANCE OF LINES WITH RESISTANCE TO RHIZOMANIA & SBCN, IMPERIAL VALLEY, 2005-2006

72 entries x 4 reps., sequential
1-row plots, 18 ft. long

Planted: September 22, 2005
Harvested: June 13, 2006

Variety	Description	Acre Yield		Beets/ 100'	Sucrose %	Bolting %	Root Rot %	Clean Beets %	NO3-N ppm	Mean Appear Score
		Sugar	Beets							
		Lbs	Tons							
Checks										
Phoenix	Holly Hybrids, 9/12/03	6804	23.19	168	14.63	0.9	4.7	97.5	265	3.9
Beta 4430R	Betaseed, 8/21/03	8656	27.51	165	15.74	0.0	0.0	97.9	167	3.9
Angelina	Betaseed, 2/25/04	6846	23.68	168	14.53	1.6	2.9	97.6	192	3.6
Roberta	Betaseed, 2/25/04	9093	27.61	174	16.43	0.0	3.1	96.6	152	3.9
US H11	Susc. check, 10/4/02	5011	18.42	175	13.64	0.0	5.6	96.0	200	3.6
1927-4H5	C833-5HO x RZM 9927-4, (C927-4)	9022	30.49	163	14.82	0.9	0.0	95.9	129	2.9
2VK0305	Betaseed, 9/16/05	11882	38.55	183	15.41	0.0	0.0	97.1	124	1.9
0VK6280	Betaseed, 9/16/05	12131	41.19	168	14.71	0.0	0.0	96.7	155	2.5
2AP0852	Betaseed, 9/16/05	9609	33.27	178	14.43	0.0	5.1	94.8	124	2.0
Hil-4	Syngenta, 9/05	10854	38.53	178	14.06	0.0	0.0	96.5	119	1.3
Hil-3	Syngenta, 9/05	9745	35.19	165	13.88	0.0	6.7	96.4	221	2.9
Beta G017R	Betaseed, 4/22/05	7794	24.18	175	16.11	0.0	1.7	97.1	92	3.0
Multigerm breeding lines										
R578(Sp)	RZM 378(Iso), (C78/3)	6126	21.14	167	14.69	5.1	0.8	96.8	165	3.4
P531CT(Sp)	Inc. P431CT, (CP09)	7721	26.67	156	14.47	10.9	0.0	96.3	150	2.8
P531CT(Iso)	PMR-RZM P431CT, (CP09)	7036	23.88	150	14.81	13.2	0.0	96.1	98	2.5
Y591	IRZM-% Y391	6748	19.60	164	17.15	0.0	0.0	97.6	86	2.8
Y595	RZM Y95(C)	9831	33.28	143	14.82	1.8	0.0	97.2	144	2.1
05-C37	Inc. 04-C37	2543	8.39	160	15.10	0.0	0.0	95.3	59	4.0
R540	IRZM-% R940,R840,R740,(C79-#s)	8071	26.99	172	14.94	11.2	0.7	96.3	114	2.9
R525	IRZM-% R324,R325,R324/5,R337,(C79-2,-3,-9)	3912	13.28	154	14.75	2.9	0.0	95.3	95	3.6
R541/2	IRZM-% R641,R642,(C79-10,-11)	4502	15.50	183	14.39	8.1	3.6	96.1	102	3.8
R522	IRZM-% R522(Sp), (C51)	5865	24.18	160	12.12	30.8	0.0	94.6	208	3.3
Y577	IRZM-% Y277,Y275	6462	22.74	163	14.20	2.7	0.0	97.4	110	3.1
R521	IRZM-% R021,R321(A,aa)	7844	26.64	174	14.73	10.2	0.0	96.9	124	3.3

(cont.)

Variety	Description	Acre Yield		Beets/ 100'	Bolting %	Root Rot %	Clean Beets %	NO3-N ppm	Mean Appear Score
		Sugar	Beets						
		Lbs	Tons						
Multigerm breeding lines (cont.)									
P527	PMR-RZM P427, (CP03)	5279	18.06	14.62	175	3.1	94.5	116	3.0
P528	PMR-RZM P428, (CP04)	7870	30.83	12.84	164	24.5	96.1	157	1.1
R578 (Iso)	RZM R378, (C78/3)	7041	22.42	15.82	145	0.0	96.7	106	3.3
P529-305	Inc. P329-305 (PmPm)	4824	13.91	17.31	149	0.0	96.3	58	3.4
P529	PMR-RZM P429, (CP05)	6733	21.74	15.49	161	0.8	96.1	92	3.0
P530	PMR-RZM P430, (CP06)	6116	19.75	15.51	150	0.0	96.6	90	3.1
P507/8	PMR-RZM P407/8, (CP07)	9917	33.65	14.73	161	0.0	97.5	109	1.1
P507-303	Inc. P307-303	10240	33.52	15.24	163	0.0	95.1	61	1.1
P507-304	Inc. P307-304 (susc. SBCN)	6499	21.35	15.17	177	0.0	96.5	61	2.6
P507-306	Inc. P307-306 (seg NR)	7875	27.23	14.40	156	0.0	94.9	63	1.6
P507-308	Inc. P307-308 (seg NR)	7399	24.21	15.35	147	0.0	97.2	86	1.9
P507-311	Inc. P307-311	10122	32.35	15.65	175	0.0	96.5	78	1.8
P518-6	PMR-RZM P418-6, (CP08)	8971	29.15	15.35	167	0.0	94.3	79	1.1
O5-C37	Inc. 04-C37	2506	8.85	14.20	158	0.0	95.2	71	4.0
Y475	RZM-ER-8 Y275	9968	32.79	15.20	147	4.4	96.9	106	2.1
Y575-305	Inc. Y375-305 (seg NR)	7547	25.99	14.51	147	0.0	98.2	143	2.6
Y575-311	Inc. Y375-311 (NR)	9003	29.60	15.22	168	6.7	97.3	92	2.0
R336	RZM-ER-8 R136, (C79-8)	5017	17.89	14.01	161	5.0	96.3	182	3.3
Multigerm, self-fertile breeding lines									
5944	944(C)aa x A	7149	21.59	16.59	172	0.0	96.2	71	3.1
5933	933(C)aa x A	7162	22.32	16.05	154	0.9	97.0	85	3.3
N524	Inc. N424(g) (A,aa) , (B.pro)	4227	14.11	14.95	154	10.6	94.2	70	3.8
4931	3931aa x A, (C931)	5613	17.14	16.30	146	3.2	94.9	48	3.5
N472 (Sp)	N272-# (C), N372aa x A, (CN72)	8272	31.93	12.96	165	25.1	95.9	227	2.9
N572-233	RZM N472-233	6569	25.44	12.90	164	7.5	97.3	292	3.3
N412 (Sp)	N212-# (C), N312aa x A, (CN12)	10687	36.57	14.64	170	8.2	96.1	94	1.1
N512-11	RZM N412-11 (A,aa)	6464	23.47	13.74	149	0.0	91.6	60	2.5

TEST B606. PERFORMANCE OF LINES WITH RESISTANCE TO RHIZOMANIA & SBCN, IMPERIAL VALLEY, 2005-2006

(cont.)

Variety	Description	Acre Yield		Beets/ 100'	Bolting %	Root Rot %	Clean Beets %	NO3-N ppm	Mean Appear Score
		Sugar	Beets						
		Lbs	Tons						
Multigerm, self-fertile breeding lines (cont.)									
N512-13	Inc. N412-13(A,aa) (susc. SBCN)	1087	4.21	12.85	1.7	0.0	91.3	84	3.6
N412-6	Inc. N212-6 (A,aa) (susc. rzm)	6230	20.84	14.97	20.8	0.0	92.5	88	1.6
N412-10	Inc. N212-10(A,aa)	7653	24.89	15.40	0.0	1.0	96.2	78	2.4
N412-202	Inc. N212-202(A,aa)	6237	22.54	13.86	1.6	0.0	91.6	73	3.0
N412-203	Inc. N212-203(A,aa)	6694	23.59	14.10	0.0	0.0	95.6	159	1.5
N412-205	Inc. N212-205(A,aa)	5613	19.68	14.30	2.0	1.1	97.3	140	1.8
N472-230	Inc. N272-230(A,aa)	4552	18.55	12.28	6.6	1.8	95.4	211	2.6
N472-231	Inc. N272-231(A,aa)	6650	26.18	12.72	65.1	1.1	95.6	192	3.1
5921-306	Inc. 3921-306, (CN921-306)	6617	22.04	14.97	42.3	0.0	97.2	107	1.9
0926	RZM-8 8926(Sp) (A,aa)	7151	24.37	14.67	1.9	0.0	96.4	125	2.4
4926-11-3-22	Inc. 2926-11-3-22, (CN927-11-3-22)	8229	25.93	15.84	0.0	0.0	96.4	56	1.8
5926-11-3-22	RZM 4926-11-3-22, (CN926-11-3-22)	7430	23.67	15.76	0.0	0.0	97.2	52	1.3
4926-11-1-3	Inc. 2926-11-1-3	7326	25.66	14.31	1.7	8.1	97.1	64	2.6
4926-11-7-61	Inc. 2926-11-7-61	6721	20.43	16.43	0.0	3.2	96.5	59	2.1
4926-11-10-91									
	Inc. 2926-11-10-91	7434	23.83	15.59	0.8	3.0	96.6	99	1.5
4927-202	Inc. 2927-4-202(A,aa) , (CN927-202)	6546	24.17	13.48	0.0	1.7	96.8	84	1.6
5927-202	Inc. 4927-202, (CN927-202)	5855	21.99	13.35	0.0	4.6	97.4	72	2.4
5927-4-302	Inc. 3927-4-302 (seg NR)	4223	14.52	14.41	0.0	3.2	96.0	59	3.8
5927-4-303	Inc. 3927-4-303 (NR)	6192	22.80	13.54	0.0	0.7	96.4	136	3.0
5927-4-307	Inc. 3927-4-307 (susc SBCN)	5427	19.84	13.72	0.0	0.0	97.6	153	3.1
5927-4-309	Inc. 3927-4-309 (susc SBCN)	0.0	0.0	0.0	0.0	0.2	--	---	5.0
3927-4	RZM 2927-4(A,aa) , (C927-4)	7276	26.55	13.70	0.0	0.8	97.5	165	2.5
Mean		7103.1	24.17	14.70	4.7	1.2	96.1	117.4	2.6
LSD (.05)		1564.3	5.07	1.01	5.9	4.7	2.0	54.1	0.7
C.V. (%)		15.8	15.03	4.95	90.3	271.9	1.5	33.0	17.9
F value		14.0**	14.97**	8.86**	1.6* 25.3**	1.6*	4.0**	7.6**	12.5**

(cont.)

Variety	Acre Yield		Beets/		Root		Mean
	Sugar	Beets	Sucrose	100'	Bolting	Rot	
	Lbs	Tons	%	No.	%	%	Appear
							Score

NOTES:

See Tests B206, B406, and B506 for hybrids produced from these lines under non-SBCN and SBCN conditions.

See Test B506 for Appearance Score scale.

Tests in Field K at the Imperial Research Center, Brawley, CA have proven to be a way to evaluate for reaction to SBCN. Soil tests have shown this field to be high in SBCN and negative for BNYV (rhizomania). In the past, appearance scores of canopy at harvest in the high heat of summer and sugar yield have been good indicators of differential reaction to SBCN. Based upon the Field K data, lines have been sorted, screened, and selected for reaction to SBCN. Nematode resistant (NR) and nematode susceptible (NS) lines and progeny families have been phenotyped and seed increases made at Salinas based on the data. In general, NR has been identified from WB242, R22 (C51), and other *B. vulgaris maritima* (Bvm) sources. The inheritance and allelism of these breeding materials are still under investigation.

C927-4 is an increase of one S₁ progeny that appeared to segregate for NR:NS in Brawley tests. 3927-4, 2927-4, 1927-4, etc. are versions of C927-4. C927-4 has an R22 component as well as R21 for resistance to rhizomania. From C927-4, S₁ families were evaluated at Brawley and Salinas and in greenhouse container tests at Salinas. CN927-202 is an increase of one S₁ family extracted from C927-4 as are 5927-4-302, 5927-4-303, 5927-4-307, 5927-4-308 (not in test B606, see B206 & B406), and 5927-4-309. Lines 5927-4-303 and 5927-4-308 appear to be homozygous resistant to SBCN. Lines 5927-4-307 and 5927-4-309 appear to be homozygous NS. Line 5927-4-308 is very susceptible to Fusarium stalk blight and seed production is difficult.

Lines N512-#s were extracted from population CN12 with NR from WB242. (also PMR from WB242). N512-11 may be homozygous NR and N512-13 homozygous NS.

Lines P507-#s were extracted as full-sib families from CP07 (P507/8). P507-304 was selected as being NS and P507-303 & P507-311 as being NR. CP07 has a WB242 component.

For B606, soil samples were taken on 2/15/06 in mid-season from Phoenix (2601 eggs+larvae/100 grams soil), Beta 4430R (3765), 2VK0305 (1479), 2AP0852 (630), N572-233 (879), N512-11 (1385), N512-13 (1600), 5921-306 (888), 5926-11-3-22 (570), 5927-202 (1115), 5927-4-302 (539), and 5927-4-307 (2124). At harvest (6/09/06), counts for eggs+larvae/100 grams soil were 3478, 2204, 1450, 1148, 962, 1085, 1813, 1131, 720, 1770, 1437, and 2055, respectively. For each variety, soil was composited across all reps before counting. For N512-11 and N512-13, in the absence of SBCN, the performance of N512-13 is superior (see B206). Under SBCN conditions, N512-13 performs poorly.

TEST B706. S₄ and S_n PROGENY PERFORMANCE UNDER RHIZOMANIA & SBCN, IMPERIAL VALLEY, 2005-2006

96 entries x 2 reps., sequential
1-row plots, 18 ft. long

Planted: September 22, 2005
Harvested: June 12, 2006

Variety	Description	Acre Yield		Beets/ 100'	Bolting %	Root		Clean Beets	NO3-N ppm	Mean Appear Score
		Sugar Lbs	Beets Tons							
Checks										
4931	3931aa x A, (C931)	4925	17.83	131	4.3	0.0	0.0	94.6	239	3.5
N412 (Sp)	N212-# (C), N312aa x A, (CN12)	6460	24.77	128	31.3	0.0	0.0	97.5	246	1.5
N472 (Sp)	N272-# (C), N372aa x A, (CN72)	7459	29.53	170	9.6	0.0	0.0	96.5	356	2.3
N512-11	RZM N412-11 (A,aa), (NR)	6115	23.24	170	0.0	0.0	0.0	94.8	98	2.3
N512-13	Inc. N412-13 (A,aa), (NS)	735	4.19	133	0.0	0.0	0.0	91.4	164	3.5
N572-233	RZM N472-233 (A,aa)	5760	28.79	156	3.6	0.0	0.0	98.4	706	2.8
05-C37	Inc. 04-C37	2931	11.96	178	0.0	1.4	0.0	94.8	191	3.5
5927-202	Inc. 4927-202, (CN927-202)	4062	15.76	192	1.5	5.9	0.0	94.4	160	3.0
N512-11-#s = N412-11⊗. Homozygous for moderate NR?										
N512-11-520	N412-11⊗, (NR)	6710	25.68	150	0.0	0.0	0.0	90.2	125	2.5
N512-11-521		6634	24.28	147	0.0	0.0	0.0	95.8	108	1.8
N512-11-522		6515	23.34	178	0.0	0.0	0.0	94.1	118	2.8
N512-11-523		6459	23.31	150	0.0	0.0	0.0	94.1	89	1.8
N512-11-524		6394	24.49	147	0.0	1.7	0.0	93.8	62	2.3
N512-11-525		5492	19.73	133	0.0	0.0	0.0	94.8	86	1.8
N512-11-526		4799	20.37	150	0.0	0.0	0.0	96.3	170	2.3
N512-11-527		3613	14.32	139	0.0	0.0	0.0	85.6	116	2.8
N512-11-528		5022	18.24	145	1.8	0.0	0.0	88.8	62	2.0
N512-11-529		6269	22.40	142	0.0	0.0	0.0	95.2	72	1.8
N512-11-530		5489	20.82	161	1.6	0.0	0.0	94.9	79	1.8
N512-11-531		6114	22.26	153	0.0	7.4	0.0	96.6	93	2.0

(cont.)

Variety	Description	Acre Yield		Beets/ 100'	Bolting %	Root Rot %	Clean Beets %	NO3-N ppm	Mean Appear Score	
		Sugar	Beets							
		Lbs	Tons							
N512-13-#s = N412-13⊗. Homozogous for NS?										
N412-13⊗, (NS)										
N512-13-550		840	3.76	11.45	117	20.1	0.0	92.6	87	3.5
N512-13-551		1642	5.34	15.88	136	0.0	0.0	93.5	160	3.3
N512-13-552		1137	4.79	12.04	145	0.0	0.0	95.6	91	3.8
N512-13-553		826	3.40	12.04	139	0.0	0.0	91.3	101	4.0
N512-13-554		1522	6.42	11.85	167	0.0	0.0	88.4	132	4.0
N512-13-555		1316	4.57	14.38	161	0.0	0.0	93.9	78	3.5
N512-13-556		1188	4.67	12.73	142	0.0	0.0	95.4	97	3.5
N512-13-557		1063	3.95	13.49	150	0.0	0.0	93.7	59	3.5
N512-19-423 to -426-#s = N412-19-423 to -426⊗										
N412-19-423⊗, (NS)										
N512-19-423-620		3228	9.69	16.87	131	0.0	0.0	96.3	56	3.5
N512-19-423-621		2846	9.39	15.22	131	0.0	0.0	96.2	75	3.0
N512-19-424-630		2450	11.56	11.29	147	0.0	0.0	94.1	86	3.3
N512-19-424-631		2908	10.48	13.87	145	0.0	0.0	94.9	114	3.0
N512-19-425-640		3779	12.79	14.85	142	0.0	0.0	95.4	146	3.0
N512-19-425-641		4077	13.03	15.61	175	0.0	0.0	96.6	78	3.0
N512-19-426-650		2525	8.15	15.50	145	0.0	0.0	96.6	55	3.3
N512-19-426-651		3079	9.90	15.53	142	0.0	0.0	96.0	75	3.0
N512-201-438 to -441-#s = N412-201-438 to 441⊗										
N412-201-438⊗, (NR/Seg)										
N512-201-438-700		4621	16.57	13.97	142	0.0	0.0	93.5	176	1.3
N512-201-438-701		4808	16.63	14.37	131	0.0	0.0	97.8	193	1.8
N512-201-438-702		4567	15.96	14.30	158	0.0	0.0	94.6	138	1.3
N512-201-438-703		3094	10.95	14.14	153	37.5	0.0	96.3	137	2.0
N512-201-439-710		3129	13.37	11.65	158	3.6	0.0	93.5	214	3.0
N512-201-439-711		3982	15.83	12.61	175	0.0	0.0	98.0	177	2.3

(cont.)

Variety	Description	Acre Yield		Beets/ 100'	Bolting %	Root Rot %	Clean Beets %	NO3-N ppm	Mean Appear Score
		Sugar	Beets						
		Lbs	Tons						
N512-201-438 to -441-#s = N412-201-438 to 441⊗ (cont.)									
N512-201-439-712		3878	12.42	15.62	0.0	0.0	97.8	73	2.0
N512-201-439-713		5455	20.09	13.56	0.0	0.0	98.5	155	3.0
N412-201-440⊗, (NR)									
N512-201-440-720		3966	16.12	12.28	2.0	0.0	96.7	222	2.0
N512-201-440-721		3487	14.63	11.95	0.0	0.0	97.7	257	2.8
N512-201-440-722		4935	19.12	12.93	0.0	0.0	97.6	305	2.0
N512-201-440-723		4578	19.01	12.02	0.0	0.0	97.6	385	2.8
N412-201-44⊗, (Seg)									
N512-201-441-730		7217	29.06	12.40	2.3	0.0	97.6	371	2.8
N512-201-441-731		8236	30.77	13.40	0.0	0.0	97.7	194	3.0
N512-201-441-732		6392	22.46	14.23	0.0	0.0	98.5	152	2.0
N512-201-441-733		7867	29.68	13.25	2.1	0.0	98.4	228	2.3
N512-204-446 to -449-#s = N412-204-446 to -449⊗									
N412-204-446⊗, (NR)									
N512-204-446-740		4771	25.47	9.22	0.0	1.9	97.3	129	1.0
N512-204-446-741		7035	29.17	12.07	0.0	6.3	97.3	278	1.0
N512-204-446-742		8362	29.99	13.93	0.0	5.4	97.4	135	1.0
N512-204-446-743		5668	21.91	12.90	8.7	6.5	96.6	250	2.3
N472-204-447⊗, (NR)									
N512-204-447-750		7448	28.91	12.84	0.0	0.0	97.4	243	1.8
N512-204-447-751		8182	29.74	13.75	0.0	0.0	97.5	148	1.5
N512-204-447-752		4513	18.04	12.50	0.0	0.0	97.6	238	1.5
N512-204-447-753		6541	23.90	13.64	0.0	0.0	98.2	154	1.5
N412-204-448⊗, (NR)									
N512-204-448-760		7150	28.36	12.58	0.0	3.8	97.9	279	2.0
N512-204-448-761		6217	25.19	12.27	3.1	0.0	97.4	292	1.8
N512-204-448-762		7214	30.32	11.94	0.0	0.0	97.6	267	1.0
N512-204-448-763		7165	26.58	13.06	3.7	0.0	96.9	200	1.3

(cont.)

Variety	Description	Acre Yield		Beets/ 100'	Bolting %	Root Rot %	Clean Beets %	NO3-N ppm	Mean Appear Score
		Sugar	Beets						
		Lbs	Tons						
(cont.)									
N512-204-446 to -449-#s = N412-204-446 to -449⊗		5992	24.39	12.03	136	0.0	1.9	293	1.5
N512-204-448-764									
N512-204-449-770	N412-204-449⊗, (NR/Seg)	8945	31.60	14.20	161	0.0	0.0	86	1.0
N512-204-449-771		7381	26.25	14.33	139	0.0	0.0	78	1.0
N512-204-449-772		6777	25.10	13.51	139	0.0	0.0	87	1.5
(cont.)									
N572-221-425 to -428-#s = N472-221-425 to -428⊗									
N572-221-425-860	N472-221-425⊗, (NR)	5829	24.86	11.66	117	77.8	0.0	356	3.3
N572-221-425-861		7106	29.98	11.80	128	4.4	0.0	323	2.0
N572-221-425-862		7900	35.12	11.23	156	20.0	16.7	439	2.5
N572-221-425-863		5347	24.06	10.84	125	36.4	9.1	304	3.0
(cont.)									
N572-221-426-870	N472-221-426⊗, (Seg)	7079	34.33	10.29	150	7.1	0.0	604	3.5
N572-221-426-871		7707	34.82	11.10	139	0.0	0.0	423	3.0
N572-221-426-872		5560	24.50	11.49	106	0.0	0.0	368	3.5
N572-221-427-873		8534	35.08	12.08	108	0.0	0.0	426	3.3
(cont.)									
N572-221-427-1001	N472-221-427⊗, (NR)	8014	36.00	11.14	111	12.4	4.5	448	3.3
N572-221-427-1002		6260	27.51	11.36	92	0.0	0.0	392	3.0
N572-221-427-1003		7582	36.68	10.37	95	2.4	0.0	470	3.3
N572-221-428-1004		5874	30.69	9.34	114	62.1	4.5	613	3.5
(cont.)									
N572-221-428-1010	N472-221-428⊗, (Seg)	6929	33.14	10.03	142	87.0	22.9	451	3.3
N572-221-428-1011		7070	27.27	12.97	100	63.9	0.0	288	3.0
N572-221-428-1012		8410	33.21	12.71	97	32.5	0.0	236	2.0
N572-221-428-1013		8023	30.95	12.87	128	71.0	0.0	178	2.5
(cont.)									
N572-223-# = N472-233⊗, (Homozygous for mod.NR)									
N572-233-650	N472-233⊗	6682	29.26	11.31	153	3.6	1.8	401	2.3
N572-233-651		4109	19.31	10.64	145	0.0	0.0	448	3.3

(cont.)

Variety	Description	Acre Yield		Beets/ 100'	Bolting %	Root Rot %	Clean Beets %	NO3-N ppm	Mean Appear Score
		Sugar	Beets						
		Lbs	Tons						
N572-223-# = N472-233⊗, (Homozygous for mod.NR) (cont.)									
N572-233-652		6687	31.47	139	2.0	0.0	97.1	438	3.0
N572-233-653		6133	27.82	125	0.0	0.0	96.8	380	3.5
N572-233-654		5736	28.39	142	31.2	7.1	96.7	413	3.5
N572-233-655		5414	24.97	161	1.6	0.0	98.6	544	3.8
N572-233-656		6028	27.42	136	0.0	0.0	98.1	521	3.3
N572-233-657		3846	20.38	153	25.6	0.0	97.9	709	3.0
5927-202-# = 4927-202⊗, (Homozygous for mod. NR)									
4927-202⊗									
5927-202-530		6164	23.38	145	0.0	0.0	98.2	96	2.8
5927-202-531		6725	24.28	145	0.0	1.9	98.3	70	1.3
5927-202-532		6861	25.51	136	0.0	0.0	98.2	119	2.3
5927-202-533		4917	17.89	156	0.0	0.0	96.5	124	1.8
Mean		5359.2	21.59	140.2	7.1	1.2	96.3	228.3	2.5
LSD (.05)		2348.7	8.32	31.5	25.8	9.9	2.8	139.8	1.1
C.V. (%)		22.1	19.51	11.3	183.8	433.4	1.5	30.9	21.2
F value		6.1**	8.76**	2.8**	3.7**	0.9NS	6.0**	9.9**	4.8**

Test B706 is a screening trial to evaluate selfed progeny lines for reaction to SBCN. With only two reps, large experimental errors are likely to occur. In part this test was used to help clarify and verify SBCN counts made in the greenhouse and previously in the field. And to determine the variability and differences within selected lines, e.g., N512-11 vs N512-13.

For B706, soil samples were taken on 2/15/06 in mid-season from 4931 (3707 eggs+larvae/100 grams soil), N512-11 (1681), N512-13 (3857), N572-233 (2903), 05-C37 (4041), 5927-202 (2167), N512-19-425-640 (2423), N512-204-446-740 (2297), N572-233-650 (665), and 5927-202-530 (1519). At harvest (6/09/06), counts were 5163, 991, 5260, 1985, 4801, 1528, 2094, 1151, 483, and 1086, respectively. For each variety, soil was composited across all reps before counting.

CURLY TOP EVALUATION, SALINAS ENTRIES, BSDF NURSERY
KIMBERLY, ID, 2006

240 varieties x 3 reps, 2-row plots, 13 ft. long, sequential

Variety	Description	BSDF	BSDF	BSDF
		1 st Rating	2 nd Rating	3 rd Rating
		8/07/06	8/28/06	9/11/06
<u>Hybrids</u>				
USH11	Resist. check, 10/14/02	3.7	4.0	4.3
HM-PM21	Resist. check, 4/05	3.3	3.7	4.0
Beta 4430R	Betaseed	4.0	5.0	6.0
Phoenix	Holly Hybrids, 3/10/06	4.0	4.7	5.7
Monohikari	Susc. check, 1/21/03	4.0	6.0	7.0
HM-E17	Susc. check	4.7	6.7	7.3
Angelina	Betaseed, 3/06 pelleted	3.7	4.7	5.7
Roberta	Betaseed, 3/06 pelleted	4.0	5.0	5.3
Alpine	Holly Hybrids, 3-10-06	3.0	4.0	4.0
HH142	Holly Hybrids,	3.0	4.0	4.0
HM-PM21	Resist. check, 4/05	3.0	3.3	4.0
USH11	Resist. check, 10/14/02	3.3	3.7	4.0
<u>Multigerm lines and populations</u>				
05-C37	Resist. check, Inc. 04-C37	4.0	4.0	4.7
EL-SP7322-0	Susc. check, SP22-0	5.3	6.7	7.3
Z510	Inc. Z210 (Polish %S)	4.3	5.3	6.0
R578(Iso)	RZM R378 Iso (C78/3)	3.0	4.0	4.3
P529	PMR-RZM P429, (CP05)	4.3	4.7	5.0
P530	PMR-RZM P430, (CP06)	3.3	4.3	4.3
P518-6	PMR-RZM P418-6, (CP08)	4.3	5.0	5.0
P507/8	PMR-RZM P407/8, (CP07)	3.7	4.3	4.7
P527	PMR-RZM P427, (CP03)	3.0	3.7	4.0
P528	PMR-RZM P428, (CP04)	3.0	3.0	4.0
04-C37	Resist. check, Inc. C37	3.7	3.7	4.3
05-US22/3	Inc. 02-US22/3	3.3	3.7	4.3
05-US75	Inc. 03-US75	3.7	3.7	4.3
R540	IRZM-% R940,R840,R740	3.7	4.0	4.3
R525	IRZM-% R325, R324, ...	4.0	3.3	4.3
R541/2	IRZM-% R641,R642 (WB169,258)	4.0	4.7	5.0
R521	IRZM-% R321, R021	4.3	5.0	5.7
R522	IRZM-% R522 (Sp), (C51)	4.3	5.3	6.3
Y577	IRZM-% Y277, Y375	4.0	4.3	5.0
Y591	IRZM-% Y391	4.0	4.7	5.0

CURLY TOP EVALUATION, SALINAS ENTRIES, BSDF NURSERY
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(cont.)

Variety	Description	BSDF 1 st Rating 8/07/06	BSDF 2 nd Rating 8/28/06	BSDF 3 rd Rating 9/11/06
<u>Multigerm lines and populations (cont.)</u>				
R539	Inc. R039, (C39R)	4.0	4.3	4.7
P531CT(Iso)	PMR-RZM P431CT, (CP09CT)	3.7	4.0	4.7
P531CT(Sp)	PMR-RZM P431CT	3.7	4.3	4.3
Y595	RZM Y95(C)	3.7	4.3	4.7
R481-22	RZM R181-22, (C81-22)	4.3	5.3	5.3
N524	Inc. N424(g)	4.7	5.3	6.3
EL-SP7322-0	Susc. check, SP22-0	4.3	6.0	6.7
05-C37	Resist. check, Inc. 04-C37	4.0	4.0	4.3
R524-2/3	Inc. R324-213,-215,-222,-223 (WB41,42)	3.7	4.0	4.7
R524-302	Inc. R324-302,-306 (WB41)	4.0	4.0	4.7
R525-301	Inc. R325-301,-302 (WB42)	4.0	4.0	4.7
R537-302	Inc. R337-302 (WB151)	3.7	4.3	4.3
HM-PM21	Resistant check, 4/05	4.0	4.0	4.3
Monohikari	Susc. check, 1/21/03	5.7	7.3	8.3
Y390	Inc. Y190-#(C), C2, Syn 1	4.0	5.0	5.0
Y492	RZM-ER-% Y292	4.0	5.0	5.0
Y393	Composite FS's, C1, Syn 1	4.0	5.0	4.7
R340	RZM-ER-% R140, (C79-#s)	4.3	5.0	5.3
R437	RZM-% R637, (C79-9, WB151)	4.3	4.7	5.3
Y369	RZM-ER-% Y169, (C69/2)	4.3	5.3	5.7
R476-89	RZM-ER-% R276-89	4.0	5.0	4.7
R481-22	RZM R181-22, (C81-22)	4.0	4.7	4.7
Y475	RZM-ER-% Y275	4.3	5.3	5.3
P531CT(Iso)	PMR-RZM P431CT, (CP09CT)	3.7	4.7	5.0
R578(Iso)	RZM P378(Iso), (C78/3)	3.7	4.7	5.0
05-US22/3	Inc. 02-US22/3	3.7	4.0	4.0
EL-SP7322-0	Susc. check, SP22-0,4/5	4.0	5.3	5.7
05-C37	Resist. check, Inc. 04-C37	3.3	4.0	4.0
<u>MM,populations with FC gp</u>				
05-FC1036	RZM 04-FC1028,1037,1038aa x A	4.0	5.0	5.3
05-FC1022	RZM-CR-% 20031022 (C931 x FC)	4.0	5.3	5.7
05-FC1018	RZM-CR-% 20031018 (C931 x FC709-2)	4.0	4.7	5.3
05-FC1019	RZM-CR-% 20031019 (FC712 x C931)	4.3	5.0	5.3
<u>MM,S^f,A:aa populations</u>				
5944	S ₁ (C1,C2,C3)aa x A	4.3	5.0	5.3
5933	933(C)aa x A	4.0	4.7	5.3
4931	RZM 3931aa x A, C931	4.3	5.0	5.3
4941	RZM 3941aa x A, C941	4.0	4.7	5.3

CURLY TOP EVALUATION, SALINAS ENTRIES, BSDF NURSERY
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(cont.)

Variety	Description	BSDF	BSDF	BSDF
		1 st Rating	2 nd Rating	3 rd Rating
		8/07/06	8/28/06	9/11/06
<u>MM,S^f,A:aa populations (cont.)</u>				
CR411	RZM CR311aa x A, CR11	4.0	4.7	5.7
Z425	RZM Z325aa x A, CZ25/2	4.3	5.7	6.7
N412 (Sp)	N312,N212-#(C)aa x A, CN12	4.0	4.7	5.0
N472 (Sp)	N372,N272-#(C)aa x A, CN72	4.3	5.3	5.3
4921	RZM-ER-% 2921	4.0	4.7	4.7
4943	RZM 3943aa x A	4.0	4.0	5.0
05-C37	Resist. check, Inc. 04-C37	3.7	4.0	4.3
EL-SP7322-0	Susc. check, SP22-0	4.3	5.7	7.0
<u>MM,S^f,Aa progeny lines</u>				
05-FC1030-15 (Sp)	03-FC1030-15aa x A	4.7	5.7	6.3
05-FC1030-15 (Iso)	RZM 03-FC1030-15 (A,aa)	5.0	6.0	7.0
05-FC1030-16 (Sp)	03-FC1030-16aa x A	4.0	5.0	5.0
05-FC1030-16 (Iso)	RZM 03-FC1030-16 (A,aa)	4.0	4.3	5.0
CR509-1-312	Inc. CR301-1-312 (A,aa)	4.3	4.7	5.0
CR510-2-305	Inc. CR310-2-305 (A,aa)	4.7	4.7	5.3
CR511-7-302	Inc. CR311-7-303,-304 (A,aa)	5.0	6.0	6.7
CR511-88	RZM CR311-88 (A,aa), (CR11-88)	4.3	5.0	5.7
CR311-6	Inc. CR111-6 (A,aa)	4.0	4.7	5.0
CR311-6H50	C790-15CMS x CR111-6	4.0	5.0	5.0
Monohikari	Susc. check, 1/21/03	5.7	8.0	8.7
HM-PM21	Resist. check, 4/05	4.0	4.7	4.7
Y575-305	Inc. Y375-305	4.3	4.7	5.3
Y575-311	Inc. Y375-311	4.0	4.7	5.3
Y590-40 (Iso)	RZM Y390-40	4.0	4.3	5.0
5930-35	Inc. 2930-35, C930-35	4.0	4.3	4.3
5943-9-6	Inc. 3943-9-6 (A,aa)	4.3	5.0	5.3
5943-9-7	Inc. 3943-9-7 (A,aa)	5.0	6.3	6.3
5943-19-312	Inc. 3943-19-312 (A,aa)	4.3	4.7	5.3
5943-35-301	Inc. 3943-35-301 (A,aa)	4.0	4.7	5.3
5943-35-318	Inc. 3943-35-318 (A,aa)	4.0	4.7	4.7
5930-19-312	Inc. 3930-19-312 (A,aa)	4.0	4.7	5.0
5930-19-325	Inc. 3930-19-325 (A,aa)	4.0	4.3	5.0
5930-35-312	Inc. 3930-35-312 (A,aa)	4.3	4.0	4.3
Z525-9-307	Inc. Z325-9-307 (A,aa)	4.0	4.7	5.7
Z525-9-308	Inc. Z325-9-308 (A,aa)	4.3	5.3	6.3
5936-10-310	Inc. 3936-10-310 (A,aa)	4.7	5.0	5.3
5936-16-313	Inc. 3936-16-313 (A,aa)	4.7	4.7	5.7
R578H23-308	Inc. R378H23-308 (A,aa)	4.0	5.0	5.0
R578H23-312	Inc. R378H23-312 (A,aa)	4.0	5.7	6.7

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(cont.)

Variety	Description	BSDF 1 st Rating 8/07/06	BSDF 2 nd Rating 8/28/06	BSDF 3 rd Rating 9/11/06
<u>MM,S^f,Aa progeny lines (cont.)</u>				
R578H23-320	Inc. R378H23-320 (A,aa)	4.3	6.0	6.0
R578H23-325	Inc. R378H23-325 (A,aa)	4.0	4.0	4.7
R578H40-306	Inc. R378H40-306 (A,aa)	4.0	4.3	4.7
R578H40-312	Inc. R378H40-312 (A,aa)	4.0	4.0	4.7
R578H40-324	Inc. R378H40-324 (A,aa)	3.7	4.0	4.0
R576H41-301	Inc. Y391H41-301 (A,aa)	3.3	4.3	4.7
Y591H23-311	Inc. Y391H23-311 (A,aa)	4.0	4.7	5.0
Y591H23-313	Inc. Y391H23-313 (A,aa)	5.3	6.3	6.3
Y591H23-314	Inc. Y391H23-314 (A,aa)	6.0	7.7	8.0
Y591H23-322	Inc. Y391H23-322 (A,aa)	6.0	6.3	6.7
R578 (Iso)	RZM R378 (Iso) , (C78/3)	3.7	4.0	4.0
Z510	Inc. Z210 (Polish %S)	4.0	5.0	5.0
EL-SP7322-0	Susc. check, SP22-0	4.0	5.3	6.3
05-C37	Resist. check, Inc. 04-C37	3.3	4.0	4.3
N412 (Sp)	N212-# (C) ,N312aa x A, (CN12)	4.0	4.7	5.0
N472 (Sp)	N272-# (C) ,N372aa x A, (CN72)	4.0	4.7	5.0
N572-233	RZM N472-233	4.0	4.0	4.3
5926-11-3-22	RZM 4926-11-3-22, (CN926-11-3-22)	4.7	5.0	5.0
N512-11	RZM N412-11 (NR)	4.7	5.0	5.0
N512-13	RZM N413-13 (NS)	4.7	5.0	5.3
P529-305	Inc. P329-305	3.7	4.3	5.0
P507-303	Inc. P307-303	4.0	4.7	4.7
P507-304	Inc. P307-304	4.3	4.7	5.0
P507-306	Inc. P307-306	4.7	4.7	4.7
P507-308	Inc. P307-308	4.3	4.7	5.7
P507-311	Inc. P307-311	4.0	4.3	4.3
3927-4	RZM 2927-4 (A,aa) , (C927-4)	4.0	5.0	5.0
5927-202	Inc. 4927-202, (CN927-202)	4.0	4.7	4.7
5927-4-302	Inc. 3927-4-302	3.7	4.3	5.0
5927-4-303	Inc. 3927-4-303	3.3	4.3	4.7
5927-4-307	Inc. 3927-4-307	5.0	5.0	5.7
5927-4-309	Inc. 3927-4-309 (NS)	4.0	5.7	6.0
5921-306	Inc. 3921-306, (CN921-306)	3.7	4.7	4.7
P531CT (Iso)	PMR-RZM P431CT, (CP09CT)	3.7	4.7	4.7
4952-222	Inc. 2952-222 (A,aa)	4.3	5.0	5.0
4953-217	Inc. 2953-217 (A,aa)	4.0	5.0	5.0
4954-210	Inc. 2954-210 (A,aa)	3.7	4.7	4.7
4931	3931aa x A, (C931)	4.0	4.7	4.7

CURLY TOP EVALUATION, SALINAS ENTRIES, BSDF NURSERY
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(cont.)

Variety	Description	BSDF	BSDF	BSDF
		1 st Rating	2 nd Rating	3 rd Rating
		8/07/06	8/28/06	9/11/06
<u>Monogerm populations and lines</u>				
3869	1869(C)mmaa x A, (C869)	3.7	4.7	4.7
EL-C869	EL-C869, ELA015028, 4/05	4.0	4.7	5.0
EL-C869CMS	EL-C869CMS, ELA015027, 4/05	4.3	4.3	4.7
3842	RZM 2842 (C)mmaa x A, (C842)	3.7	4.3	4.3
4842 (Iso)m	RZM-% 2842 (A,aa) , (C842)	3.7	4.0	4.7
5842	RZM 4842mmaa x A, (C842)	4.0	4.7	4.7
4842-226m	Inc. 2842-226 (A,aa) (T-O)	4.3	5.0	5.3
4842-256m	Inc. 2842-256 (A,aa) (T-O)	4.7	5.3	5.7
4842-262m	Inc. 2842-262 (A,aa)	4.7	5.0	5.0
4837-6-203m	Inc. 2837-6-203 (A,aa) (T-O)	4.0	4.3	5.0
4836-13m	RZM-T-O 3836-13-# (C) (A,aa)	4.0	5.0	5.0
5843-10CT	Inc. 3843-10 (A,aa)mm	4.3	4.7	5.0
5848-1m	RZM 2848-1mm	3.7	4.0	4.3
2833-5 (Sp)	RZM,T-O 1833-5-# (C)mmaa x A	4.7	5.3	5.7
2833-5HO (Sp)	1833-5HO x ", (C833-5CMS) (C833-5)	4.3	5.0	5.3
04-C790-15m	Inc. CO-C790-15	4.3	5.0	5.7
05-C562HO	97-C562HO x 97-C562, (C562HO)	4.0	4.7	5.3
05-C562	Inc. 97-C562, (C562)	4.0	4.3	5.0
05-C718	Inc. 97-C718, (C718)	3.7	4.0	5.0
05-C718HO	97-718HO x 97-C718, (C718HO)	3.0	4.0	4.3
05-C546	Inc. 97-C546, (C546)	3.3	4.0	4.3
05-C762-17	Inc. 0762-17, (C762-17)	3.7	4.0	4.0
3849m	RZM 2251-2255 (C)mmaa x A	4.7	5.7	5.7
5849m	Inc. 4849-# (C)mm (A,aa)	4.0	5.0	5.7
4850	Inc. 2252-2MmAa	4.0	5.0	5.7
4851	Inc. 2252-5MmAa	4.7	5.7	5.0
5845	RZM 845 (C1,C2)mmaa x A	3.7	4.0	4.7
5812	Inc. 3812-2,-5,-6,-42 (A,aa)mm	4.0	4.3	5.0
5819m	Inc. 3819-26,-27,-28 (A,aa)mm	4.7	5.3	5.3
N569m	Inc. N469-# (C)g, N469 (g)mm	5.0	5.3	5.7
05-FC1023M	Inc. FC20021023 (A,aa)	4.0	4.7	4.7
05-FC1023M	FC20021023aa x A	4.0	4.0	4.7
03-FC1014-22	Inc. 01-FC1014-22 (A,aa)	4.0	4.0	4.7
03-FC123-31	Inc. 01-FC123-31 (A,aa)	4.0	5.0	5.0
20051007HOMS	Rhizoc. 03-FC1014-22	4.7	5.3	6.0
20051007HOPF	Rhizoc. 03-FC1014-22	3.7	4.7	5.7
EL-SP7322-O	Susc. check, SP22-0, 4/05	4.0	5.7	5.7
04-C37	Resist. check, C37	4.0	4.0	5.0
4843m	RZM,T-O 3843-# (C)mmaa x A	4.0	5.0	5.7
4891m	RZM,T-O 3891-# (C)mmaa x A	3.7	4.7	4.7

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(cont.)

Variety	Description	BSDF 1 st Rating 8/07/06	BSDF 2 nd Rating 8/28/06	BSDF 3 rd Rating 9/11/06
<u>Hybrids with C790-15CMS tester</u>				
US H11	Resist. check	4.0	4.0	5.0
HM-PM21	Resist. check	3.0	4.0	4.0
Monohikari	Susc. check	4.0	5.0	6.0
Beta 4430R	Betaseed	3.3	4.7	5.7
R578H50	C790-15CMS x R378, (C78/3)	4.0	4.7	5.0
P531CTH50	C790-15CMS x PMR-RZM P431CT, (CP09CT)	4.3	5.0	5.3
Y595H50	C790-15CMS x RZM Y95 (C)	4.3	5.0	5.0
Y590-40H50	C790-15CMS x Y390-40	4.0	5.7	5.7
05-FC1036H50	C790-15CMS x RZM 04-FC1028, 37, 38	4.0	5.0	5.3
05-FC1030-15H50	C790-15CMS x 05-FC1030-15	4.0	5.0	5.7
05-FC1030-16H50	C790-15CMS x 03-FC1030-16	4.3	5.0	5.0
5933H50	C790-15CMS x popn-933 (C)	4.3	5.0	5.0
5944H50	C790-15CMS x popn-944 (C)	4.0	4.7	4.7
05-FC1023H50	C790-15CMS x 20021023	4.0	5.0	5.0
05-FC1022H50	C790-15CMS x RZM-CR-% 20031022	3.7	5.0	5.0
05-FC1018H50	C790-15CMS x RZM-CR-% 20031018	4.0	4.3	4.7
05-FC1019H50	C790-15CMS x RZM-CR-% 20031019	3.7	4.0	4.7
R578H23-325H50	C790-15CMS x R378H23-325	3.0	4.0	4.0
R578H40-306H50	C790-15CMS x R378H40-306	4.0	4.0	4.0
5943-19-312H50	C790-15CMS x 3943-19-312	4.0	4.7	5.0
5930-35-312H50	C790-15CMS x 3930-35-312	4.0	4.3	4.7
Z525-9-307H50	C790-15CMS x Z325-9-307	5.0	6.0	7.0
5930-35H50	C790-15CMS x 2930-35, (C930-35)	4.0	4.3	4.3
Y591H50	C790-15CMS x IRZM-% Y391	4.0	4.7	4.7
CR509-1-312H50	C790-15CMS x CR309-1-312	3.7	4.7	4.7
CR510-2-305H50	C790-15CMS x CR310-2-305	4.0	4.7	4.7
CR511-7-302H50	C790-15CMS x CR311-7-303, -304	4.3	4.7	5.3
CR511-88H50	C790-15CMS x CR311-88, (CR11-88)	4.3	5.0	5.3
<u>Hybrids with C833-5CMS tester</u>				
5933H5	C833-5CMS x popn-933 (C)	4.0	4.0	5.0
5944H5	C833-5CMS x popn-944 (C)	4.0	5.0	5.0
Y595H5	C833-5CMS x RZM Y95 (C)	4.3	5.0	5.0
P531CTH5	C833-5CMS x PMR-RZM P431CT (CP09CT)	4.3	4.7	5.3
R578H5	C833-5CMS x RZM R378, (C78/3)	4.0	4.7	5.0
R578H33	4842-226H5 x RZM R378	3.7	4.0	4.3
R578H34	4842-256H5 x RZM R378	3.7	4.0	4.3
R578H35	4842-262H5 x RZM R378	4.0	4.3	5.0

CURLY TOP EVALUATION, SALINAS ENTRIES, BSDF NURSERY
KIMBERLY, ID, 2006

(cont.)

Variety	Description	BSDF	BSDF	BSDF
		1 st Rating	2 nd Rating	3 rd Rating
		8/07/06	8/28/06	Hybrids
Hybrids with C833-5CMS tester (cont.)				
R578H37	4837-6-203H5 x RZM R378	4.0	5.0	5.0
R578H36	4836-13H5 x RZM R378	4.0	5.0	5.0
R578H42	3842HO x RZM R378	3.7	4.0	4.3
R578H70	3869HO x RZM R378	4.0	4.0	4.7
HM-PM21	Resistant check, 4/05	4.0	4.0	4.0
Monohikari	Susc. check, 1/21/03	4.7	7.0	7.7
R521H5	C833-5CMS x RZM-% R321,R021	4.0	5.0	5.0
R540H5	C833-5CMS x IRZM-% R940,R840,...	4.3	5.0	5.3
R525H5	C833-5CMS x IRZM-% R325,R324,...	4.3	5.0	5.0
R537-302H5	C833-5CMS x R337,302	4.3	5.3	5.0
N512-11H5	C833-5CMS x RZM N412-11	4.3	5.3	5.3
P507-306H50	C790-15CMS x P307-306	4.3	4.7	4.7
5927-4-302H5	C833-5CMS x 3927-4-302	4.7	5.0	5.0
5927-4-303H5	C833-5CMS x 3927-4-303	4.0	5.0	5.0
N412H5	C833-5CMS x N312, (CN12)	4.0	4.7	5.0
N472H5	C833-5CMS x N372, (CN72)	4.3	5.0	5.0
N572-233H5	C833-5CMS x RZM N472-233	4.0	5.0	5.0
5926-11-3-22H5	C833-5CMS x RZM 4926-11-3-22 (CN926-11-3-22)	4.3	5.0	5.0
5921-306H5	C833-5CMS x 3921-306 (CN921-306)	4.7	5.3	5.0
5927-202H50	C790-15CMS x 4927-202, (CN927-202)	4.0	4.7	5.0
Mean		4.1	4.8	5.1
LSD (.05)		0.8	1.1	1.0
C.V. (%)		12.4	13.8	12.6
F value		2.7**	3.4**	4.3**

USDA-SALINAS ENTRIES IN DISEASE NURSERIES, BETASEED, SHAKOPEE, MN and USDA-ARS, FORT COLLINS, CO, 2006

Variety	Description	Shakopee, MN				Fort Collins			
		RA ⁴	Cercospora Leaf Spot	Aphanomyces		Rhizoctonia			
		Score	4 th reading	Mean	1 st reading	2 nd reading	Mean	DI ¹	%H ² %H(0-3) ³
<u>Checks</u>									
HM-E17	Michigan hybrid		5.9	4.0	2.3	1.8	2.1		
EL-SP22-0	EL-SP7322-0, 4/05		5.9	3.8	2.0	1.2	1.6		
Beta 4430R	Betaseed		8.6	6.4	3.5	3.2	3.3		
<u>Salinas lines</u>									
Y595	RZM Y95 (C)	3.5	7.7	5.4	3.8	4.2	4.0	4.5	6
P531CT (Sp)	PMR-RZM P431CT (CP09CT)		7.7	5.3	3.2	3.0	3.1	3.9	8
R522	IRZM- $\frac{8}{5}$ R522 (C50,C51)	3.7	8.3	5.9	3.5	4.0	3.8	4.7	0
R521	IRZM- $\frac{8}{5}$ R321,R221	3.3	8.2	5.5	3.0	3.0	3.0	4.1	12
R539	Inc. R039 (C39R)		8.0	5.3	3.3	3.2	3.3		
Z510	Inc. Z210 ($\frac{8}{5}$ S Polish C)		8.0	5.3	3.2	2.8	3.0		
5944	944(C)aa x A		7.6	5.1	3.2	3.0	3.1	4.6	3
5933	933(C)aa x A	2.4	8.0	5.5	3.2	3.3	3.3	4.8	6
CR411	RZM CR311,CR311aa x A(CR11)		6.8	4.5	4.5	4.7	4.6	4.3	9
<u>Salinas CR lines and selections</u>									
CR311-6	Inc. CR111-6 (A,aa)		5.7	3.8	3.3	3.3	3.3		
CR511-88	RZM CR311-88(A,aa) , (CR11-88)		6.7	4.7	3.3	3.7	3.5		
CR509-1-312	Inc. CR301-1-312 (A,aa)		6.7	4.3	2.8	3.2	3.0		
CR510-2-305	Inc. CR310-2-305 (A,aa)		5.6	3.8	3.5	3.8	3.7		
CR511-7-302	Inc. CR311-7-303,304(A,aa)		5.9	3.6	3.3	3.3	3.3		
<u>Salinas CR experimental hybrids</u>									
CR311-6H50	C790-15CMS x CR111-6		6.8	4.5	3.8	3.7	3.8		
CR511-88H50	C790-15CMS x CR311-88		7.0	4.8	2.8	2.3	2.6		
CR509-1-312H50	C790-15CMS x CR301-1-312		6.8	4.4	3.2	3.3	3.3		
CR510-2-305H50	C790-15CMS x CR310-2-305		7.2	4.7	4.0	4.2	4.1		
CR511-7-302H50	C790-15CMS x CR311-7-303		6.6	4.3	3.7	4.0	3.8		

(cont.)

Variety	Description	Shakopee, MN				Fort Collins				
		RA ⁴	Cercospora	Leaf Spot	Aphanomyces	Rhizoctonia				
		Score	4 th reading	Mean	1 st reading	2 nd reading	Mean	DI ¹ %H ² %H(0-3) ³		
Fort Collins lines and populations										
05-FC1036	RZM 04-FC1028, 1037, 1038	2.5	7.0	4.5	3.7	3.8	3.8	3.2	17	55
04-FC1028	RZM-% FC2002 1028(A,aa)		7.0	4.7	4.7	5.0	4.8	3.9	16	43
04-FC1037	RZM-% FC2002 1037(A,aa)		6.6	4.2	2.8	3.2	3.0	3.0	27	66
04-FC1038	RZM-% FC2002 1038(A,aa)		6.8	4.4	3.8	3.8	3.8	3.3	15	58
05-FC1022	RZM-CR-% 2003 1022(A,aa)	3.2	7.7	5.1	4.7	4.7	4.7	4.2	9	35
05-FC1018	RZM-CR-% 2003 1018(A,aa)	3.0	7.0	4.5	3.7	4.0	3.8	2.5	35	74
05-FC1019	RZM-CR-% 2003 1019(A,aa)	2.6	7.7	5.2	3.8	3.3	3.6	3.0	16	64
05-FC1030-15(Sp)	03-FC1030-15aa x A	2.7	6.9	4.8	3.5	3.7	3.6	1.8	50	95
05-FC1030-16(Sp)	03-FC1030-16aa x A	4.0	7.4	4.7	3.8	3.5	3.7	2.4	33	78
05-FC1023M(Iso)	Inc. FC2002 1023M(A,aa)	3.7	7.9	5.0	4.3	4.5	4.4			
Fort Collins experimental hybrids										
05-FC1036H50	C790-15CMS x 04-FC(C)		7.7	5.1	3.2	3.3	3.3	3.9	12	39
05-FC1030-15H50	C790-15CMS x 03-FC1030-15		7.9	5.2	4.2	5.0	4.6	3.7	10	52
05-FC1030-16H50	C790-15CMS x 03-FC1030-16		7.4	5.0	3.3	2.8	3.1	3.3	9	60
05-FC1023H50	C790-15CMS x FC20021023		7.9	5.2	3.7	3.7	3.7			
05-FC1022H50	C790-15CMS x RZM-CR-% 1022							4.0	13	40
Check for Root Aphid, CR, & APH										
Monohikari	Seedex, 1/21/03	2.6	7.3	5.0	3.7	3.7				
Betaseed Checks										
Tol Check			4.5	3.0	2.3	1.5	1.9			
Tol Check 2					2.8	2.0	2.4			
Susc Check		3.8	9.1	6.6	5.5	6.7	6.1			
Susc Check 2		3.2			4.7	6.0	5.3			
Mod Susc Check			8.6	6.0	4.3	5.3	4.8			
Mod Susc Check 2			8.0	6.1	5.0	4.8	4.9			

USDA-SALINAS ENTRIES IN BETASEED DISEASE NURSERIES, SHAKOPEE, MN and FORT COLLINS, CO, 2006

(cont.)

Variety	Description	Shakopee, MN				Fort Collins					
		RA ⁴ Cercospora Leaf Spot		Aphanomyces		Rhizoctonia					
		1 st reading		2 nd reading		DI ¹ %H ² %H(0-3) ³					
		Score	4 th reading	Mean	Mean	Mean	Mean	Mean			
Fort Collins Checks											
FC901/C817	Susc Check						4.2	10	33		
FC705/1	Highly Resist Check						1.8	32	98		
FC703	Resist Check						2.2	32	81		
LSD (.05)		0.79	0.49	1.31	1.47	1.31			1.18		
C.V. (%)		7.97	7.45	23.41	25.72	23.16					

- ¹ DI = disease index. Based on a scale of 0 (=healthy) to 7 (= plant dead).
² %H = percent of healthy roots (disease classes 0 and 1 combined).
³ Percent of diseased roots likely to be taken for processing (disease classes 0 through 3 combined).
⁴ RA = Root Aphid mean where 1 & 2 are considered resistant and 3 & 4 are considered susceptible.
 Test run by Margaret Rekoske, Betaseed.

Tests at Shakopee, MN were run by Margaret Rekoske and Jay Miller, Betaseed.
 Rhizoctonia test at Fort Collins was run by Linda Hanson and Lee Panella, USDA-ARS.

2006 SALINAS ENTRIES FOR EAST LANSING CERCOSPORA LEAF SPOT TEST,
E. LANSING, MI, 2006

1-row plots, 15 ft. long, 3 reps, RCB

Variety	Description	Cercospora Leaf Spot	
		Score	Standard Deviation
		Mean	Score
<u>Checks</u>			
HM-E17	Michigan hybrid	4.33	1.53
EL-SP22-0	EL-SP7322-0, 4/05	5.67	1.53
Beta 4430R	Betaseed	10.00	0.00
<u>Salinas lines</u>			
Y595	RZM Y95 (C)	7.33	2.89
P531CT (Sp)	PMR-RZM P431CT (CP09CT)	6.67	2.31
R522	IRZM-% R522 (C50,C51)	10.00	0.00
R521	IRZM-% R321,R221	6.33	4.62
R539	Inc. R039 (C39R)	7.00	2.65
Z510	Inc. Z210 (%S Polish C)	8.67	2.31
5944	944 (C)aa x A	5.67	2.52
5933	933 (C)aa x A	7.33	2.08
CR411	RZM CR311,CR311aa x A (CR11)	5.33	1.15
<u>Salinas CR lines & selections</u>			
CR311-6	Inc. CR111-6 (A,aa)	4.00	2.00
CR511-88	RZM CR311-88 (A,aa) , (CR11-88)	6.33	0.58
CR509-1-312	Inc. CR301-1-312 (A,aa)	8.33	2.08
CR510-2-305	Inc. CR310-2-305 (A,aa)	5.67	1.15
CR511-7-302	Inc. CR311-7-303,304 (A,aa)	2.67	1.15
<u>Salinas CR experimental hybrids</u>			
CR311-6H50	C790-15CMS x CR111-6	6.33	2.52
CR511-88H50	C790-15CMS x CR311-88	6.67	2.52
CR509-1-312H50	C790-15CMS x CR301-1-312	7.00	2.65
CR510-2-305H50	C790-15CMS x CR310-2-305	5.67	1.15
CR511-7-302H50	C790-15CMS x CR311-7-303,-304	6.00	1.00
<u>Fort Collins lines and populations</u>			
05-FC1036	RZM 04-FC1028,1037,1038aa x A	6.33	1.53
04-FC1028	RZM-% FC2002 1028 (A,aa)	7.67	1.53
04-FC1037	RZM-% FC2002 1037 (A,aa)	6.33	1.53
04-FC1038	RZM-% FC2002 1038 (A,aa)	6.50	0.71
05-FC1022	RZM-CR-% 2003 1022 (A,aa)	7.33	2.52
05-FC1018	RZM-CR-% 2003 1018 (A,aa)	4.00	1.00
05-FC1019	RZM-CR-% 2003 1019 (A,aa)	8.00	1.00
05-FC1030-15 (Sp)	03-FC1030-15aa x A	6.00	3.00
05-FC1030-16 (Sp)	03-FC1030-16aa x A	6.00	2.65
05-FC1023M (Iso)	Inc. FC2002 1023M (A,aa)	8.00	1.00
<u>Fort Collins experimental hybrids</u>			
05-FC1036H50	C790-15CMS x 04-FC (C)	5.67	1.53
05-FC1030-15H50	C790-15CMS x 03-FC1030-15	9.00	1.00
05-FC1030-16H50	C790-15CMS x 03-FC1030-16	8.33	2.89
05-FC1023H50	C790-15CMS x FC20021023	8.67	1.53

Notes: Test scored on a scale of 0 to 10. Test run by Dr. Mitch McGrath and staff. Inoculated with *C. beticola* by Michigan Sugar.

California Entries in Rhizomania Test, Heyburn area, Idaho, 2006

Planted:

Variety	Description	Verticillium Symptomatic Plants	RZM DI
		%	Mean
2992RZ	Hilleshog variety - Rz1 control	1	25.9
Y591	IRZM-% Y391, (CY91)	3	22.4
05-US75	Inc. 03-US75	5	29.8
R540	IRZM-% R940, R840, R740	5	16.4
Y577	IRZM-% Y277, Y375	5	19.8
R522H5	C833-5CMS x IRZM R522(Sp)	5	20.3
P518-6	PMR-RZM P418-6, CP08	7	32.7
N412(Sp)	N312, N212-#(C) aa x A, CN12	7	18.8
Y375-311	Inc. Y575-311	7	19.8
Y371(C72)	see KA0060	8	23.7
R541/2	IRZM-% 12641, R642 (WB169, 258)	9	23.6
N472(Sp)	N372, N272-#(C) aa x A, CN72	9	26.5
Y375-305	Inc. Y575-305	9	19.9
Beta GO17R	Betaseeds - Rz2 variety	9	24.6
05-FC1019	RZM-ER-% 20031019, (FC712 x C931)	10	20.6
05-FC1030-16(Sp)	03-FC1030-16 aa x A	10	27.5
Y590-40(iso)	RZM Y390-40	10	25.1
R537-302H5	C833-5CMS x R337-302	10	18.4
2992RZ	Hilleshog variety - Rz1 control	10	22.1
P529	PMR-RZM P429, (CP05)	11	23.3
Y595	RZM Y95 (C)	11	20.3
R522	IRZM-% R522(sp), (C51)	11	24.3
R525	IRZM-% R325, R324, R324/5. R337	11	30.1
R424/5	see KA0056	11	28.7
R5324-302H5	C833-5CMS x IRZM-% R324-302, -306	12	22.7
R525-301H5	C833-5CMS x R525-301, 302	12	27.4
R525H5	C833-5CMS x IRZM-% R325, R324, R324/5, R337	12	28.0
P507/8	PMR-RZM P407/8, CP07	12	22.6
P528	PMR-RZM P528, CP04	12	17.9
05-FC1018	RZM-ER-% 20031078, (C931 x FC709-2)	12	25.0
N524	Inc. N424(g) (Hslpro1)	12	27.2
5933	933(C) aa x A, CR933	12	27.6
4931	RZM 3931aa x A, C931	12	21.0
4941	RZM 3941aa x A, C941	12	21.9
R537-302	INC. R337-302 (WB151)	12	21.6
Y577H5	C833-5CMS x IRZM Y277, Y375	12	19.0
Y5977H5	C833-5CMS x IRZM Y95(C)	12	24.0
R540H5	C833-5CMS x IRZM-% R940, R840, R740	12	21.6

California Entries in rhizomania Test, Heyburn area, Idaho, 2006

(cont.)

Variety	Description	Verticillium Symptomatic Plants	RZM DI
		%	Mean
R539H5	C833-5CMS x R039, (C39R)	12	19.1
4921	RZM-ER-% 2921	12	21.6
05-US22/3	Inc. 03-US22/3	13	34.0
R481-22	RZM R181-22, (C81-22)	13	22.3
R521	IRZM-% R321, R021	13	24.3
05-FC1022	RZM-ER-% 20031022, (C931 x FCRhizoc)	13	23.5
CR411	RZM CR311 aa x A, CR11	13	25.8
R524-302	Inc. R324-302, -306 (WB41)	13	32.1
R521H5	C833-5CMS x IRZM-% R321, R021	13	19.8
Beta GO17R	Betaseeds - Rz2 variety	13	21.0
P527	PMR-RZM P427, CP03	15	29.0
R539	Inc. R039, C39R	15	22.6
05-FC1030-15 (Sp)	03-FC1030-15 aa x A	15	27.7
R4541/2H5	C833-5CMS x IRZM-% R641, R642	15	20.8
4842 (iso)	C842	15	17.3
Phoenix	Holly Hybrids, 3-10-06	15	24.4
05-C37	Inc. 04-C37	16	27.4
R525-301	Inc. R325-301, -302 (WB42)	16	31.5
Y393	see KA0051	16	20.6
EL-SP7322-0	Inc. SP22-0	17	27.4
P530	PMR-RZM P430, CP06	17	20.4
Phoenix	Holly Hybrids, 3-10-06	17	22.2
R524-2/3	Inc. R324-213, -215, -222, -223 (WB41, 42)	18	22.7
P531CTH5	C833-5CMS x P431CT, (CP09CT)	18	23.0
Z510	Inc. Z210 (%S Polish composite)	19	23.6
05-FC1036	RZM 04-FC1028, 1037, 1038 aa x A, (LSR)	19	20.4
Y591H50	C790-15cms x IRZ-% Y391	19	24.4
P531CT (iso)	PMR-RZM P431CT	20	23.7
5944	S1 (C1,2,3) aa x A	20	20.5
R578H5	C833-5CMS x R378, (C78/3)	21	26.5
R524-2/3H5	C833-5CMS x R324-213, -215, -222, -223	22	21.7
Roberta	Betaseed 3/06 pelleted	22	20.4
Beta4430R	Betaseed 8-21-03/	24	12.9
Z425	RZM Z325 aa x A, CZ25/2	25	24.0
R578 (iso)	RZM R378 (iso), (C78/3)	26	23.9
Roberta	Betaseed 3/06 pelleted	27	21.2
4943	RZM 3943 aa x A	28	26.5
Beta4430R	Betaseed 8-21-03/	28	14.3
Angelina	Betaseed 3/06 pelleted	37	22.0
Angelina	Betaseed 3/06 pelleted	43	21.7

California Entries in rhizomania Test, Heyburn area, Idaho, 2006

(cont.)

Variety	Description	Verticillium	RZM
		Symptomatic Plants	DI
		<u>%</u>	<u>Mean</u>
		LSD 12	

Notes:

Seed from Salinas was provided for a rhizomania test in Idaho and planted in a field near Heyburn, Idaho, purported to have rhizomania. 2006 test means suggested that rhizomania was mild and disease ratings may not be reliable. Test was grown and data were obtained by Anne Gillen and Carol Strausbaugh.

In the Heyburn rhizomania test, foliar yellowing was observed. Initially foliar yellowing was thought to be due to *Fusarium*. Isolations and evaluations by Carl Strausbaugh, however, revealed that *Verticillium* was the primary pathogen. The plots were scored for *Verticillium* yellowing by Carl Strausbaugh.

TEST 106. EVALUATION OF PLANT INTRODUCTIONS (PI's), SALINAS, CA, 2006, BLOCK 2

48 entries* x 4 reps, sequential
1-row plots, 11 ft. long

Planted: May 5, 2006
Harvested: September 6, 2006

Variety	Description	Stand Count		Harv Count	Roots/Acre		Sucrose		RJAP		Bolt		PM		Leaf Color		Bolt Tend		Plant Type	DI	%R (0-3)
		No.	No.		Tons	%	%	%	%	%	Score	Score	Score	Score	Score	Score					
Checks																					
US H11	Susc. check	14	13	15.49	10.11	67.1	0.0	1.5	2	2	3	4.2	35.2								
R539	Inc. R039, (C39R)	15	14	24.73	11.13	68.8	0.0	0.0	2	2	3	2.9	94.5								
Y577	IRZM-% Y277, Y375	15	15	22.18	11.71	65.6	0.0	0.0	2	2	3	2.9	91.9								
R521	IRZM-% R021, R321	15	15	20.91	11.42	65.1	0.0	0.3	2	2	3	2.9	91.5								
P528	PMR-RZM P428, (CP04)	14	14	19.95	10.17	63.5	0.0	0.3	2	2	3	3.2	81.4								
O5-C37	Inc. 04-C37	15	15	15.07	11.18	69.4	0.0	0.8	2	2	3	3.7	63.9								
R540	IRZM-% R940,R840,R740	14	14	22.50	11.51	66.1	0.0	1.0	2	2	3	3.0	91.5								
R524-302	Inc. R321-302,-306	15	14	13.69	11.65	65.1	0.0	2.3	2	2	3	3.3	80.9								
R525	IRZM-% R325,R324, ...	14	14	17.72	11.98	67.4	0.0	2.0	2	2	3	3.0	89.5								
R537-302	Inc. R337-302	13	13	17.41	12.98	68.0	0.0	1.8	2	2	3	3.0	94.2								
P527	PMR-RZM P427, (CP03)	13	14	20.80	11.21	63.4	0.0	0.0	2	2	3	3.0	92.6								
P529	PMR-RZM P429, (CP05)	14	14	22.50	12.76	69.4	0.0	0.0	2	2	3	2.9	92.6								
P530	PMR-RZM P430, (CP06)	15	16	25.79	11.26	64.9	0.0	0.0	2	2	3	2.9	95.0								
EL-SP7322-0	Inc. SP22-0, 4/05	15	14	12.95	9.51	66.3	0.0	0.3	1	2	3	3.9	49.8								
Roberta	Betaseed, pelleted	14	14	14.65	10.78	72.4	0.0	1.5	2	2	3	4.7	30.9								
Angelina	Betaseed, pelleted	15	15	31.63	12.95	68.6	0.0	7.0	2	2	3	2.9	98.5								
PI 504204	Wildbeet, Italy	10	10	2.02	7.88	56.4	93.2	0.0	3	1	5	4.1	44.8								
PI 504272	Wildbeet, France	14	13	1.80	1.84	16.6	88.0	0.0	3	1	5	4.4	28.9								
PI 518355	IDBNR 5849, UK	13	15	5.10	8.68	48.3	54.6	0.0	3	3	5	3.2	77.2								
PI 518377	IDBNR 5871, Ireland	14	15	3.93	9.26	50.7	58.8	0.0	3	3	5	3.4	65.5								
PI 518426	IDBNR 5920, UK	13	14	4.88	10.42	59.4	0.0	0.0	3	2	5	3.7	58.9								
PI 518433	IDBNR 5927, UK	14	14	6.69	10.27	67.1	41.2	0.0	3	3	5	3.1	84.4								
PI 540563	WB 814, France	14	14			63.1		0.0	3	2	5	3.3	73.4								
PI 540565	WB 816, France	13	13			87.2		0.0	3	1	5	3.2	78.1								

TEST 106. EVALUATION OF PLANT INTRODUCTIONS (PI's), SALINAS, CA, 2006, BLOCK 2

(cont.)

Variety	Description	Stand Count		Harv Count		Roots/ Acres		Sucrose		RJAP		Bolt		PM		Leaf		Bolt		Plant Type	DI		%R (0-3)
		No.	No.	No.	No.	Tons	%	%	%	%	%	%	%	Score	Score	Score	Score	Score	Score	Score	%	%	
PI 540566	WB 817, France	5	4									86.5		0.0		3		1		5	3.0	3.0	95.0
PI 540567	WB 818, France	12	12	1.49	2.29	20.2	93.0	0.0				93.0		0.0		3		1		5	3.8	61.7	
PI 540573	WB 827, France	12	11	1.91	4.62	28.2	93.5	0.0				93.5		0.0		3		1		5	3.3	73.9	
PI 540574	WB 828, France	4	4	3.71	5.02	34.4	86.7	0.0				86.7		0.0		3		2		5	3.8	45.8	
PI 540577	WB 831, France	11	10	4.88	7.86	52.2	69.4	0.0						0.0		3		3		5	4.2	33.6	
PI 540632	WB 886, UK	15	15	2.34	9.99	56.7	81.9	0.0						0.0		3		1		5	2.8	96.5	
PI 540633	WB 887, UK	12	12	5.20	5.83	36.1	86.5	0.0						0.0		3		1		5	3.2	84.7	
PI 540666	WB 920, France	12	11	0.70	9.40	57.9	54.9	0.0						0.0		3		3		5	3.1	81.1	
PI 546379	IDBENR 5657, Spain	12	10	1.81	0.33	4.5	81.1	0.0						0.0		3		1		5	3.3	74.4	
PI 546387	IDBENR 5631, USA (CA)	10	10	3.18	3.62	30.5	85.7	0.0						0.0		3		2		5	4.6	29.4	
PI 546388	IDBENR 5656, USA (CA)	9	8	2.87	3.15	28.4	78.5	0.0						0.0		3		2		5	4.4	25.6	
PI 546389	IDBENR 5632, USA (CA)	11	10	2.34	7.19	50.4	0.0	0.0						0.0		1		2		3	4.3	25.8	
PI 546393	IDBENR 5593, USA (CA)	14	14				80.9	0.0						0.0		3		1		5	3.3	72.3	
PI 546403	IDBENR 5600, UK	15	14	2.23	2.23	14.9	91.2	0.0						0.0		3		1		5	3.2	79.1	
PI 546416	IDBENR 5610, Greece	12	9	2.23	7.72	59.9	61.0	0.0						0.0		3		2		5	3.8	54.5	
PI 546508	IDBENR 9675, Greece	12	3				51.3	0.0						0.0		3		1		5	7.8	0.0	
PI 546520	IDBENR 9687, Greece	9	5				79.6	0.0						0.0		2		1		5	7.1	15.6	
PI 562586	IDBENR 9737, Egypt	14	7				80.1	0.0						0.0		3		1		5	7.6	19.4	
PI 562591	IDBENR 9742, Egypt	13	13				97.9	0.0						0.0		3		1		5	3.8	56.2	
PI 562600	IDBENR 9749, Egypt	13	10				85.5	0.0						0.0		3		1		5	3.8	47.6	
PI 562601	IDBENR 9750, Egypt	12	11	2.76	5.46	45.0	96.2	0.0						0.0		3		1		5	3.6	65.2	
PI 562604	IDBENR 9753, Egypt	13	14	2.02	4.10	42.0	94.4	0.0						0.0		3		1		5	4.3	41.7	
Checks																							
C28	Syngenta lot, 4/06	15	13	17.94	9.76	63.2	0.0	0.3						0.3		2		2		3	3.6	63.0	
R524-2/3	Inc. R324-213,-215, -222,-223	14	14	15.92	11.12	62.7	0.0	1.5						1.5		2		2		3	3.1	85.6	

(cont.)

Variety	Description	Stand		Harv Count	Roots/ Acre		RJAP	Bolt %	PM	Leaf		Bolt Tend	Plant		%R (0-3)	
		No.	Count		Tons	%				Score	Color		Score	Type		%
Mean		12.7	12.0	10.66	8.47	52.7	45.9	0.4	2.5	1.7	4.2	3.7	64.9			
LSD (.05)		2.6	3.2	3.11	2.26	13.8	20.4	0.8	0.4	0.5	0.0	1.1	25.3			
C.V. (%)		14.8	18.7	20.83	19.02	18.6	31.8	138.4	12.8	21.5	0.0	20.6	28.0			
F value		6.5**	8.0**	66.04**	19.27**	13.6**	31.4**	15.3**	14.2**	11.8**	--	8.3**	8.3**			

*Analyses were performed on available data.

48V x 4R data available for: stand & harvest counts, %bolting, powdery mildew, leaf color, bolt tendency, plant type, disease index (DI); %resistant(%R) 0-3.

39V x 4R data available for: clean weight, %sucrose, %soluble solids, %NSSS, RJAP
(data missing for: V23 = PI540563 (WB 814, France); V24 = PI 540565 (WB 816, France);
V25 = PI 540566 (WB 817, France); V37 = PI 546393 (IDBBNR 5593, USA (CA));
V40 = PI 546508 (IDBBNR 9675, Greece); V41 = PI 546520 (IDBBNR 9687, Greece);
V42 = PI 562586 (IDBBNR 9737; Egypt); V43 = PI 562591 (IDBBNR 9742, Egypt);
V44 = PI 562600 (IDBBNR 9749; Egypt).

Leaf Color scored 1-5 (1 = light green; 2 = green; 3 = green-red mixture; 4 = red; 5 = chlorophyll mutant)

Bolting Tendency scored 1-4 (1 = annual; 2 = biennial; 3 = mixed annual and biennial; 4 = perennial)

Plant Type scored 1-5 (1 = fodder; 2 = leaf; 3 = sugar; 4 = table; 5 = wild)

Rhizomania scored 0-9, where 9 = highly susceptible. DI = average rhizomania score per root. %R = classes 0-3/total roots. Rhizomania was moderated. Growth habits of wild, annual beets made scoring for rhizomania difficult. The reported frequency of resistant plants is greater than the actual number based on the performance of sugarbeet checks. For rhizomania, test was fair and only within broad ranges identified reaction to rhizomania.

Harvest was early and plants were still growing under high nitrogen conditions. Development of powdery mildew was in early stage. Bolted, annual plants had been repeatedly cut back through season to prevent hard seed development and wild beet from establishing in the field.

**SUGAR BEET RESEARCH
USDA-ARS SUGARBEET RESEARCH UNIT
FORT COLLINS, COLORADO**

2006 REPORT

SECTION B

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In Cooperation with:

Colorado Agricultural Experiment Station

**Much of this research was supported in part by funds provided through the
Beet Sugar Development Foundation
(Projects 421, 423, 430, 440, 441, 443, 445, 446 and 903)**

USDA-ARS-NPA Sugar Beet Research Unit's Mission Statement

Utilize distinctive site environmental and disease-free characteristics and specifically developed team expertise to:

- ❖ develop new knowledge and adapt biotechnologies to modify host-pathogen relations that affect disease resistance, pathogenesis and epidemiology in sugar beet and other plant species pertinent to sugar beet cultivation;**
- ❖ discover new information and techniques to identify and produce genotypes exhibiting superior disease and stress tolerance and agronomic qualities;**
- ❖ provide new knowledge that improves production efficiency and biochemical processing characteristics of sugar beet.**

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BSDF PROJECT 421 – VARIABILITY IN *FUSARIUM OXYSPORUM* FROM SUGAR BEETS IN THE UNITED STATES

L.E. Hanson, L. Panella and A.L. Hill
USDA-ARS, Fort Collins, Colorado

Fusarium yellows causes significant reduction in root yield, sucrose percentage and juice purity in affected sugar beets. Research in our laboratory and others on variability in *Fusarium oxysporum* associated with sugar beets demonstrated that isolates that are pathogenic on sugar beet can be highly variable. A better understanding of this variability is important in the efforts to test for *Fusarium* yellows resistance in beets and efforts to breed for resistance.

From 2002-2005, 647 *Fusarium* isolates were obtained from sugar beet. Isolates of species have been identified every year of the study, included, in order of frequency, *F. oxysporum*, *F. equiseti*, *F. solani*, *F. acuminatum*, *F. avenaceum*, *F. proliferatum*, *F. subglutinans*, and *F. verticillioides*. Two other species, *F. culmorum* and *F. graminearum* have not been isolated every year, but have been isolated from several fields or a larger proportion of beets than some of the above species during some years. A small number of isolates of three additional species have been identified, but only rarely. None of these isolates were pathogenic in greenhouse tests, and so they are not discussed further.

In 2006, isolates of *Fusarium* were obtained from diseased beets, and the majority identified. Several isolates were obtained that did not match any of the previously identified species from this survey. Genetic tests indicate that it is in the *Giberella fujikori* complex of strains, but do not give an exact match to any known species. The isolates of this unknown species tested to date have not caused any foliar symptoms on sugar beet, but additional isolates remain to be tested. This fungus will be examined further.

Of the remaining isolates from 2006, 56% were *Fusarium oxysporum*. The second most common species was *F. equiseti*, followed by *F. solani*, *F. acuminatum* and *F. graminearum*. Other species identified included *F. avenaceum*, *F. culmorum*, *F. proliferatum*, *F. subglutinans*, and *F. verticillioides*. In 2006, *F. avenaceum* was isolated less frequently than *F. acuminatum*. This is similar to what was observed in 2005, but unlike previous years in which these two species were isolated at approximately equal frequencies.

All years of this project, the majority of the isolates collected (52%) being *Fusarium oxysporum*. Of the *F. oxysporum*, approximately 25% of the isolates tested to date are pathogenic on sugar beet. In addition, isolates of at least five other *Fusarium* species have been determined to cause yellows-type foliar symptoms on sugar beet. No isolates of *F. equiseti* have been found pathogenic on sugar beet in our greenhouse assay, but this species has been associated with postharvest mold problems in sugar beet (Bosch & Mirocha 1992). While these other species can cause similar foliar symptoms to yellows, the most virulent isolates in our collection are all *F. oxysporum*. *F. oxysporum* isolates can be separated into highly virulent and moderately virulent isolates, with the highly virulent isolates causing 20% or more of the beets in the greenhouse screen to die within 6 weeks after inoculation, while the moderately virulent isolates cause yellowing, wilting, and stunting, but usually do not kill plants in this time period. Of the other species, the majority of the isolates tested are mildly or moderately virulent. In 2006, one isolate of *F. acuminatum* was identified that could be considered highly virulent because it caused a 30% loss of plants. This is still less virulent

than several of the *F. oxysporum*, which can cause 70-100% plant loss.

In addition to *Fusarium* yellows, for which there are no external root symptoms, some of the beets in this study had root rot symptoms. Species isolated from these beets included *F. culmorum*, *F. graminearum*, *F. oxysporum*, and *F. solani*. *F. culmorum* has been reported to cause a root or crown rot under drought conditions in Europe (Hull 1960). *Fusarium solani* also has been reported to cause root rot in beets (Abada 1994, Maxon 1948). In Texas, some *F. oxysporum* isolates have been demonstrated to cause a tip rot of sugar beet (Martyn et al. 1989). These have been designated *F. oxysporum* f. sp. *radicis-betae* (FORB) rather than FOB (Harveson and Rush 1998). None of the samples from which our isolates were obtained were from Texas, but it is clear that root rotting *F. oxysporum* occurs in other areas. *F. oxysporum* isolates were identified from Colorado and Montana that caused a tip rot symptom similar to that reported for isolates from Texas. Additional isolates are being tested. *F. graminearum* has been reported from rotted beets at harvest (Bosch and Mirocha 1992), but the role of this species in sugar beets in the field is still being investigated. It does not cause any evident root rot in young beets (6-week-old or 8-week-old), but can cause a reddish rot in beet root if inoculated into mature roots.

In addition to isolates from sugar beet, *F. oxysporum* f. sp. *spinaciae* (FOS) isolates were kindly provided by Dr. L. duToit. These isolates were obtained from spinach and had been demonstrated to be pathogenic on spinach. In greenhouse tests, all spinach isolates tested were pathogenic on sugar beet with a moderate level of virulence. While these isolates are pathogenic on sugar beet, and 12 of 16 isolates from sugar beet tested were pathogenic on spinach, genetic evidence (Fig. 1) indicates that the FOS are more similar to one another than to isolates from beet.

Isolates of *F. oxysporum* so far obtained in this study include isolates from California, Colorado, Michigan, Minnesota, Montana, Nebraska, North Dakota, Oregon, Washington, and Wyoming. Pathogenic isolates identified so far are from California, Colorado, Michigan, Minnesota, Montana, North Dakota, Oregon, Washington, and Wyoming. Some variability has been observed in the other species obtained in different areas. For example, the majority of the *F. graminearum* isolates are from Minnesota or North Dakota, with a few from northern Wyoming or northern Nebraska. This species was very rarely isolated in Colorado (one isolate in the course of 6 years) and we have not found it in any samples from Oregon or California.

Following up on evidence from RAPD analysis indicating a high degree of variability, three sections of the *Fusarium* genome were sequenced and used in comparison of isolates. All three sequenced areas gave similar results, with greater or lesser discrimination between individual isolates. With all three types of sequence information (β -tubulin, α -elongation factor, and ITS region), three distinct genetic groups were found for isolates of *F. oxysporum* pathogenic on sugar beet. An example is shown in Figure 1. One of these groups had higher similarity to another species, *F. proliferatum*, than to the other two *F. oxysporum* groups. Two of the three groups (designated group 1 and group 2, Fig. 1) included isolates that varied in their degree of virulence on the sugar beet germplasm used in pathogenicity screening. Two of the three groups (groups 1 and 3) contained both pathogenic and non-pathogenic isolates of *F. oxysporum* f. sp. *betae*. Group 3 showed similarity to isolates of FOS and included one isolate of FORB.

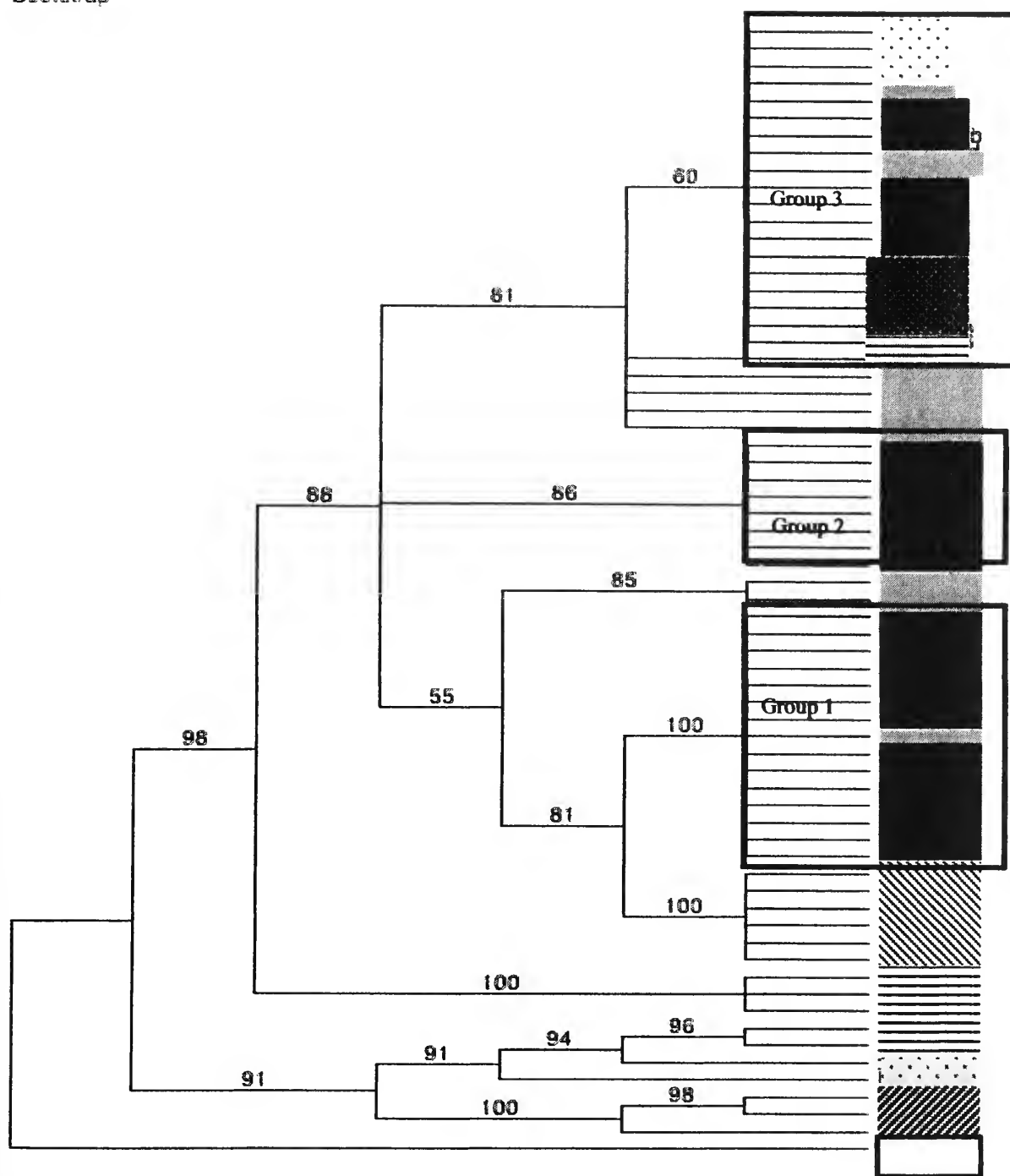


Figure 1. Nucleotide sequence analysis shows a high degree of genetic variability in *Fusarium oxysporum* from sugar beet, with at least three genetically distinct groups that cause yellows-type symptoms on sugar beet. Sugar beet isolates (FOB, black) are compared to *Fusarium oxysporum* isolates from spinach (FOS, black with white spots) or dry bean (FOP, gray with black spots), non-pathogenic *F. oxysporum* (gray), *F. oxysporum* of unknown pathogenicity (bars), and isolates of closely related species, *F. proliferatum* (diagonal lines left to right), and *F. solani* (diagonal lines right to left), as well as a more distantly related species, *F. avenaceum* (white). Both the *F. proliferatum* and *F. solani* fell within the same broad group that contained the *F. oxysporum* isolates. FOB isolates fell into three distinct groups. Groups 1 and 2 contain both highly and moderately virulent isolates, and group 3 includes an isolate of *F. oxysporum* f. sp. *radicis-betae* from Texas that causes root rot of sugar beet.

The finding of several species of *Fusarium* causing similar foliar yellowing is of concern since current disease control measures are aimed at controlling *F. oxysporum*. Rotation with small grains and corn has been recommended for *Fusarium* yellows control, but *F. acuminatum*, *F. avenaceum*, *F. graminearum*, and *F. verticillioides* can be pathogens on small grains and *F. graminearum* and *F. verticillioides* on corn. Thus these rotations might not aid in disease control.

The presence of several of these species of sugar beet also could be of concern for other crops grown in rotation with sugar beet, whether or not they cause disease on sugar beet. Several of the species isolated from sugar beet are generally reported to be grain pathogens. For example, *F. equiseti* was the second most commonly isolated species after *F. oxysporum*. While no isolates of this species were pathogenic on growing sugar beet, isolates of this species are important pathogens of cereal grains. Similarly, isolates of *F. avenaceum*, *F. acuminatum*, *F. culmorum*, *F. graminearum*, and *F. verticillioides* are pathogens of grains. In addition, isolates of *F. avenaceum*, *F. acuminatum*, *F. culmorum*, *F. graminearum*, and *F. solani* have been reported to cause dry rot in potatoes, *F. graminearum* can be pathogenic on soybean, and *F. solani* cause a root rot of crops such as dry beans. Isolates of *F. graminearum* collected in this survey have been provided to other researchers who have found that these isolates can be pathogenic on potato and wheat. The ability of isolates of other species to infect rotation crops is not known, but this could be of concern for infection of crops in the rotation.

BSDF PROJECT 423 – DETERMINATION OF POTENTIAL RACES OF *FUSARIUM OXYSPORUM* F.SP. *BETAE* (FOB), THE CAUSAL AGENT OF FUSARIUM YELLOWS

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Fusarium yellows can cause significant reduction in root yield, sucrose percentage and juice purity in affected sugar beets. The disease is caused by *Fusarium oxysporum* f. sp. *betae* (FOB). Research in our laboratory and others on variability in FOB demonstrated that isolates that are pathogenic on sugar beet can be highly variable. A better understanding of this variability is important in the efforts to test for Fusarium yellows resistance in beets and efforts to breed for resistance.

Nineteen sugar beet lines were generously provided by the sugar beet seed companies. The majority of these lines had shown resistance to Fusarium yellows in at least one test, except that two lines were provided as susceptible material. These lines, along with the Fort Collins germplasms FC716, as a standard, were tested in 2005 for their reaction to FOB isolates that were from different geographic regions and showed genetic variability or variable virulence in our initial screening on germplasm FC716 (see report for BSDF project 421) or in tests in other laboratories. The lines were tested both in Fort Collins, CO and in Bozeman, MT. In Fort Collins, lines were rated for foliar disease severity using a 0-5 rating scale (0=no disease, 5=plant dead) for six weeks and the area under the disease progress curve was determined. In addition, in both locations, the percent of plant death at 4 and 6 weeks after inoculation was determined. The isolates differed in the amount of disease they caused, with isolates Fob13, Fo24, Fo25, and Fo37 generally killing few plants during the tests. Differences were found in the response of the various sugar beet lines to the FOB isolates (Figure 1). Some lines were quite susceptible to all or most of the isolates, while other lines showed resistance to some isolates

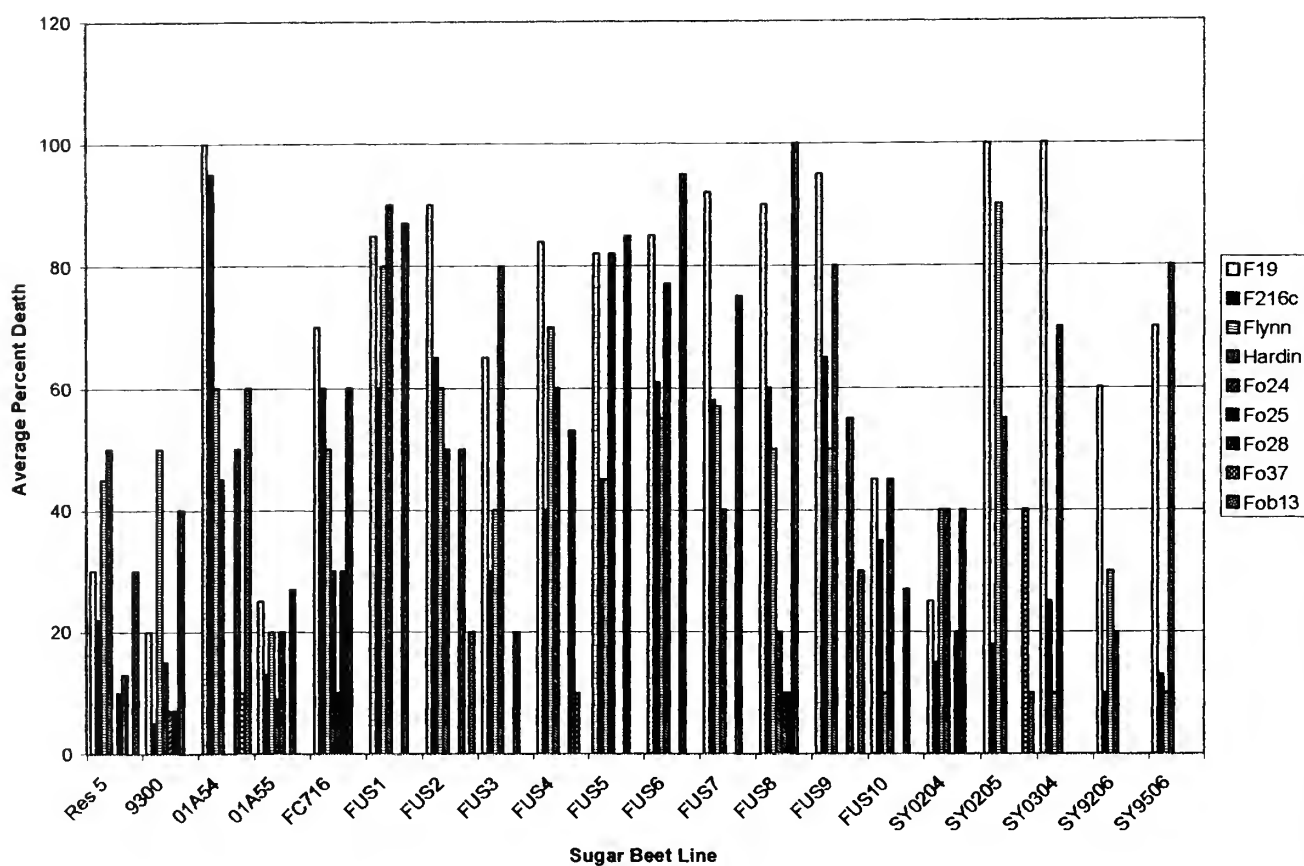


Figure 1. Average percent death of sugar beet plants of different lines treated with various isolates of *Fusarium oxysporum* f.sp. *betae*. Note isolates F19, F216c, Flynn, Hardin, and Fob13 were tested at both Fort Collins and Bozeman, and results shown are the average for the two locations. The other isolates were tested at only one location, and results shown are for those tests only. Isolates Fo24, Fo25, and Fo28 were not tested on the last three varieties due to insufficient plants.

In 2006, additional smaller screenings were done with subsets of the above lines that had shown variable reactions to different sugar beet isolates in the initial screening using a smaller number of isolates. In these test, it was observed that FOB isolates that had been classified as highly virulent in initial screening generally gave more consistent results from experiment to experiment (correlation coefficients 0.7 – 0.9 between experiments) as compared to moderately virulent FOB isolates (correlation coefficients 0.2-0.5). Thus additional screenings focused primarily on highly virulent isolates. Differences between the responses of lines continued to be observed (Figure 2).

In examining genetic variability of FOB isolates (see project 421), three distinct genetic groups had been observed within this *forma specialis*. Isolates used in the screening included material from two of these genetic groups. Isolates from the third group will be included in future screenings.

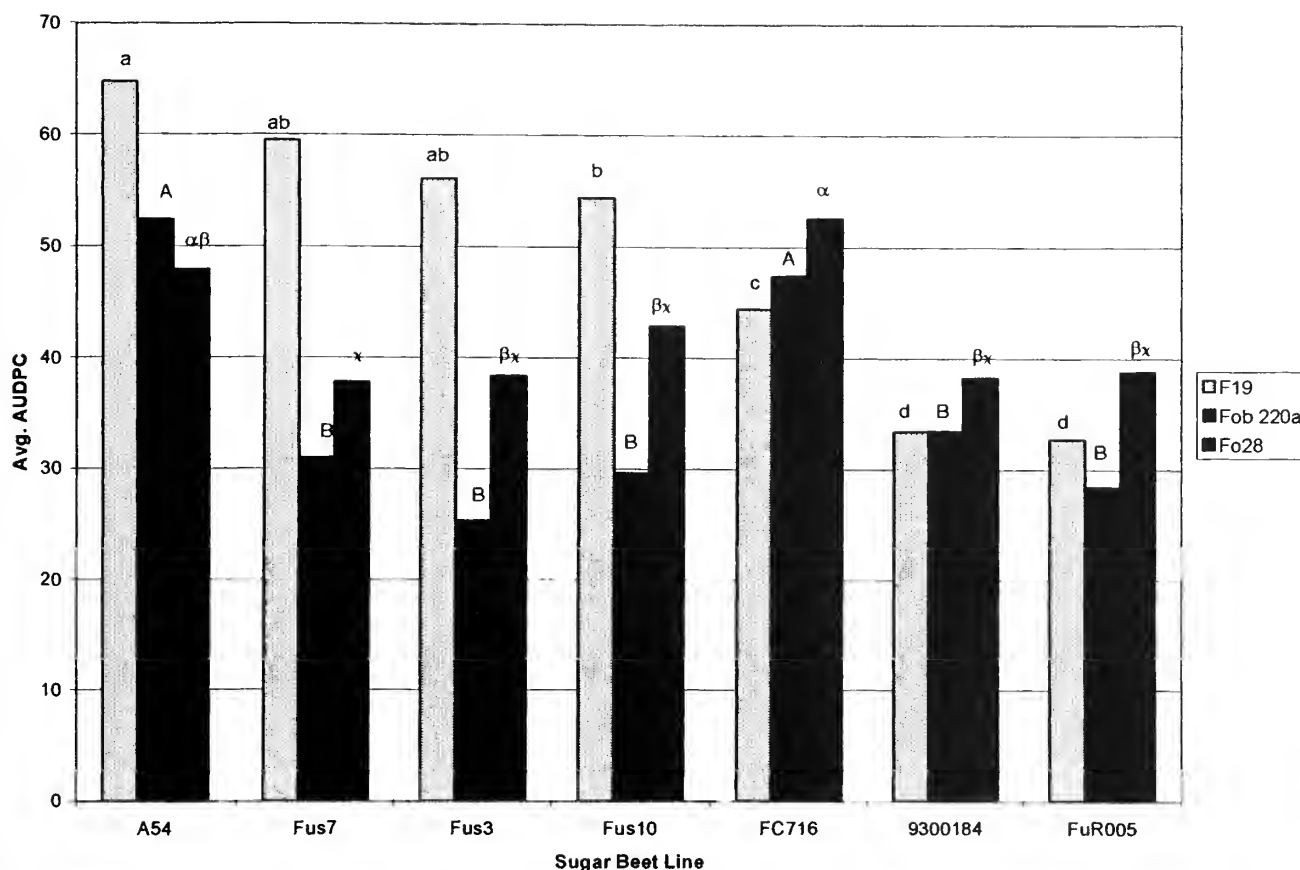


Figure 2. Response of a subset of the sugar beet lines to three highly virulent isolates of *Fusarium oxysporum* f. sp. *betae*. Lines of the same pattern with the same letter are not significantly different ($\alpha=0.05$) by Tukey's.

As well as variability within FOB, in 2006, an isolate used in some of the screenings of sugar beet germplasm was determined to cause a root rot on several sugar beet lines, similar to what has been reported as *Fusarium oxysporum* f. sp. *radicis-betae*. Differences in line responses to this isolate were found, similar to those found for the FOB isolates. In addition, two other isolates were found which appeared to cause some rotting symptoms, starting with the root tip, on some sugar beet lines, but not on other lines. This will be examined further.

Also in 2006, Dr. Barry Jacobsen screened several sugar beet lines for their response to different *Fusarium oxysporum* isolates in the presence and absence of the sugar beet cyst nematode. Lines were observed which showed no difference in response associated with the nematode, which had increased diseases severity, or potentially decreased disease severity.

Table 1. Percentage dead or dying plants six weeks after inoculation for sugarbeet lines inoculated with *Fusarium oxysporum* f.sp. *betae* (FOB) isolates H7/8 or 216c alone or grown in soil inoculated with three viable eggs and larvae/ cc of *Heterodera schachtii* and inoculated with the two FOB isolates.

Sugarbeet line	FOB isolate H7/8 Percent plant death		FOB isolate 216C Percent plant death	
	+CN	-CN	+CN	-CN
FC 716	56	44	16	11
A54	86	47	94	85
A55	36	12	50	18
FUS1	20	94	40	60
FUS2	60	67	50	63
FUS3	74	88	77	29
FUS4	54	67	44	58
FUS5	42	84	32	56
FUS6	60	58	30	48
FUS8	30	27	28	30
FUS9	60	83	58	68
FUS10	64	45	74	50
SY 0204	34	40	26	20
SY0205	60	40	73	25
SY0304	42	70	20	15
SY9206	38	42	36	25
SY9506	48	100	22	15

FLSD P=0.05 for H7/8 between +CN and -CN = 6.7%

FLSD P=0.05 for 216C between +CN and -CN = 5.4%

Finding differences in the response of sugar beet lines to varying FOB isolates, examinations were done to further examine the interaction. When epidermal peels were taken from sugar beet root following inoculations, no significant differences were found in the timing of penetration between resistant and sensitive lines. Similarly, no significant differences were observed in the timing of spread from the epidermis into the cortex. However, when root segments were collected and plated on media to look at colonization, differences were observed in the rate and level of colonization of the vascular tissue over time in resistant and sensitive sugar beet lines with the first FOB isolate tested (Figure 3). Preliminary tests with a second FOB isolate showed similar results.

This may give one indication for a factor involved in resistance. If such differences in spread are consistent for additional lines and FOB isolates, a more rapid screen might be developed based on host colonization.

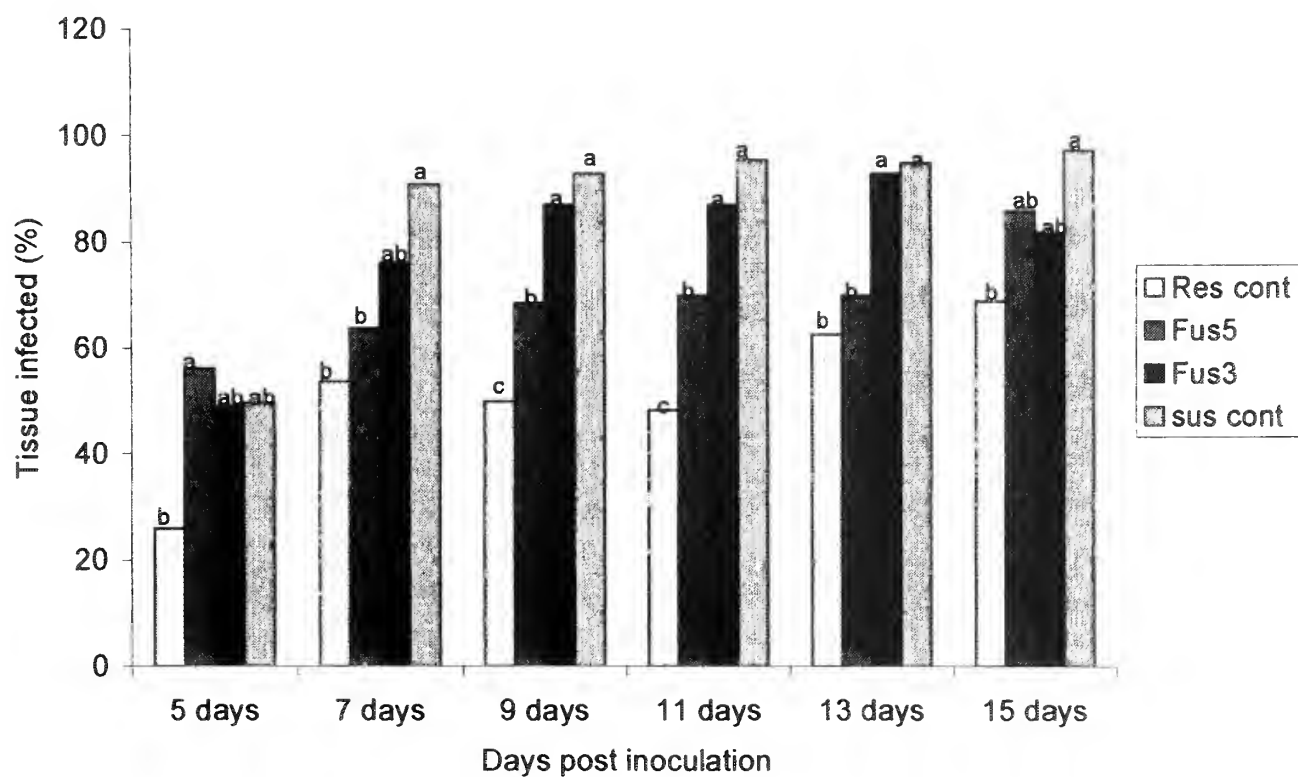


Figure 3. Amount of root tissue showing evidence of infection with *Fusarium oxysporum* f. sp. *betae* at different time periods following inoculation. Bars for each time with the same letter are not significantly different by Tukeys ($\alpha=0.05$).

BSDF PROJECT 430

COMPARATIVE PROTEOMICS FOR UNDERSTANDING SUGARBEET RESISTANCE TO *FUSARIUM* SPP.

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Introduction: *Fusarium spp.* are a serious threat to sugarbeet production worldwide. There are resistance sources that exist, but the basis for resistance is poorly understood. Furthermore, resistance appears to vary by geographic location. This variability may be a result of the tremendous diversity within the pathogen population, since sugarbeet falls prey to a wide array of pathogenic species and isolates. This is further complicated by evidence that resistance can be genotype-specific and vary depending on the species, isolate or possible race of *Fusarium* infecting the beet. The first objective of this study was to examine proteins affected by *Fusarium oxysporum* isolate F-19 in a resistant and susceptible line of sugarbeet. This information contributes to a broad-based ARS multidisciplinary investigation of *Fusarium*-sugarbeet interactions and these combined efforts in genetics, pathology and biochemistry will ultimately help us develop better disease management strategies and methods for resistance selection.

Several other crops are affected by *Fusarium spp.* Many genes/proteins involved in plant defense are found in a wide array of distantly-related crop species, therefore the second objective of this study was to examine the degree of conservation of proteins induced by *Fusarium* in corn and sugarbeet. Comparison of sugarbeet resistance to the resistance response of other crops will serve two purposes: 1) comparisons across large genetic distances help determine which proteins are functionally related to defense (i.e. clarify findings in the sugarbeet studies) and 2) if major constituents of defense are conserved, resistance genes from other crops may be introduced into sugarbeet to provide more sources of resistance to *Fusarium*.

Results: Protein extracts from sugarbeet genotypes C1200.XH024 (resistant, R) and Fus7 (susceptible, S) were analyzed by multidimensional liquid chromatography at 2- and 5-days post inoculation (dpi) and compared to mock-inoculated controls. One hundred twenty-one (R) and 73 (S) protein peaks were induced/repressed by F-19, approximately 12% (R) and 8% (S) of the total proteome detected. Temporal protein regulation occurred within and between each genotype indicating timing of expression may be important for resistance (Figure 1).

Thirty-one (R) and 48 (S) of the differentially expressed peaks were identified using MALDI-TOF/TOF mass spectrometry, others were below detection level. Comparison between the two genotypes uncovered R- and S-specific proteins with potential roles in resistance and disease development, respectively. Of particular interest was the R line responded to F-19 by inducing a larger subset of oxidative and anti-fungal enzymes when compared to the S line. Pathogenesis-related (PR) proteins 1a, 7 and 10 were all unique to the resistance response. However, chitinase, an antifungal enzyme, was induced in both lines, only to a much greater extent in the R line. The late and/or transient expression of some of the defense-related proteins in the S line may explain their lack of activity against F-19. Another striking difference between the R and S line was the notable inhibition of cell wall strengthening/cross-linking enzymes in the S line and

a noted increase in R line. Creating physical barriers against pathogen ingress appears to be an important defensive mechanism for sugarbeet. This line of investigation also uncovered susceptibility-specific proteins. One, a tonoplast aquaporin, is a protein pore, which in other systems, is manipulated by pathogens and symbiotic microorganisms to derive food from the host plant. Interestingly, controlling expression of aquaporins has been an effective mechanism for controlling disease in other crops. Exploitation of similar mechanisms in beet could be explored as a novel *Fusarium* Yellows disease control strategy.

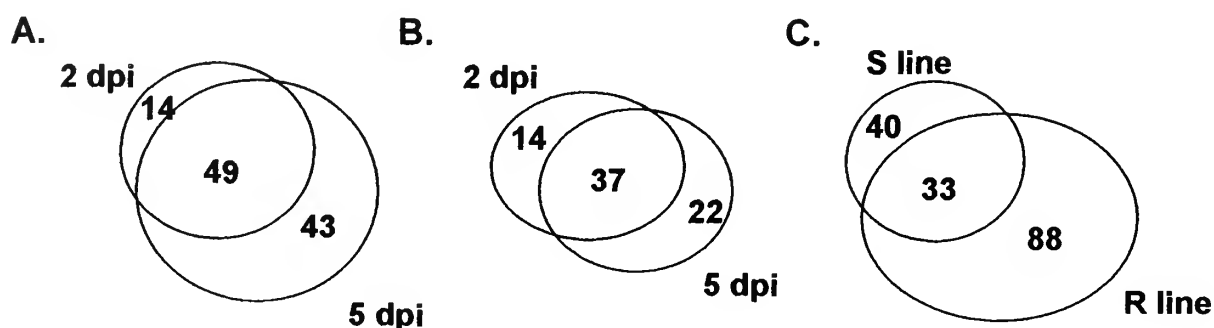


Figure 1. Temporal regulation of proteins induced in sugarbeet resistant (A) and susceptible (B) to *F. oxysporum* isolate F-19. Some proteins were similarly affected by F-19 in both genotypes, while others were specific to the resistant (R) or susceptible (S) line (C).

For experiments examining corn resistance, kernel samples, from varieties 441 (R) and B73 (S, provided by Dr. Linda Harris, Oilseed and Cereal Research Center, Ottawa, Canada) were analyzed at 2 dpi with *F. graminearum* and compared to mock-inoculated controls. Surprisingly little overlap exists between the corn and sugar beet system. The only proteins in common included: hydrogen peroxide generating enzymes, ubiquitination proteins, protein kinases, and profilin. Several of the similar proteins are classically tied to plant defense. With the acceptance of transgenic technology by the sugar beet production community, some of these conserved proteins may be potential gene candidates for creating novel resistance through overexpression.

Conclusions and Implications: Initial investigation into the conservation of resistance responses in a diverse array of crops in response to *Fusarium* infection provided some pertinent clues for developing future lines of investigation. We have begun to uncover some protein constituents necessary for resistance to *F. oxysporum* in sugar beet. Although there was a lack of overlap between the corn and sugar beet system, the underlying reason for that remains unknown and could be due to the fact a large subset of proteins were unable to be identified, once identified more overlap may become apparent. Furthermore, the major gene resistance response of sugar beet could be fundamentally different from the quantitative resistance response of corn (i.e. we are comparing apples to oranges). Therefore it may be necessary to gain a better understanding of how sugar beet responds to a wider array of *Fusarium* species. Ultimately, we hope to use this information to develop methods for increasing the speed and accuracy of resistance identification and develop novel disease strategies to increase the durability of the resistance already employed.

BSDF PROJECT 445
PRE-BREEDING: THE INTROGRESSION OF NEW SOURCES OF
HOST-PLANT RESISTANCE FROM *BETA VULGARIS* SSP. *MARITIMA*
AND OTHER EXOTIC SOURCES INTO SUGAR BEET-TYPE
POPULATIONS

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USDA-ARS, Salinas, California
USDA-ARS, Fargo, North Dakota

BACKGROUND

This project combines and re-directs components of previous BSDF projects 440, 441, and 443. (Final reports on those projects follow.) It is an attempt to respond to many of the BSDF plant breeders with whom I have discussed the ARS breeding program at Fort Collins. The general consensus has been that the ARS programs should concentrate on bringing novel resistance genes into the sugar beet gene pool. The private breeders would then fit that raw germplasm into their own breeding programs. This point in time is a good place to refocus the effort of this breeding program for a number of reasons. Most of the material from R. J. Hecker has been released and worked through. There is a good chance that my administrative duties will increase into another crop(s) in the near future. All of these factors coming together make this a propitious time to narrow the focus and increase the intensity of the breeding program. That said, I still plan to release a number of germplasm in the next few years that have been under development with other ARS breeders (R. T. Lewellen, J. M. McGrath, and L. G. Campbell). I would only ask that I continue to receive the excellent feedback from the BSDF members that I have received in the past. Please feel free to ask questions on any part of this project.

JUSTIFICATION FOR BREEDING RESEARCH

A major emphasis of the research mission of the USDA-ARS plant scientists is the collection, documentation, characterization, evaluation, regeneration (maintenance), distribution, and utilization of plant germplasm, especially Plant Introduction (PI) accessions in the USDA-ARS National Plant Germplasm System (NPGS). The Sugar Beet Research Unit at Fort Collins is coordinating the national program for *Beta* germplasm evaluation. In addition to the evaluation for *Rhizoctonia* resistance, it is crucial that the ARS scientist be involved in the long range, high risk research problems involved in sugar beet 'germplasm enhancement' or 'pre-breeding' from exotic germplasm or wild relatives. This is an important component in the overall sugar beet improvement effort of the Fort Collins Sugar Beet Research Unit. The major emphasis in this project will be on *Cercospora* Leaf Spot and *Rhizoctonia* Root Rot resistance; however, as the screening techniques become better for some of the other major pests and diseases of sugarbeet, host-plant resistance to them will also be explored.

This is an integrated breeding program with greenhouse and laboratory studies, and a field program based on testing in an artificial epiphytotic created in the unique Colorado environment.

It involves close collaboration with the other USDA-ARS sugar beet programs in the U.S. and sugar beet seed industry customers. Genetic information, which is developed during this research, will be used to execute additional cycles of pathogen inoculation, plant selection, and recombination among germplasms that we have in our germplasm enhancement program. Results of these tests will be the basis of decisions about specific germplasm, i.e., retain, discard, recombine, release, etc. Germplasms likely to be useful for variety improvement will be identified and released for use by other sugar beet breeders.

Rhizoctonia:

Rhizoctonia root rot (caused by the fungus *Rhizoctonia solani* Kühn) continues to be a problem in most sugar beet-growing areas in the United States, and is a growing problem worldwide. The practice of short rotations and the expansion of growing areas into infested areas compound the problem. The result is a reduction in net returns to growers as well as processing losses due to reduced sucrose and purity of rotted or partially rotted beets. Genetic resistance, coupled with judicious cultural measures, is a more economical and practical method of reducing losses caused by this fungus than is a strictly chemical control regime.

This has been an ongoing and productive project, and has been the only research project with the goal of discovering, developing, and releasing Rhizoctonia-resistant germplasm to industry breeders, our major external customers. Although several relatively resistant germplasms have been developed, we need to continue to combine this resistance with resistance to other diseases, uncover new sources of resistance, and work to more quickly introgress this resistance into germplasm with higher sucrose yield potential.

Cercospora:

Cercospora leaf spot (caused by the fungus *Cercospora beticola* Sacc.) is one of the most widespread diseases of sugar beet and is a serious problem in many sugar beet production areas throughout the U.S. The disease damages the leaves, which, consequently, reduces root yield, percent sucrose of roots, and purity of the extracted juice. Cercospora leaf spot currently is controlled by combining spraying with commercial fungicides and the use of disease tolerant germplasm. That continued improvement in genetic resistance to this serious pathogen still is needed, is evident by the occurrence of *Cercospora* strains that are resistant or increasingly tolerant to our most potent fungicides. Additionally, some of these fungicides may be removed from the market because of their perceived or real threat to the environment. The development of Cercospora leaf spot resistant sugar beet lines and hybrids with greater levels of host-plant resistance offers a more sustainable solution to this disease problem.

Previously, this element of the breeding program at Fort Collins was built on germplasm developed at Fort Collins over the last fifty years. The genepool for resistance to Cercospora leaf spot in this germplasm is extremely narrow and has been characterized by consisting of all biennial, sugarbeet-type germplasm (no exotic material). Therefore many of the resistant lines are highly inbred, i.e., closely related to one another, and stem from germplasm coming out of Italy in the early 1900s and only a few other sources. In the germplasm developed at Fort Collins, continued inbreeding has increased the level of disease resistance, but at the cost of plant vigor. Over the long term, a secure, sustainable response to this disease requires commercial quality hybrids with good host-plant resistance. Therefore, the focus of this project will shift to finding novel sources of resistance and work to more quickly introgress this resistance into germplasm with sucrose yield potential.

OBJECTIVES

1. The formation of long-range breeding populations through the introgression of resistant germplasm from "exotic" sources (*Beta vulgaris* ssp. *maritima*, fodder beet, table beet, Swiss chard, foreign sugar beet landraces from the PI collection, etc.).
2. The development of germplasm populations from these long range populations that are of sufficient agronomic quality to be of use to commercial breeders. They will be sources of disease resistance with differing genetic backgrounds.
3. The development of techniques (both traditional and molecular) to more efficiently introgress the exotic germplasm into sugar beet breeding populations
4. Long terms goals include discovery of genes in sugar beet which condition resistance to pathogens and pests using Suppressive Subtractive Hybridization, proteomics, and other methodologies.

MATERIALS AND METHODS:

The USDA-ARS National Plant Germplasm System Beta collection has over 2,000 Plant Introduction (PI) accessions. The germplasm used most often in sugar beet breeding is from *Beta vulgaris* spp. *vulgaris*, which includes all of the biennial, cultivated beet types, or from *Beta vulgaris* spp. *maritima*, which contains the closely related wild sea beet and has both annual and biennial types. Germplasm with a biennial flowering habit is easier both to introgress and screen. Annual *Beta vulgaris* spp. *maritima* has, nonetheless, been used as a source of resistant germplasm. Much of the CLS-resistant germplasm in use today, which came out of Munerati's program in Italy, had annual *B. vulgaris* spp. *maritima* as the source of resistance genes. There have been very few new efforts to locate and incorporate other sources of resistance into the commercial sugar beet germplasm base. Munerati's success, and the research of others, has shown that it can be done if we have the persistence to do it.

Artificial field and greenhouse inoculation and disease scoring will be used to identify the resistant germplasm sources and make selections in the donor parent populations. The exotic materials will be crossed into sugar beet populations that have been selected for higher agronomic quality (recoverable sucrose yield). These sucrose populations are based on a number of sources. Old commercial varieties – i.e., MonoHy T6, A7, A4 and breeding lines received from American Crystal Sugar Co. and Seedex, Inc. have been used. Other parents include high sucrose germplasm from Poland and other Eastern European countries. Older USDA-ARS developed germplasm, such as L-19, East Lansing smooth root germplasm, and higher sucrose lines out of the Salinas program, are available as well. This parental material is being put into or already is in populations that are self-fertile (S^f) and segregating for nuclear male sterility ($A-:aa$).

Hybrid populations will be handled in the following manner: 1) Following the initial cross, a population will be random mated (using *aa* females because of the self-fertility) for three to four generations to break up linkage groups and remove annual plants. 2) Sugar beet-type mother roots will be selected, selfed or sib-mated, and progeny tested for agronomic performance and disease resistance. 3) Selected roots will be recombined (and backcrossed if desirable) and re-selected until they are ready for release.

Population development will be done with the thought of concurrent development of populations suitable for genetic analyses, both molecular and traditional. Molecular markers (RFLPs, RAPDs, SSRs, AFLPs, SNPs, etc.) as they become available may be used to expedite the backcrossing program, to define the genetic control of resistance, compare genetic diversity among populations, and search for markers to use in marker aided selection. Advanced populations will be released to the sugar beet seed industry.

TIME LINE OF ANTICIPATED ACCOMPLISHMENTS:

Development of a resistant germplasm line generally takes seven years. A longer time will be necessary to incorporate disease resistance from more exotic sources. Some of the *Cercospora*-resistant material is close to being released; once that happens, there will be a "pipeline" of germplasm in various stages of development and the release of new germplasm will occur every two to four years. The incorporation of exotic sources into agronomically acceptable germplasm is a long term proposition - results will not appear overnight. This is the type of long-term germplasm development that ARS is well suited to perform.

PROJECT ACCOMPLISHMENTS IN GERMPLASM RELEASES:

Germplasm released from the Fort Collins Breeding and Genetics Program over the last fifteen years

Beta	vulgaris	FC404	Crop Sci. 35(6):1721.
Beta	vulgaris	FC404CMS	Crop Sci. 35(6):1721.
Beta	vulgaris	FC716	Crop Sci. 35(1):291-292.
Beta	vulgaris	FC717	Crop Sci. 35(1):291-292.
Beta	vulgaris	FC718	Crop Sci. 35(1):291-292.
Beta	vulgaris	FC719	Crop Sci. 35(1):291-292.
Beta	vulgaris	FC715	Crop Sci. 35(1):290.
Beta	vulgaris	FC715CMS	Crop Sci. 35(1):290.
Beta	vulgaris	FC725	Crop Sci. 36(3):819-820.
Beta	vulgaris	FC726	Crop Sci. 36(3):819-820.
Beta	vulgaris	FC728	Crop Sci. 36(3):819-820.
Beta	vulgaris	FC721	Crop Sci. 37(5):1675-1676.
Beta	vulgaris	FC721CMS	Crop Sci. 37(5):1675-1676.
Beta	vulgaris	FC709-2	Crop Sci. 39(1):298-299.
Beta	vulgaris	FC727	Crop Sci. 39(1):298-299.
Beta	vulgaris	FC712(4X)	Crop Sci. 41(5):1374.
Beta	vulgaris	FC724	Crop Sci. 44(1):361-362.
Beta	vulgaris	FC710(4X)	Crop Sci. 44(5):1885-1886.
Beta	vulgaris	FC201	Crop Sci. 45(3):1169-1170.
Beta	vulgaris	FC301	Crop Sci. 45(6):2666-2667
Beta	vulgaris	FC720	Crop Sci. 46(2):1009-1010
Beta	vulgaris	FC722	Crop Sci. 46(2):1009-1010
Beta	vulgaris	FC722CMS	Crop Sci. 46(2):1009-1010

Germplasm released from the Fort Collins Breeding and Genetics Program over the last fifteen years

Beta	vulgaris	FC723	released 1/27/06
Beta	vulgaris	FC723CMS	released 1/27/06
Beta	vulgaris	FC220	in process
Beta	vulgaris	FC221	in process

Allotment of Fort Collins "FC" numbers (3-digit numbers)

"FC" numbers are "convenience" numbers for "seed releases" or purposes where a permanent line designation is needed — i.e. a number that does not change from generation to generation where little or no selection pressure is applied. Initially, an "FC" no. was written thus "FC 501" [now FC727], "FC 502 CMS" [now FC715CMS], etc. Sublines (from selfing) were designated thus, "FC 502/2" [now FC709-2], "FC502/3" [now FC502-3], etc. The same applies when the line is substantially changed by selection without selfing.

100's	Early releases
200's	Rhizoctonia, rhizomania resistant, combined with other resistances
300's	Leaf Spot Resistant (LSR), combined with rhizomania resistance
400's	Parental lines and special genetic stocks
Below 500	Originally LeRoy Powers -
500's	Leaf Spot Resistant (LSR), Type-O lines & male steriles [CMS]
600's	LSR-Curly Top Resistant (CTR), type-O lines & male steriles [CMS]
700's	Rhizoctonia Resistant
800's	LSR-CTR-Rhizoctonia resistant
900's	Pollinators, LSR-CTR type

SUMMARY OF LITERATURE

Rhizoctonia

Twenty-five years ago, Leach and Garber (1970) reviewed resistance to Rhizoctonia infection and concluded, "In general, while it has been possible to identify differences among cultivars or selections in susceptibility to Rhizoctonia infection, it is extremely rare that a high degree of resistance has been found or produced by selection or breeding within a susceptible host species." However, one of the most effective and environmentally safe ways to manage plant disease is with resistant germplasm (Sherf and MacNab, 1986). Soilborne pathogens like Rhizoctonia are often difficult to control chemically. Fumigation is expensive, providing only a temporary solution. The use of Quadris™¹ provides the first real chemical control for this disease.

¹ Mention of a trademark or manufacturer by the USDA does not imply its approval to the exclusion of other products or manufacturers.

However, timing of application is crucial (Stump et al., 2004). Additionally, spot spraying can be time consuming, and spraying a whole field because of a few patches of disease also can be expensive. The use of resistant germplasm, coupled with crop rotation and other cultural practices, can provide excellent management of diseases caused by *Rhizoctonia solani*.

In sugar beet (*Beta vulgaris* L.), *Rhizoctonia* root- or crown-rot is caused by *Rhizoctonia solani* (AG-2-2). Seedling damping-off in sugar beet is caused by *R. solani* of both AG-2-2 and AG-4. Root-rot is endemic in sugar beet growing areas across the United States. John Gaskill began breeding for resistance in the late 1950s and released his first resistant germplasm in 1966 (Gaskill, 1968). Current *Rhizoctonia* resistant germplasm has a level of resistance in which there is no yield loss under disease pressure in the field (Ruppel and Hecker, 1994). It was realized early that natural field epiphytotics did not produce the necessary consistent, uniform disease pressure for recurrent mass selection (Pierson and Gaskill, 1961). Artificially induced epiphytotics (Ruppel et al., 1979; Schneider et al., 1982) were developed to provide uniform, heavy disease pressure to be able to perform mass selection or recurrent field selection (Hecker and Ruppel, 1977).

The resistance to *R. solani* in sugar beet developed by John Gaskill is polygenic, involving at least two loci, two or three alleles, and modifying genes in some populations (Hecker and Ruppel, 1975). Broad-sense heritability has been estimated at about 0.65, and there are nonadditive components of the variance (Hecker and Ruppel, 1975). In a study by Hecker and Ruppel (1976) dominance effects were present in diploid, triploid, and tetraploid resistant hybrids. Relatively high heritability has aided in the development of increasing host plant resistance to *Rhizoctonia* root- and crown-rot, and we have released over 15 germplasm lines in the last 10 years. *Rhizoctonia* Resistance has been released in O-type maintainer, CMS female, and multigerm-pollinator germplasm and remains a very important means of reducing crop damage by this disease (Herr, 1996). Genetic resistance to *Rhizoctonia* root rot has been an ongoing development from this project at Fort Collins. Several resistant germplasms have been released in the last five year to use as parents of hybrid cultivars or to provide source populations from which *Rhizoctonia* resistant parents were selected or which were crossed to provide resistant parents (Panella, 1999; Panella, 2001; Panella and Hanson, 2004a, b; Panella and Lewellen, 2005).

Epidemiological and control studies have been reported regularly from this project (Ruppel et al., 1988). Pathogen survival in varied crop debris and soil and the interaction of pesticides with *Rhizoctonia* have been reported on the literature (Ruppel, 1985; Ruppel 1991; Ruppel and Hecker, 1982; Ruppel et al., 1982). In a 3-year study, positive significant or highly significant correlations between disease severity indices and percent decreases in yield and purity parameters indicated that there were no hidden losses to *Rhizoctonia* root rot in our resistant germplasms (Ruppel and Hecker, 1994).

Recently, researchers attempting to determine the anastomosis group (AG) of *Rhizoctonia solani* isolates have used several new biotechnological techniques (including RFLP, RAPD, and isozyme analyses), with some notable successes in distinguishing among, and even within some, of these groups. Recently there was a report of a definitive assay to distinguish those isolates in AG-2-2 or AG-4 that cause sugar beet root rot and damping-off, respectively, from nonpathogenic isolates obtained from soil (Lubeck and Poulsen, 2001).

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Cercospora:

Cercospora leaf spot (CLS) has been a continual problem in sugar beet growing areas of the United States where the summers can be hot and humid (Red River Valley, Michigan, Ohio, and, less often, Great Plains growing areas and California). It has been estimated that a severe epidemic can cause up to a 42% loss of gross sugar (Smith and Martin, 1978; Smith and Ruppel, 1973), or up to a 43% relative dollar loss (Shane and Teng, 1992).

Resistance to CLS has long been a goal of the USDA-ARS sugar beet research program at Fort Collins. The resistance to CLS could more accurately be described as a tolerance, rather than true resistance. Tolerance or "field resistance" means that, although some symptoms of the disease are present, the plant still is able to perform well (Fehr, 1987 p.307).

Much of the *Cercospora*-resistant germplasm in use today came out of Munerati's program in Italy, in which *B. vulgaris* spp. *maritima* was the source of resistance genes (Lewellen, 1992). In this genetic source, there are an estimated 4 or 5 genes responsible for CLS resistance (Smith and Gaskill, 1970) and broad-sense heritability estimates ranged from 12 to 71% (Bilgen et al., 1969).

Narrow-sense heritability estimates of about 24% compared well with realized heritability values, and 44 to 62% of the variation was due environment in this test (Smith and Ruppel, 1974). The large environmental variation has made it difficult to make progress in developing resistance through mass selection. Incorporation of high levels of leaf spot resistance into varieties with superior agronomic performance also is difficult (Smith and Campbell, 1996) and, therefore, commercial resistant varieties require some fungicide application to provide adequate levels of protection against *Cercospora* (Miller et al., 1994).

A major problem in the development of CLS-resistant sugar beet is the loss of vigor due to the continual inbreeding. Coons (1955) noted this and it has been a concern ever since (McFarlane, 1971). The use of hybrid varieties has ameliorated this problem to some extent, but seed production on the highly inbred O-type males and CMS females still is a problem. This is seen in germplasm from both the FC 500 and FC 600 series developed at Fort Collins (Panella, 1998; Panella and Frese, 2000). This creates an urgent need to continue to develop a broader genetic base in our CLS-resistant germplasm than we have today. Also as commercial hybrid parents become more inbred, the germplasm base from which these inbred parents are developed must have the diversity necessary to provide for maximum gain through heterosis. In addition to broadening the genetic base of the commercial sugar beet germplasm, novel genes for resistance to CLS might lead to transgression of the currently available tolerance to CLS. Simply defined, transgression is when a population contains individuals with a phenotype that is beyond the phenotype found in the parents of the population (de Vicente & Tanksley, 1993).

The USDA-ARS National Plant Germplasm System *Beta* collection has over 2,000 Plant Introduction (PI) accessions. The germplasm used most often in sugar beet breeding is from *Beta vulgaris* spp. *vulgaris*, which includes all of the biennial sugar beet types, or from *Beta vulgaris* spp. *maritima*, which contains the closely related wild sea beet and has both annual and biennial types. Germplasm with a biennial flowering habit is easier both to introgress and screen. Annual *Beta vulgaris* spp. *maritima* has, nonetheless, been used as a source of resistant germplasm. Much of the CLS-resistant germplasm in use today, which came out of Munerati's program in Italy, had annual *B. vulgaris* spp. *maritima* as the source of resistance genes (Lewellen, 1992). There have been very few new efforts to locate and incorporate other sources of resistance to *Cercospora* into this narrow germplasm base. Munerati's success, and the research of others, has shown that it can be done if we have the persistence to do it (Bilgen et al., 1969; Doney, 1993; Lewellen, 1995)

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BSDF PROJECT 445 PROGRESS

2006 Research on *Rhizoctonia* Root Rot of Sugar Beet

Field screening

Annually, for over thirty years, the sugar beet program in Fort Collins has included the production of an artificial epiphytotic through inoculation with *Rhizoctonia solani* to evaluate and select for resistance to *Rhizoctonia* root rot. We have been pleased to participate and lead this cooperative research project between the ARS and the BSDF. In 2006, the project involved field studies conducted at the Crops Research Lab-Fort Collins Research Farm (CRL-FCRF) near Wellington, CO.

Randomized, complete-block designs with five replicates were used to evaluate ARS breeding germplasm and Plant Introduction accessions. *Rhizoctonia*-resistant line FC703, highly resistant FC705-1, and susceptible FC901/C817 were included as internal controls. The field was treated with Telone II April 11, 2006 and then manure worked in. One-row plots, planted May 24, 2006 were 14 feet long with 22 inches between rows and 8-10 inches within-row spacing. The field was sprayed once with Betamix Progress, Upbeet, and Stinger (July 20) to control weeds. The field was thinned by hand and irrigated as necessary.

Inoculation (July 13, 2006) was with dry, ground, barley-grain inoculum of *Rhizoctonia solani* AG2-2 isolate R-9, and, immediately after inoculation, a cultivation was performed to throw soil into the beet crowns. Beets were harvested Sept. 19 through 21, 2006. Each root was rated for rot on a scale of 0 to 7 (dead) as previously described. ANOVAs were performed on disease indices (DIs), percent healthy roots (classes 0 and 1 combined), and percentage of roots in classes 0 thru 3. Percentages were transformed to arcsin-square roots to normalize the data for analyses. LSDs are provided for comparing entries with those of our internal checks.

The high daytime temperatures in the summer of 2005, combined with a moderate inoculum load, contributed to a mild root rot epidemic. Due to water restrictions, sprinkler irrigation could not be applied immediately after applying inoculum which reduced severity. In addition, timing of irrigation could not be regulated sufficiently to provide moderate water stress at desired intervals. Mild disease developed by mid-September. Mean DIs across all tests for highly resistant FC705-1, resistant FC703, and susceptible FC901/C817 controls were 1.7, 1.8, and 3.5 respectively. Mean DIs for these controls in 2005 were 2.7, 3.1 and 4.9 respectively. Percentages of healthy roots were 51.5, 43.7, and 21.3% for these controls. Percentages of roots in disease classes zero thru three were 97.4, 91.5, and 50.9% respectively. The highest and lowest DIs for the evaluated lines were 5.8 and 1.0, respectively.

2006 *Rhizoctonia*-Resistant Populations under Development with R. T. Lewellen

This has been an ongoing and productive project, and has been the only research project with the goal of discovering, developing, and releasing *Rhizoctonia*-resistant germplasm to industry breeders, our major external customers. With the release of FC723 and FC723CMS last fall, the germplasm remaining from the program of Dr. Richard Hecker has been evaluated, recombined, improved and released, or shelved. Although relatively resistant germplasms have been developed, we have worked to continue to combine this resistance with resistance to rhizomania (*Rz1*), uncover new sources of resistance, and are working to introgress this resistance into germplasm with higher sucrose yield potential (Table below).

Accession	Salinas No.	Description	
2007A049	06-FC103 6	<p>04-FC1028 = RZM-% FC20021028 FC1028 = FC709-2 x 9933</p> <p>04-FC1037 = RZM-% FC20021037 FC1037 = (FC-LSR x EL-LSR) x CR11</p> <p>04-FC1038 = RZM-% FC20021038 FC1038 = (FC-LSR x EL-LSR) x CR10</p>	<p>{RZM-CR-% 04-FC1028} {RZM-CR-% 04-FC1037} {RZM-CR-% 04-FC1038}</p>
2007A050	06-FC102 0	<p>Mother roots selected from test 5205 under mod. Severe RZM, mild CLS. Selected for %S. Recombine sources of resistance to CLS with rzm. 06-FC1036 will be MM, Sf, A:aa, Rzi, CR, %S</p> <p>05-FC1018=RZM-CR-% 20031018 (A,aa)FC20031018=F₃ (C931aa x FC709-2)</p> <p>05-FC1019=RZM-CR-% 20031019 (A,aa) FC20031019=F₃ (FC712 x C931)</p> <p>05-FC1022=RZM-CR-% 20031022 (A,aa) FC20031022=F₃ [931aa x (FC907 x FC709-2)]</p> <p>MM, Sf, Aa, Rzi, Rhizoc. Population</p>	<p>{05-FC1018} {05-FC1019} {05-FC1022} (A,aa)</p>
2007A051	06-FC124- 425	<p>Inc. 04-FC124-425mm (A,aa)</p> <p>04-FC124-425 = RZM 03-FC124mmø; 03-FC124 = C833-5mmaa x FC123</p> <p>Increased fr 1 S1 progeny selected from progeny test at Salinas in 2005 from seed produced in 2004.</p> <p>C83305 = mm, T-O, Rzi, NB, MCT; FC123 = mm line with fair CR and high %sugar</p> <p>*Seed saved at Salinas for PI, Pullman</p>	
2007A052	06-FC124- 425H5	<p>C833-5CMS x Inc. 04-FC124-425mm (A,aa)</p> <p>CMS of above</p> <p>*Seed saved at Salinas for PI, Pullman</p>	
2007A053	06-FC101 5-403	<p>Inc. 04-FC1015-403mm (A,aa)</p> <p>04-FC1015-403 = RZM 03-FC1015mmø; 03-FC1015 = C833-5mmaa x FC1014; FC1014 = mm line (CMS)with fair CR, high %sugar & sugar yield</p> <p>*Seed saved at Salinas for PI, Pullman</p>	

2007A054	04-FC101 5-403H5	04-FC1015-403H5 C833-5CMS x Inc. 04FC1015-403mm (A,aa) CMS of above *Seed saved at Salinas for PI, Pullman
2007A055	06-FC101 5-420	Inc. 04-FC1015-420mm (A,aa) 04-FC1015-420 = RZM 03-FC1015mmø; 03-FC1015 = C833-5mmaa x FC1014; FC1014 = mm line with fair-good CR, mod. %sugar, high SY & RJAP *Seed saved at Salinas for PI, Pullman
2007A056	06-FC101 5-420H5	06-FC1015-420H5 C833-5CMS x Inc. 04FC1015-420mm (A,aa) CMS of above *Seed saved at Salinas for PI, Pullman
2007A057	06-FC101 5-427	Inc. 04-FC1015-427mm (A,aa) 04-FC1015-427 = RZM 03-FC1015mmø; 03-FC1015 = C833-5mmaa x FC1014; FC1014 = mm line with good CR, fair %sugar, high SY *Seed saved at Salinas for PI, Pullman
2007A058	06-FC101 5-427H5	06-FC1015-427H5 C833-5CMS x Inc. 04-FC1015-427mm (A,aa) CMS of above *Seed saved at Salinas for PI, Pullman
2007A059	06-FC123- 31	Inc. 03-FC123-31 03-FC123-31 = 01-FC123-31; 01 FC123-31 = 06-FC123-31M mm, A:aa, Sf, CR, Rz1 line that may be released in 2006. *Seed saved at Salinas for PI, Pullman
2007A060	06-FC123- 31HO	03-FC123-31HO x Inc. 03-FC123-31 03-FC123-31H5 - C833-5HO x 01-FC123-31: CMS of above *Seed saved at Salinas for PI, Pullman
2007A061	06-FC101 4-22	Inc. 03-FC1014-22 03-FC1014-22 = Inc. 01-FC1014-22; 01-FC1014 = mm, A:aa, Sf, Rhizoc, Rz1 line that may be released in 2006. *Seed saved at Salinas for PI, Pullman
2007A062	06-FC101 4-22HO	03-FC1014-22H5 x Inc. 03-FC1014-22 03-FC1014-22H5 = C833-5HO x 01-FC1014-22 CMS of above *Seed saved at Salinas for PI, Pullman

Some of the populations under development are:

Rhizoctonia root rot resistance multigerm base population developed by a cross between FC709-2 and a Salinas germplasm, 2915, which has been tested in Salinas & Fort Collins as FC1030). – includes populations 03-FC1030-15 and 03-FC1030-16 being reselected in Fort Collins for Rhizoctonia resistance and Salinas for rhizomania resistance. Sib-lines with increase sucrose are also being developed.

- a) 2915 (sp) RZM 1915-#m 1913-# aa x A (Salinas); Seed harvested from aa (ms) plants open-pollinated by A- (fertile) plants. This population will segregate for A-:aa, Rz-:rzzr, s^ss^s:s^f-, (>1/2 s^f), R-:rr, It will be multigerm, have moderate to good tolerance to virus yellows, curly top, bolting, Erwinia; variable for reaction to powdery mildew, production traits. Individual plants will be either Aa or aa. Background of population is mostly from OP, MM lines such as C46, C37.

20021028; FC709-2 (Fort Collins release) x 9933 (Salinas germplasm) [(2000A011 x 19921024)rr blk F₂]; Should segregate for □Rhizoctonia and cercospora leafspot resistance (FC709-2), multigermity, root aphid resistance (FC709-2 and 9933), tolerance to curly top, Virus Yellows, powdery mildew, Erwinia, rhizomania (9933) S^f-, A-, in a fertile cytoplasm – tested in Salinas as 04-FC1028.

Sib-lines of FC201 – 01-FC1014-22 (A,aa); 01-FC1014A; 01-FC1014H5 – C833-5 CMS x 01-FC1014A; 03-FC1015 – Rzm (C833-5 mmaa x FC1014) mmaa x A; 03-FC1015HO, CMS equivalent of the previous – (C833-5 CMS x 01-FC1014A) x Rzm (C833-5 mmaa x FC1014) mmaa x A.

20021022 – [2000A010aa [9931] x 20001009 [sel(FC907 x FC709-2)F3]blk increase-blk – was sent to Salinas and reselected in Fort Collins.

- b) 9931 = Advanced Base breeding population at Salinas with resistance/tolerance to Rz, CT, VY, Pm, Erwinia, bolting – segregates for Aa:aa, Sf, Multigerm.

Progress in 2006

Sib-lines from the population (20001004, 19991030, 10001031, and 19991032), 051030-15 and 05-1030-16 – seed has been distributed and will be released as FC220 and FC221. They have a high frequency of the *Rz1* allele conferring resistance to rhizomania caused by *Beet necrotic yellow vein virus*, and excellent resistance to root-rotting strains (AG-2-2) of *Rhizoctonia solani* Kühn.

Seed received from R.T. Lewellen for testing and evaluation includes Accession seed numbers from 2007A049 to 2007A062 (Table above). The results of 2006 screening are below.

Experiment 5R, 2006. Rhizoctonia Resistance Evaluation of USDA-ARS, Salinas contributed lines.						
Entry	Description	DI¹	% Hlthy²	% 0 - 3³	Z%⁴ Hlthy	Z% 0 - 3⁴
	LSD⁵	1.18			19.46	20.14
1631	Susceptible Check⁶	4.2	10	33	11.7	31.9
1632	Highly Resistant Check⁷	1.8	32	98	30.8	85.9
1633	Resistant Check⁸	2.2	32	81	32.8	72.4
	Experiment Mean	3.5	17	54	19.5	48.3
1611	Y595	4.5	6	36	8.8	36.4
1612	P531CT	3.9	8	45	7.6	41.2
1613	R521	4.1	12	34	15.1	35.5
1614	R522	4.7	0	40	0.0	36.0
1615	CR411	4.3	9	38	13.4	35.2
1616	5944	4.6	3	31	4.8	30.4
1617	5933	4.8	6	26	9.2	27.4
1618	05-FC1036	3.2	17	55	19.2	48.1
1619	05-FC1028	3.9	16	43	18.4	40.4
1620	05-FC1037	3.0	27	66	27.3	57.7
1621	05-FC1038	3.3	15	58	20.5	50.2
1622	05-FC1022	4.2	9	35	13.0	33.2
1623	05-FC1018	2.5	35	74	29.7	63.2
1624	05-FC1019	3.0	16	64	20.1	56.4
1625	05-FC1030-15	1.8	50	95	44.7	79.8
1626	05-FC1030-16	2.4	33	78	34.1	64.8
1627	05-FC1030-15H50	3.7	10	52	11.8	46.5
1628	05-FC1030-16H50	3.3	9	60	15.5	51.2
1629	05-FC1036H50	3.9	12	39	17.7	38.7
1630	05-FC1022H50	4.0	13	40	18.8	36.4
¹ Disease Index is based on a scale of 0 (=healthy) to 7 (= plant dead). ² Percent of healthy roots (disease classes 0 and 1 combined). ³ Percent of diseased roots likely to be taken for processing (disease classes 0 through 3 combined). ⁴ Percentages were transformed to arcsin-square roots to normalize the data for analyzes. ⁵ P=0.05 ⁶ FC901/C817 ⁷ FC705/1 ⁸ FC703						

Experiment 11R, 2006. Rhizoctonia Resistance Evaluation of USDA-ARS, Fort Collins lines.						
Description		DI¹	% Hlthy²	% 0 - 3³	Z%⁴ Hlthy	Z% 0 - 3⁴
LSD⁵		0.98			17.8	19.0
CV		32.0			44.2	21.9
	Susceptible Check⁶	3.4	20	57	20	50
	Highly Resistant Check⁷	1.9	31	98	33	86
	Resistant Check⁸	1.8	42	96	40	82
	Experiment Mean	2.5	32	81	32	69
19921019	FC729 – FC712/A4, 3 cycles Rhizoc, MM	2.0	27	98	25	86
19951016HO	FC723 – EL44/FC708 mm	2.2	29	89	32	76
19951016HO1	FC723CMS – EL44/FC708 CMS	2.1	36	89	38	73
19961010HO1	FC722CMS – C718/FC708CMS	2.0	35	90	38	76
19961010HO	FC722 – C718/FC708	1.6	51	97	46	86

Experiment 11R, 2006. Rhizoctonia Resistance Evaluation of USDA-ARS, Fort Collins lines.						
Description		DI ¹	% Hlthy ²	% 0 - 3 ³	Z% ⁴ Hlthy	Z% 0 - 3 ⁴
		LSD ⁵	0.98		17.8	19.0
		CV	32.0		44.2	21.9
Susceptible Check ⁶		3.4	20	57	20	50
Highly Resistant Check ⁷		1.9	31	98	33	86
Resistant Check ⁸		1.8	42	96	40	82
Experiment Mean		2.5	32	81	32	69
19961014	FC724	1.7	43	100	41	90
20001017	FC720 -- C718/(C718/FC708)	2.2	28	92	29	80
20041007	FC709-2	1.6	57	94	52	84
19921024	FC709-2	1.3	72	100	61	90
20011007	F3 (907 x 709-2) for RhzcR - hs 10A-1775	2.1	45	91	41	76
20041010HO	FC712/MonoHy A4	1.9	35	98	38	87
20041010HO1	FC712/MonoHy A4 - CMS equivalent	2.1	33	91	34	76
2004A029	04-FC1028; (9933rr x FC709-2)F3	2.9	20	75	23	63
2005A009	05-FC1030-15H5	2.7	29	71	29	60
2005A008	05-FC1030-15(Sp)	2.3	29	86	31	73
2005A010	05-FC1030-15H5	2.8	35	69	35	59
2005A011	05-FC1030-16(Sp)	2.6	32	79	31	68
2005A012	05-FC1030-16H5	3.5	13	60	18	51
2005A013	05-FC1030-16H50	3.7	18	48	21	44
2005A014	05-FC1030-15(Iso) FC220	2.2	42	87	40	74
2005A015	05-FC1030-16(Iso) FC221	2.5	34	77	32	67
2005A022	05-FC1022-C391aa x (FC907 x FC709-2)	2.5	24	75	26	61
2005A023	05-FC1022H50 - CMS equivalent	4.0	6	49	9	45
2005A024	05-FC1018 [(C931XFC709-2)F3	2.5	30	77	32	67
2005A025	05-FC1018H50 - CMS equivalent	2.2	35	86	33	73
2005A026	05-FC1019 (FC712 x 9931)F3	2.8	29	73	32	60
2005A027	05-FC1019H50 - CMS equivalent	3.7	20	54	23	47
20051021	FC201	2.4	27	83	28	71
20051007HOPF	03-FC1014-22 - 201 sib line	2.3	31	89	27	75
20051027	9931 x [sel(FC907 x FC709-2)F3]	3.2	27	62	28	52
20051030	FC220-1	2.7	40	67	36	55
20051031	FC221-1	2.6	22	80	25	64

¹Disease Index is based on a scale of 0 (=healthy) to 7 (= plant dead).
²Percent of healthy roots (disease classes 0 and 1 combined).
³Percent of diseased roots likely to be taken for processing (disease classes 0 through 3 combined).
⁴Percentages were transformed to arcsin-square roots to normalize the data for analyzes.
⁵P=0.05
⁶FC901/C817
⁷FC705/1
⁸FC703

New 2006 Rhizoctonia-Resistant Populations under Development

A number of accessions from the NPGS *Beta* collection that had shown Rhizoctonia-resistance in the Sugarbeet CGC screening program have been identified. Those PIs with seed available were re-screened in 2003. Special attention was given to those accessions screened in 1987 and 1992 because the tests in those years appear to have been unreliable. These and other wild accessions were screened (from the European GENRES Project). Parents are growing in the greenhouse and crosses will be made this spring. The non-sugarbeet accessions will

be crossed using a female (male sterile – *aa*) parent with high sucrose yield potential and with Rhizomania resistance. The goal is to develop Rhizoctonia-resistant populations from potentially different sources of resistance, from which breeders will be able to select resistant hybrid parents or germplasm to cross into programs developing Rhizoctonia-resistant hybrid parents (See tables below). Screening PI accessions is an ongoing project and the results of the 2006 test are in the table below.

Initial rhizoctonia-resistant males used in crosses to develop rhizoctonia resistant populations.		
Males		
Acc NR	Donor NR	type
2007A012	BGRC 28938	<i>B. v. ssp. maritima</i>
2007A015	BGRC 32375	<i>B. v. ssp. maritima</i>
2007A016	BGRC 32376	<i>B. v. ssp. maritima</i>
2007A048	PI 504173	<i>B. v. ssp. maritima</i>
2007A029	BGRC 54748	<i>B. v. ssp. vulgaris</i> - fodder beet
2007A041	BGRC 62124	<i>B. v. ssp. vulgaris</i> - leaf beet
2007A045	BGRC 62708	<i>B. v. ssp. vulgaris</i> - fodder beet
Females		
Acc NR	Donor NR	type
2003A044	Z325	<i>aa</i> X <i>Aa</i>
20011021H1	Sucrose mm in Dogget Equilibrium	<i>aa</i> X <i>Aa</i>
1997A050	FC607CMS	CMS

Experiment 4R, 2006. Rhizoctonia Resistance Evaluation of USDA-ARS, Fargo, ND contributed lines.

Entry	Description	DI ¹	% Hlthy ²	% 0 - 3 ³	Z% ⁴ Hlthy	Z% 0 - 3 ⁴
LSD ⁵		1.23			17.77	18.81
1605	Susceptible Check ⁶	3.7	33	46	34.7	42.7
1606	Highly Resistant Check ⁷	1.1	94	99	80.7	86.9
1607	Resistant Check ⁸	1.0	96	100	83.0	90.0
Experiment Mean		2.9	54	66	48.2	57.5
1601	04N0063	3.5	45	55	41.3	48.0
1602	04N0064	2.9	58	66	52.4	57.2
1603	04N0068	3.8	31	56	33.0	51.6
1604	04N0072	2.4	65	73	57.0	61.5

¹Disease Index is based on a scale of 0 (=healthy) to 7 (= plant dead).

²Percent of healthy roots (disease classes 0 and 1 combined).

³Percent of diseased roots likely to be taken for processing (disease classes 0 through 3 combined).

⁴Percentages were transformed to arcsin-square roots to normalize the data for analyzes.

⁵P=0.05

⁶FC901/C817

⁷FC705/1

⁸FC703

Note, the given Mean and LSD values are for the entire plot, which included 20 other entries.

Experiment 2R, 2006. Rhizoctonia Resistance Evaluation of USDA-ARS Plant Introductions, Pullman WA.

	Description	LSD ⁵	DI ¹ 1.6	% Hlthy ²	% 0 - 3 ³	Z% ⁴ Hlthy 16.8	Z% 0 - 3 ⁴ 33.3
	Susceptible Check⁶		3.2	17.4	54.5	22.1	47.6
	Highly Resistant Check⁷		1.6	32.0	98.0	30.8	85.9
	Resistant Check⁸		1.7	40.3	98.5	39.1	86.8
	Experiment Mean		4.1	8.9	49.8	9.9	45.2
PI518355	IDBBNR 5849, UK		4.0	0.0	60.5	0.0	51.7
PI540577	WB 831, France		4.1	4.0	41.4	5.3	39.8
PI546416	IDBBNR 5610, Greece		5.2	0.0	31.7	0.0	31.1
PI562585	IDBBNR 9796, Egypt		4.8	6.7	43.3	7.1	38.0
PI504204	Wildbeet, Italy		4.5	17.4	32.1	19.3	31.0
PI518377	IDBBNR 5871, Ireland		2.8	12.4	68.4	13.5	62.0
PI518426	IDBBNR 5920, UK		3.8	6.0	51.8	11.1	46.1
PI540563	WB814, France		3.7	17.0	49.3	18.9	46.4
PI540565	WB816, France		4.4	6.7	42.4	7.1	40.5
PI540567	WB818, France		4.1	5.0	47.2	8.3	43.3
PI540573	WB827, France		5.6	5.7	20.9	6.5	21.0
PI540574	WB828, France		3.0	20.0	71.7	18.0	67.1
PI540633	WB887, UK		2.3	15.0	90.0	15.9	80.2
PI540666	WB920, France		3.7	8.7	57.4	13.4	49.5
PI546379	IDBBNR 5657, Spain		3.9	2.2	60.0	3.9	54.0
PI546387	IDBBNR 5631, USA		3.8	5.7	70.5	6.5	60.5
PI546388	IDBBNR 5656, USA		3.3	10.0	70.0	11.9	59.8
PI546389	IDBBNR 5632, USA		4.2	0.0	44.4	0.0	41.7
PI546393	IDBBNR 5593, USA		4.5	2.5	43.8	4.1	38.2
PI546426	IDBBNR 5642, Italy		4.1	3.1	46.7	6.5	40.8
PI546437	IDBBNR 5650, Greece		6.3	0.0	12.5	0.0	14.8
PI546509	IDBBNR 9676, Greece		5.2	6.7	26.2	7.1	24.7
PI546517	IDBBNR 9684, Greece		3.6	7.3	64.6	7.4	56.9
PI546519	IDBBNR 9686, Greece		3.6	0.0	63.3	0.0	56.0
PI546520	IDBBNR 9687, Greece		5.8	0.0	20.0	0.0	18.0
PI546528	IDBBNR 9695, Italy		5.2	6.7	35.0	7.1	33.0
PI546529	IDBBNR 9696, Italy		4.2	6.9	45.3	9.8	42.1
PI562587	IDBBNR 9738, Egypt		4.7	0.0	26.5	0.0	30.2
PI562588	IDBBNR 9739, Egypt		5.7	2.9	7.9	4.4	10.4
PI562589	IDBBNR 9740, Egypt		4.0	4.0	46.8	5.3	40.3

¹Disease Index is based on a scale of 0 (=healthy) to 7 (= plant dead).

²Percent of healthy roots (disease classes 0 and 1 combined).

³Percent of diseased roots likely to be taken for processing (disease classes 0 through 3 combined).

⁴Percentages were transformed to arcsin-square roots to normalize the data for analyzes.

⁵P=0.05

⁶FC901/C817

⁷FC705/1

⁸FC703

2006 Research on Cercospora Leaf Spot of Sugar Beet

Field screening

The breeding program in Fort Collins had created an annual artificial epiphytotic through inoculation with *Cercospora beticola* for over forty years. This epiphytotic has been used to evaluate and select for resistance to leaf spot caused by *C. beticola*. Because of the droughty situation in the West, and the difficulty in getting good epiphytotics in our semi-arid climate, this nursery was relocated to Michigan last summer (2006) and managed by Mitch McGrath, USDA-ARS, East Lansing, Michigan. Linda Hanson (Plant pathologist, USDA-ARS, currently in Fort Collins, Colorado) will join the ARS research program in East Lansing this summer, and will work with Mitch to manage the *Cercospora* screening nursery.

In 2006, we tested germplasm at East Lansing, where disease pressure was strong and early. Because the earliness caught the researchers off guard, evaluations were begun after the peak of the epidemic (see table below) and interpretation of the results is a bit difficult. We also had germplasm screened by Betaseed at their Rosemount nursery (see table below). We will continue to work with Mitch McGrath in the development of *Cercospora* Leafspot resistant sugarbeet germplasm.

Germplasm under Development

FC301 population and sib lines

- 1) *Cercospora* leaf spot and curly top resistant monogerm base population from a polycross of FC607 and FC604 with two Salinas germplasms 2859 and 2890 (**Tested in Salinas as FC123**).
 - a) 2890 (sp) = 0790 mm aa x 1890 (Salinas); is seed from aa plants open pollinated by A- plants. 0790 = population-790 cycle 5 synthetic by S₁ progeny, aa, mm, O-type, good combining ability, adapted to California, S^f. 1890 = BC population to population 790 to get Rz equivalent, remains variable for M-:mm, Rz-:rzz, etc.
 - b) 2859 m (sp) = 1859, 1859R aa x A- (Salinas); Released in 1992 as C859. S^f, similar to 2890, but should have higher curly top resistance. Segregates and variable for M-:mm, Rz-:rzz, A-:aa, predominant background is lines like C563.
- 2) *Cercospora* leaf spot and curly top resistant multigerm base population from a polycross of FC902 with two Salinas germplasms 278 and 4918.
 - a) 278 (Iso 83) = RZM R078; R278 is Rz (segregates Rz-:rzz) version of C46. It should be S^sS^s, MM.
 - b) 4918 (sp) = RZM 3918aa X A-, 142 aa plants; This is an increase of released material C918. It should be Multigerm, over 75% S^f and segregating for A-, R-, Rz-, VY, CT, Erw, & PM.
- 3) 20021037; (Best FC LSR x Best EL LSR) x CR011 (Salinas LSR/RhzmR) [(20011001 x 2001A031)blk F₂] – tested in Salinas as 04-FC1037
 - a) Salinas CR9110 = more broad based rhizomania and leaf spot resistant population, will segregate A- and S^f-
 - b) 20011001 = (Best Fort Collins leaf spot resistant x Best East Lansing leaf spot resistant), population cross and bulk made using hypocotyl color
- 4) 20021038; (Best FC LSR and EL LSR) x CR910 – [(20011001 x 2001A032)blk F₂] – tested in Salinas as 04-FC1038.
 - a) Salinas CR910 = fairly inbred rhizomania and leaf spot resistant population, will segregate A- and S^f-

- b) 20011001 = (Best Fort Collins leaf spot resistant x Best East Lansing leaf spot resistant), population cross and bulk made using hypocotyl color.
- 5) Seed from FC709-2 x FC907 was sent to Larry Campbell at Fargo to cross to Sugar beet root maggot resistant germplasm to develop a population that will produce pollinators with resistance to Rhizoctonia, Cercospora, and Root maggot.

Progress in 2006

A number of leafspot resistant half-sib families were lost in 2006 at Fort Collins when droughty conditions delayed the availability of irrigation water after the first rainfall. We had good germination but hot dry conditions with no water killed the seedlings. A number of these were planted in the Fort Collins mother root nursery and half-sib families are being re-synthesized this winter and spring for testing in 2007.

Seed from (FC709-2 x FC907) F_2 has been sent to Larry Campbell at Fargo to cross to Sugar beet root maggot resistant germplasm and be selected for Cercospora resistance. Sib lines were selected last year for Cercospora resistance and recombined. The seed was sent to Fargo for root maggot screening. The resulting population will provide pollinators with resistance to Cercospora leaf spot and the sugar beet root maggot.

2006 Cercospora evaluation - East Lansing, MI

The evaluation date with the highest (most susceptible) rating is boxed for each germplasm in this test. Look at the experimental mean for each evaluation (Grand Mean), it is clear that many of the entries were defoliated at the first evaluation and looked progressively better as they regained lost leaves (at the expense of store sucrose). Nonetheless, a few germplasm had their worst scores in the 3rd or 4th evaluation and did quite well.

2006 Cercospora evaluation - East Lansing, MI

		Grand Mean	6.19	6.07	5.77	4.86
		LSD (0.05)	3.07	2.15	1.86	1.54
		CV (%)	39.69	31.66	30.11	23.82
		F value	2.97***	4.15***	4.71***	2.31***
Source	Pedigree	8/9/2006 Mean	8/15/2006 Mean	8/22/2006 Mean	9/5/2006 Mean	
EL-A012194	EL50	1.7	2.0	1.7	3.0	
C355 - resistant check		2.7	2.7	2.0	3.0	
1997A050	FC607	3.7	4.0	3.0	3.0	
EL-A013702	EL55 / TBA	2.0	3.0	3.3	3.0	
19971017	FC710(4X)	4.0	4.3	4.3	3.0	
821051H2	LSR	3.3	4.0	3.7	3.3	
20001017	FC720	3.0	4.3	5.0	3.5	
20011002bbPF	WB850 x SucroseMM	8.3	7.3	6.0	3.7	
EL-A012858	EL0204	9.0	7.3	6.7	3.7	

2006 Cercospora evaluation - East Lansing, MI

		Grand Mean	6.19	6.07	5.77	4.86
		LSD (0.05)	3.07	2.15	1.86	1.54
		CV (%)	39.69	31.66	30.11	23.82
		F value	2.97***	4.15***	4.71***	2.31***
		8/9/2006	8/15/2006	8/22/2006	9/5/2006	
Source	Pedigree	Mean	Mean	Mean	Mean	
20041010HO1	FC712/MonoHyA4	5.0	6.0	5.0	4.0	
	05-FC1018	4.0	5.3	4.0	4.3	
	04FC1038	6.5	6.7	6.3	4.3	
19931007	FC720	5.7	7.7	7.0	4.3	
20051021	FC201	8.7	6.7	7.3	4.3	
19771082	LSR CTR population	7.0	7.0	5.3	4.5	
19961010HO1	FC722 CMS – C718/FC708 CMS	5.3	5.0	6.0	4.5	
	LSR	3.7	3.3	3.3	4.7	
EL-A019294	Mix: O-Type	7.7	4.7	5.0	4.7	
19831085HO	FC708	2.7	4.0	5.3	4.7	
	05-FC1036H50	6.3	6.3	5.7	4.7	
20051022	FC301	4.7	4.7	5.7	4.7	
19921025	FC728	6.0	5.7	6.0	4.7	
19961010HO	FC722 – C718/FC708	3.7	4.0	6.0	4.7	
20011045PF	(SucroseMM x PI540599)F2	7.7	6.7	6.3	4.7	
EL-A012172	SR94	7.3	6.7	6.3	4.7	
20041010HO	FC712/MonoHyA4	6.7	7.0	6.7	4.7	
20021018HO1	FC712/MonoHy A4 CMS	8.0	7.0	7.3	4.7	
	HM-E17	4.3	4.3	4.7	5.0	
19741026H	maritima backcross	4.7	4.7	4.7	5.0	
	05-FC1030-15(sp)	6.0	6.0	5.7	5.0	
19921019	FC729 – FC712/A4, 3 cycles Rhizoc, MM	4.7	5.3	5.7	5.0	
20001007	LSR w/ Fargo	4.3	5.0	5.7	5.0	
20031025	FC720 New Release 2005	7.0	7.0	6.0	5.0	
20041012	20021022 – inc. 03=FC123MM, ½ sib FC301	7.0	7.0	6.0	5.0	
20051007HOPF	half sib selection within FC201 - sel in 6R	5.7	5.0	6.0	5.0	
	04-FC1037	6.3	6.7	6.7	5.0	
19961014	FC724	5.3	5.7	6.7	5.0	
19951016HO1	FC723 CMS – EL44/FC708 CMS	8.0	8.0	7.0	5.0	
	04-FC1028	7.7	8.0	7.3	5.0	
	05-FC1022	7.3	7.3	7.3	5.0	
	05-FC1019	8.0	7.7	7.3	5.0	
19921021	FC703-5	5.3	4.7	4.7	5.3	

2006 Cercospora evaluation - East Lansing, MI

		Grand Mean	6.19	6.07	5.77	4.86
		LSD (0.05)	3.07	2.15	1.86	1.54
		CV (%)	39.69	31.66	30.11	23.82
		F value	2.97***	4.15***	4.71***	2.31***
Source	Pedigree	8/9/2006 Mean	8/15/2006 Mean	8/22/2006 Mean	9/5/2006 Mean	
19981025	FC717	5.0	6.0	5.7	5.3	
EL-A015032	USH20	7.3	7.3	6.3	5.3	
	05-FC1030-16(sp)	6.0	7.0	6.7	5.3	
20021018HO	FC712/Mono-Hy A4	6.0	6.0	6.7	5.3	
EL-A015028	C869	9.3	8.3	7.3	5.3	
19941027	LSS = synthetic check	9.7	8.3	7.7	5.3	
19911026HO	FC715	3.0	3.7	5.3	5.5	
19951017	FC727	7.3	7.0	6.3	5.7	
EL-A012189	SR96	8.3	7.7	6.7	5.7	
	051030-16H50	8.3	7.7	7.3	5.7	
19931012	FC901	7.3	7.7	7.3	5.7	
	05-FC1030-15H50	9.0	8.3	7.7	5.7	
	05-FC1023H50	8.7	7.3	7.7	5.7	
19911043HO1	FC403CMS	8.3	8.3	7.7	5.7	
19951016HO	FC723 – EL44/FC708 mm	8.0	7.3	8.0	5.7	
19921022	FC702-7	4.7	6.0	6.0	6.0	
20011007	F3 LSR MM x RhzcR/LSR sel RhzcR	5.7	5.3	6.3	6.0	
	05-FC1023M(Iso)	8.0	8.0	6.7	6.0	
	05-FC1036H50	5.7	6.0	7.0	6.0	
19821052	FC709-2 (20001016H)	8.3	7.0	7.7	6.0	
20051020	FC710(4X) (20001022)	5.7	5.0	5.7	6.3	
19911043HO	FC403	9.0	7.7	8.0	6.3	
	BETA 4430R	10.0	9.7	8.0	7.0	
19941027	LSS = synthetic check	9.7	8.7	8.0	7.0	

Other Evaluations

Germplasm also was screened by Betaseed in Rosemount, MN and in the BSDF curly top nursery in Kimberly, ID (below).

Betaseed Leaf Spot Disease Nursery Rosemount, MN 2006					
	CV	21.1	15.1	10.2	10.4
	LSD	0.65	0.74	0.87	1.02
Source	ID	Jul 28	Aug 4	Aug 11	Aug 16

	tolerant	1.3	2.3	3.8	4.5
821051H2	LS Resistant check	1.8	2.5	4.8	5.5
	mod susceptible 2	2.8	5.3	8.3	8.0
19941027	LS Susceptible check	3.0	5.0	8.0	8.3
	mod susceptible	2.8	4.8	7.5	8.5
	susceptible	2.8	5.8	8.8	9.0
1997A050	FC607	1.8	2.8	4.3	5.5
19911026HO	FC715	1.8	2.5	5.0	5.8
WC040022	EL53	2.0	3.0	5.0	6.0
20011002bbPF	WB850 x SucroseMM	2.3	3.0	5.5	6.3
19831085HO	FC708	2.0	2.3	5.0	6.3
20001017	FC720	2.3	3.3	5.5	6.5
20001007	LSR w/ Fargo	2.0	3.3	5.3	6.8
19921022	FC702-7	2.3	3.0	5.8	6.8
20051020	FC709-2	1.8	3.0	4.8	6.8
19951017	FC727	2.3	3.5	6.0	6.8
2005A005	FC709-2, 9933,LSR,CR10-11	2.3	3.3	6.0	7.0
19921021	FC703-5	2.0	2.8	5.8	7.0
19981025	FC717	2.0	3.8	6.8	7.0
20011045PF	(SucroseMM x PI540599)F2	2.0	3.5	6.5	7.3
20051022	FC301	2.3	3.5	6.0	7.3
20011007	F3 hs(907 x 709-2)	2.0	3.5	6.8	7.5
19921025	FC728	2.8	3.3	6.0	7.5
20051021	FC201	2.5	4.0	6.8	8.0
19951016HO	FC723	2.5	4.0	7.8	8.5

2006 Curly Top Nursery, Kimberly, ID

Source	Description	8/7/2006	8/28/2006	9/11/2006
	LSD	0.94	1.22	1.27
	CV	13.0	14.3	13.4
1996A008	Beta G6040 - Resistant Check	3.7	4.0	4.7
19931012	FC901	4.0	4.0	5.0
20021022	2859/FC607&FC604 MM	4.0	4.7	5.0
20051022	FC301	4.0	4.7	5.0
19911043HO	FC403	4.0	4.3	5.0
2005A009	2005A008 x C833-5cms	4.3	5.0	5.0
2005A018	C833-5cms x FC20021023	4.3	5.0	5.0
2005A027	C790-15cms x (FC712 x 9931)F3]	4.0	5.0	5.0
20031017	LSR x maritima BC - 75119H	4.0	4.3	5.3
20051021	FC201	4.0	5.3	5.3
19911043HO1	FC403CMS	4.0	4.3	5.3
20051007HOPF	half sib selection within FC201	4.0	4.3	5.3
2005A005	FC709-2, 9933, LSR (FC x EL), CR11, CR10	4.0	5.0	5.3
2005A006	C833-5cms x FC1036	4.0	4.7	5.3

2006 Curly Top Nursery, Kimberly, ID

Source	Description	8/7/2006	8/28/2006	9/11/2006
	LSD	0.94	1.22	1.27
	CV	13.0	14.3	13.4
1996A008	Beta G6040 - Resistant Check	3.7	4.0	4.7
2005A012	2005A008 x C833-5cms	4.0	5.0	5.3
2005A013	2005A008x C790-15cms	3.7	4.7	5.3
2005A024	rzmm-%-ER (C931 x FC709-2)F3	5.0	5.3	5.3
2005A019	C790-15cms x FC20021023	4.5	5.5	5.5
19771082	LSR CTR population	4.3	5.3	5.7
19741026H	maritima backcross	4.3	5.0	5.7
2005A007	C790-15cms x FC1036	4.0	5.0	5.7
2005A015	½ sib 2005A008	4.7	5.0	5.7
2005A023	C790-15cms x 20031022	4.3	5.3	5.7
2005A025	C790-15cms x (C931 x FC709-2)F3]	4.7	5.3	5.7
19961014	FC724 New Release 2003	5.0	5.3	6.0
20031013	SucroseMM x PI35826 LSR Fodder Beet	4.0	5.0	6.0
20031014	(SucroseMM x PI540605)F3	4.3	5.0	6.0
20041012	20021022 – '2859/FC607&FC604 MM	5.0	5.7	6.0
19951016HO1	FC723 CMS – EL44/FC708 CMS	4.0	5.0	6.0
20041010HO	FC712/MonoHyA4	4.0	5.0	6.0
2005A010	2005A008 x C790-15cms	4.7	5.3	6.0
2005A011	½ sib 2005A008	4.3	5.3	6.0
2005A014	4918aa, FC902, FC607, 2915, FC709-2	5.0	6.0	6.0
2005A026	rhzm-ER-%S (FC712 x 9931)F3	5.0	5.7	6.0
19931007	FC720 New Release 2005	5.0	5.7	6.3
19911026HO	FC715	4.3	5.3	6.3
19961010HO	FC722 – C718/FC708	4.0	5.0	6.3
1997A050	FC607	5.0	6.0	6.3
20001016H	FC709-2	4.7	5.7	6.3
20011045PF	(SucroseMM x PI540599)F2	5.0	6.0	6.3
2005A022	(C931aa x (FC907 x FC709-2)	4.3	5.0	6.3
20031025	FC720 New Release 2005	4.0	5.5	6.5
19951016HO	FC723 – EL44/FC708 mm	5.0	6.0	6.5
20041010HO1	FC712/MonoHyA4	4.5	6.0	6.5
19961010HO1	FC722 CMS – C718/FC708 CMS	4.7	5.7	6.7
20011002bbPF	WB850 x SucroseMM	4.7	6.0	6.7
20001017	FC720 New Release 2005	6.0	7.0	7.0
20001007	LSR w/ Fargo	5.7	6.7	7.3
2005A008	4918aa, FC902, FC607, 2915, FC709-2	5.7	7.0	7.7

FINAL REPORT BSDF PROJECT 440 RHIZOCTONIA ROOT ROT RESISTANCE AND DEVELOPMENT OF GENETIC RESISTANCE IN SUGAR BEET

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2005 Field Research on Rhizoctonia Root Rot of Sugar Beet

Annually, for over thirty years, the sugar beet breeding program in Fort Collins has included the production of an artificial epiphytotic through inoculation with *Rhizoctonia solani* to evaluate and select for resistance to root rot caused by this pathogen. In 2005 the project involved field studies conducted at the Crops Research Lab-Fort Collins Research Farm near Wellington, CO. Randomized, complete-block designs with five replicates were used to evaluate ARS breeding germplasm and Plant Introduction accessions. *Rhizoctonia*-resistant line FC703, highly resistant FC705-1, and susceptible FC901/C817 were included as internal controls. One-row plots (56 cm row spacing) were 4 m long and were planted at the Crops Research Lab-Fort Collins Research Farm, CO, on May 25. Inoculation with dry, ground, barley-grain inoculum of *Rhizoctonia solani* isolate R-9 (AG-2-2) was performed on July 28 at a rate of 25 g/m row with inoculum applied to the crown of the plant. Immediately after inoculation, plots were cultivated to throw soil into the beet crowns. The plant population was thinned to 20-25 cm spacing by hand and irrigated as necessary. Beets were harvested September 19, and each root was rated for rot on a scale of 0 (no damage) to 7 (dead plants). The average disease severity was determined to create a disease index for each PI. Analyses of variance (PROC ANOVA – SAS) were performed on disease indices (DI), percent healthy roots (classes 0 and 1 combined) and percentage of roots in classes 0 through 3 (harvestable roots). Percentage of roots in classes 0-1 and 0-3 were transformed using arcsine-square root to normalize the data for analyses (AP 0-1 and AP 0-3, respectively)

Rhizoctonia root rot reached moderate severity levels in early September. Differences in the DI among entries were highly significant ($P < 0.001$). The average DI across all tests in the 2005 nursery for highly resistant FC705-1, resistant FC703, and highly susceptible FC901/C817 controls were 2.7, 3.1, and 4.9, respectively. Percentages of healthy roots (those in disease classes 0-1) were 27.6, 25.4, and 6.4% for these controls, respectively. The percentages of harvestable roots (those in disease classes 0-3) were 59.1, 56.7, and 18.3% for these controls, respectively. The highest and lowest DI for all of the lines evaluated in the nursery, including materials not in the PI tests, were 7.0 and 1.5, respectively.

Table 4. Allotment of Fort Collins "FC" numbers (3-digit numbers)

"FC" numbers are "convenience" numbers for "seed releases" or purposes where a permanent line designation is needed — i.e. a number that does not change from generation to generation where little or no selection pressure is applied. Initially, an "FC" no. was written thus "FC 501" [now FC727], "FC 502 CMS" [now FC715CMS], etc. Sublines (from selfing) were designated thus, "FC 502/2" [now FC709-2], "FC502/3" [now FC502-3], etc. The same applies when the line is substantially changed by selection without selfing.

100's	Early releases
200's	Rhizoctonia, rhizomania resistant, combined with other resistances
300's	Leaf Spot Resistant (LSR), combined with rhizomania resistance
400's	Parental lines and special genetic stocks
Below 500	Originally LeRoy Powers -
500's	Leaf Spot Resistant (LSR), Type-O lines & male steriles [CMS]
600's	LSR-Curly Top Resistant (CTR), type-O lines & male steriles [CMS]
700's	Rhizoctonia Resistant
800's	LSR-CTR-Rhizoctonia resistant
900's	Pollinators, LSR-CTR type

Rhizoctonia-Resistant Populations under Development

Rhizoctonia root rot continues to be a problem in most sugar beet-growing areas in the United States, and is a growing problem world wide. The practice of short rotations and the expansion of growing areas into infested areas compound the problem. The result is a reduction in net returns to growers as well as processing losses due to reduced sucrose and purity of rotted or partially rotted beets. Genetic resistance, coupled with judicious cultural measures, is a more economical and practical method of reducing losses caused by this fungus than is a strictly chemical control regime. There is also a strong need of combining Rhizoctonia root rot resistance with Rhizomania resistance.

This has been an ongoing and productive project, and has been the only research project with the goal of discovering, developing, and releasing Rhizoctonia-resistant germplasm to industry breeders, our major external customers. Although several relatively resistant germplasms have been developed, we need to continue to combine this resistance with resistance to other diseases, uncover new sources of resistance, and work to more quickly introgress this resistance into germplasm with higher sucrose yield potential.

Current Research 2005 – Germplasm under development:

Current Rhizoctonia-resistant germplasm under development consists of populations being jointly developed with Dr. Robert Lewellen in Salinas. These populations are being improved to combine Rhizoctonia and Rhizomania resistant in a genetic background with good sucrose yield potential. Additionally, a population providing root maggot resistance along with Rhizoctonia and Cercospora resistance is under development with Larry Campbell in Fargo. Finally, potential new sources of Rhizoctonia have been identified, are being retested and will be crossed to sugar beet with high sucrose potential and Rhizomania resistance.

With the release of FC723 and FC723CMS last fall, the germplasm remaining from the program of Dr. Richard Hecker has been evaluated, recombined, improved and released, or shelved.

Salinas:

Seed Sent to R. T. Lewellen

Release	Seed No.	Germplasm, release no. or description	Date Sent	Salinas ID
FC201	19951014	(941009H2 + 941009H3) – 951014; ((2890aa x FC708) + (2859aa x FC708))F1 – blk F2	04/01/99	FC1014
FC301	19981010H	[(2859aa x (FC607 & FC604))] + [2890aa x (FC607 & FC604)] – blkF1 –blkF2 – S1 – blkLSR; 981010 = Mix of 20 g 971011 with 11 g of 971013MS and 11 g of 971013PF.	05/01/98	FC123
FC301	19981011H	[(2859aa x (FC607 & FC604))] + [2890aa x (FC607 & FC604)] – blkF1 –blkF2- S1 – RMCTR(1s, 6s, 26s, 88s, 94s)aa – blk PF; (941007H2 + 941007H3) – 951013 – 961007 – 971012ms	05/01/98	FC123
FC301	19981012	CTR/LSRmmpop – [(2859aa x (FC607 & FC604))] + [2890aa x (FC607 & FC604)] – blkF2 – S1 – blk rem CTR	05/01/98	FC123
FC301	19991012	971012 – [(2859aa x (FC607 & FC604))] + [2890aa x (FC607 & FC604)] – blkF2 – S1 – blkCTR(1s, 6s, 26s, 88s, 94s) – selected by G Koch via leaf disc	07/25/00	FC123
√ 05-1030- 15	19991030MS	((2915aa x FC709-2) + (FC709-2rr x 2915A_))blkF1-blkF2-RMF3- Hs; (941011H2 +941012H2) – 961004 – 971015Aa – 981006-x [Polycross increase of 981006-10, -15, -17, -21, -60, -70] – male sterile harvested	07/25/00	FC1030
√05-130- 16	19991030PF	((2915aa x FC709-2) + (FC709-2rr x 2915A_))blkF1-blkF2-RMF3- Hs; (941011H2 +941012H2) – 961004 – 971015Aa – 981006-x [Polycross increase of 981006-10, -15, -17, -21, -60, -70] - pollen fertile harvested	07/25/00	FC1030
	19991031MS	((2915aa x FC709-2) + (FC709-2rr x 2915A_))blkF1-blkF2-RMF3- Hs; (941011H2 +941012H2) – 961004 – 971015Aa – 981006-x [Polycross increase of 981006-6, -12, -19, -27, -34, -37, -38, -41, -43, -48, -65, -68] – male sterile harvested	07/25/00	FC1030
	19991031PF	((2915aa x FC709-2) + (FC709-2rr x 2915A_))blkF1-blkF2-RMF3- Hs; (941011H2 +941012H2) – 961004 – 971015Aa – 981006-x [Polycross increase of 981006-6, -12, -19, -27, -34, -37, -38, -41, -43, -48, -65, -68] - pollen fertile harvested	07/25/00	FC1030
	19991032MS	((2915aa x FC709-2) + (FC709-2rr x 2915A_))blkF1-blkF2-RMF3- Hs; (941011H2 +941012H2) – 961004 – 971015Aa – 981006-x [Polycross increase of 981006-18, -54, -56, -59, -71, -110] –	07/25/00	FC1030

Release	Seed No.	Germplasm, release no. or description	Date Sent	Salinas ID
		male sterile harvested		
	19991032PF	((2915aa x FC709-2) + (FC709-2rr x 2915A_))blkF1-blkF2-RMF3- Hs; (941011H2 +941012H2) – 961004 – 971015Aa – 981006-x [Polycross increase of 981006-18, -54, -56, -59, -71, -110] - pollen fertile harvested	07/25/00	FC1030
	20001004	(961002aa x 961001)F2blk; (((4918(sp)aa x (FC902 x 278R-)) + (4918(sp)aa x (278R- x FC902))) – blkF1 –aa} X {(FC607 x (MonoHy-T6, -A7, -A4, & SR87)) – blk(Ss?)F2} – F2blk	07/25/00	FC1030
	20021028	(2000A011 x 19921024)rr blk F2; 9933rr x FC709-2; RhzcR, LSR, RtAphidR, Sf, A-, Rz-, fertile cytoplasm	04/08/03	04-FC1028
	20021038	[2001A032=CR910 blk]x[(20001014H2+20001014H4+20001015H2+20001015H4+20001015H5+20001015H6+20001015H7) blk increase]F2	04/08/03	04FC1038
	20021037	[2000 Seed Production Sp5 – (Rzm CR910, 911, 912 aa x A-) blk] x [(20001014H2+20001014H4+20001015H2+20001015H4+20001015H5+20001015H6+20001015H7) blk increase]F2	04/08/03	04-FC1037
	20031018	(2000A010[9931rr] x 9210124[FC709-2R-])F1-blkF2-blkF3; 74 females harvested, 24 males in F1	04/14/04	FC????
	20031019	(981007-x & 981006-x)blk; ((941011H2 +941012H2) – 961004 – 981007-x Rhzc sel & (941011H2 +941012H2) – 961004 – 971015Aa – 981006-x Rhzc sel)blk-blk-blk	04/14/04	FC????
	20031022	[2000A010aa [9931] x 20001009 [sel(FC907 x FC709-2)F3]blk increase-blk	04/14/04	FC????
	20021023	reselection of FC123 for LSR	07/27/04	

Some of the populations under development are:

Rhizoctonia root rot resistance multigerm base population developed by a cross between FC709-2 and a Salinas germplasms, 2915, which has been tested in Salinas & Fort Collins as FC1030). – includes populations 03-FC1030-15 and 03-FC1030-16 being reselected in Fort Collins for Rhizoctonia resistance.

- c) 2915 (sp) RZM 1915-#m 1913-# aa x A (Salinas); Seed harvested from aa (ms) plants open-pollinated by A- (fertile) plants. This population will segregate for A-:aa, Rz-:rzz, s^ss^s:s^f-, (>1/2 s^f), R-:rr, It will be multigerm, have moderate to good tolerance to virus yellows, curly top, bolting, Erwinia; variable for reaction to powdery mildew, production traits. Individual plants will be either Aa or aa. Background of population is mostly from OP, MM lines such as C46, C37.

20021028; FC709-2 (Fort Collins release) x 9933 (Salinas germplasm) [(2000A011 x 19921024)rr blk F₂]; Should segregate for □Rhizoctonia and cercospora leafspot resistance (FC709-2), multigermity, root aphid resistance (FC709-2 and 9933), tolerance to curly top, Virus Yellow, powdery mildew, Erwinia, rhizomania (9933) S^f-, A-, in a fertile cytoplasm – tested in Salinas as 04-FC1028.

Sib-lines of FC201 – 01-FC1014-22 (A,aa); 01-FC1014A; 01-FC1014H5 – C833-5 CMS x 01-FC1014A; 03-FC1015 – Rzm (C833-5 mmaa x FC1014) mmaa x A; 03-FC1015HO, CMS equivalent of the previous – (C833-5 CMS x 01-FC1014A) x Rzm (C833-5 mmaa x FC1014) mmaa x A.

20021022 – [2000A010aa [9931] x 20001009 [sel(FC907 x FC709-2)F₃]blk increase-bk – was sent to Salinas and reselected in Fort Collins.

- d) 9931 = Advanced Base breeding population at Salinas with resistance/tolerance to Rz, CT, VY, Pm, Erwinia, bolting – segregates for Aa:aa, Sf, Multigerm.

Progress in 2005

Sib-lines from the population (20001004, 19991030, 10001031, and 19991032), 051030-15 and 05-1030-16 will be released as FC220 and FC221. They have a high frequency of the *Rz1* allele conferring resistance to rhizomania caused by *Beet necrotic yellow vein virus*, and excellent resistance to root-rotting strains (AG-2-2) of *Rhizoctonia solani* Kühn.

Seed received from R.T. Lewellen for testing and evaluation includes Accession seed numbers from 2005A005 to 2005A027 (Table below).

A number of accessions from the NPGS *Beta* collection that had shown Rhizoctonia-resistance in the Sugarbeet CGC screening program have been identified. Those PIs with seed available were re-screened in 2003. Special attention will be paid to those accessions screened in 1987 and 1992 because the tests in those years appear to have been unreliable. These and other PIs are being screened (Table below). Crosses will be made between any that appear to have resistance using a female parent with high sucrose yield potential and with Rhizomania resistance. The goal is to develop Rhizoctonia-resistant populations from potentially different sources of resistance, from which breeders will be able to select resistant hybrid parents or germplasm to cross into programs developing Rhizoctonia-resistant hybrid parents (See table below).

Germplasm Received from RT Lewellen at Salinas for evaluation, crossing, and selection.			
Number	PARENTDESC	Designation	Pedigree
2005A005	bulk increase of (FC709-2 x 9933) & (Best LSR FC x EL x CR11) & (Best LSR	05-FC1036	05-FC1036 = [(rzm 04-FC1028, RZM 04-FC1037, RZM 04-FC1038)aa x A]; 04-FC1028 = rzm-%S FC20021028 (FC709-2 x 9933); 04-FC1037 = rzm-%S FC20021037

Germplasm Received from RT Lewellen at Salinas for evaluation, crossing, and selection.			
Number	PARENTDESC	Designation	Pedigree
	FC x EL x CR10)		(Best LSR FC x EL x CR11); 04-FC1037 = rzm-%S FC200210378(Best LSR FC x EL x CR10)
2005A006	C833-5cms x FC1036	05-FC1036H5	05-FC1036H5 = C833-5cms x FC1036A; FC1036=2005A005; C833-5 cms = mm, Rz1Rz1, ♀ tester, cms
2005A007	C790-15cms x FC1036	05-FC1036H50	05-FC1036H50 = C790-15cms x FC1036A; FC1036=2005A005; C790-15 cms = mm, Rz1Rz1, ♀ tester, cms
2005A008	{{(4918aa x (FC902, FC607, Commercial))F2; (2915 x FC709-2) reciprocal} blk	05-1030-15(Sp)	= 03-FC1030-15aa x A; 03-FC1030-15 = Inc. 01-FC1030-15(A,aa); 01-FC1030-15 = FC1030@aa x A (½ sib); FC(C1)=rzm MR of 20001004(48), 19991030MS(27), 19991030PF(23), 19991031MS(10), 19991031PF(5), 19991032MS(24), 199910302PF(24); 40 stecks/each
2005A009	{{(4918aa x (FC902, FC607, Commercial))F2&(2915 x FC709-2) reciprocal} blk x C833-5cms	05-FC1030-15H5	05-FC1030-15H5 = C833-5cms x FC1030-15A; FC1030-15=2005A008; C833-5 cms = mm, Rz1Rz1, ♀ tester, cms
2005A010	{{(4918aa x (FC902, FC607, Commercial))F2&(2915 x FC709-2) reciprocal} blk x C790-15cms	05-FC1030-15H50	05-FC1030-15H50 = C790-15cms x FC1030-15A; FC1030-15=2005A008; C790-15 cms = mm, Rz1Rz1, ♀ tester, cms
2005A011	1/2 sib 2005A008 {{(4918aa x (FC902, FC607, Commercial))F2; (2915 x FC709-2) reciprocal} blk	05-FC1030-16(Sp)	= 03-FC1030-16aa x A; 03-FC1030-16 = Inc. 01-FC1030-16(a,aa); 01-FC1030-16 = FC1030@aa x A (½ sib); see 2005A008; ½ sib = one aa plant pollinated by A_ (fertile) plants from composite of MR & stecklings. Source of single♀ seed bearing plant not known.
2005A012	{{(4918aa x (FC902, FC607, Commercial))F2; (2915 x FC709-2) reciprocal} blk x C833-5cms	05-FC1030-16H5	05-FC1030-16H5 = C833-5cms x FC1030-16A; FC1030-16=2005A011; C833-5 cms = mm, Rz1Rz1, ♀ tester, cms
2005A013	{{(4918aa x (FC902, FC607, Commercial))F2&(2915 x FC709-2) reciprocal} blk x C790-15cms	05-FC1030-16H50	05-FC1030-16H50 = C790-15cms x FC1030-16A; FC1030-16=2005A011; C790-15 cms = mm, Rz1Rz1, ♀ tester, cms
2005A014	{{(4918aa x (FC902, FC607, Commercial))F2; (2915 x FC709-2) reciprocal} blk	05-FC1030-15(iso)	05-FC1030-15(iso) = rzm 03-FC1030-15(A,aa) ; bulk increase in greenhouse isolation chamber (not distributed)
2005A015	1/2 sib 2005A008 {{(4918aa x (FC902, FC607, Commercial))F2; (2915 x FC709-2) reciprocal} blk	05-FC1030-16(iso)	05-FC1030-16(iso) = rzm 03-FC1030-16(A,aa) ; bulk increase in greenhouse isolation chamber (not distributed)
2005A016	half sibs of	05-FC1023M(sp)	05-FC1023M(Sp) = Inc. 20021023Maa x A;

Germplasm Received from RT Lewellen at Salinas for evaluation, crossing, and selection.			
Number	PARENTDESC	Designation	Pedigree
	FC123mm (FC301); multigerm		Multigerm, aa plants, x all A ₋ plants; Only a fair seed plot. Risk of out crossing to other mm populations.
2005A017	half sibs of FC123mm (FC301); monogerm	05-FC1023m(Sp)	05-FC1023m(Sp) = Inc. 20021023mmaa x A; monogerm, aa plants, x all A ₋ plants, mostly M ₋ ; Only a fair seed plot. Risk of out crossing to other mm populations.
2005A018	C833-5cms x FC20021023 (mm of LSRmm pop & CTR/LSRmm pop & CTR/LSRmm pop)	05-FC1023H5	05-FC1023H5 = C833-5cms x 20021023mmA; C833-5 cms = mm, Rz1Rz1, ♀ tester; 20021023 = half sibs of (mm of LSRmm pop & CTR/LSRmm pop & CTR/LSRmm pop); Only a fair seed plot. Risk of out crossing to other mm populations.
2005A019	C790-15cms x FC20021023 (mm of LSRmm pop & CTR/LSRmm pop & CTR/LSRmm pop)	05-FC1023H50	05-FC1023H50 = C790-15cms x 20021023mmA; C790-15cms = mm, Rz1Rz1, ♀ tester, cms; Only a fair seed plot. Risk of out crossing to other mm populations.
2005A020	half sibs of FC123mm (FC301); monogerm	05-FC1023m(iso)	05-FC1023m(iso) = Inc. 20021023(A,aa) mm; mm (A & aa) plants in bulk increase
2005A021	half sibs of FC123mm (FC301); multigerm	05-FC1023M(iso)	05-FC1023M(iso) = Inc. 20021023(A,aa) M ₋ ; M ₋ (A & aa) plants in bulk increase
2005A022	rzm-ER-%S [(C931aa x (FC907 x FC709-2))F3 (20031022)]	05-FC1022	= rzm-ER-% 20031022 (A,aa); 20031022 = [(C931aa x (FC907 x FC709-2))F3; 47 MR increased in bulk after mild selection for rzm and CLS. Re-selected for size, shape, % sucrose. MR averaged 20.2% sucrose. Free of Erwinia after field inoculation (ER).
2005A023	C790-15cms x rhzm-ER-%S [(C931aa x (FC907 x FC709-2))F3 (20031022)]	05-FC1022H50	05-FC1022H50 = C790-15cms x rzm-ER-%S 20031022; 20031022 = [(C931aa x (FC907 x FC709-2))F3; C790-15cms = mm, Rz1Rz1, ♀ tester, cms
2005A024	rzm-%-ER (C931 x FC709-2)F3	05-FC1018	05-FC1018 = rzm-%-ER 20031018(A,aa); FC20031018=(C931 x FC709-2)F3; 47 MR selected for resistance to rzm, CLS, Erwinia, %S, size, shape (see above). MR averaged 18.5% sugar.
2005A025	C790-15cms x [rhzm-%-ER (C931 x FC709-2)F3]	05-FC1018H50	05-FC1018H50 = C790-15cms x rzm-%-ER 20031018(A,aa); FC20031018=(C931 x FC709-2)F3; 47 MR selected for resistance to rzm, CLS, Erwinia, %S, size, shape (see above). MR averaged 18.5% sugar. C790-15cms = mm, Rz1Rz1, ♀ tester, cms
2005A026	rhzm-ER-%S (FC712 x 9931)F3	05-FC1019	05-FC1019 = rzm-ER-%S 20031019; FC20031019 = (FC712 x 9931)F3; 32 MR selected for resistance to rzm, CLS, Erwinia, %S, size, shape (see above). MR averaged 18.0% sugar.
2005A027	C790-15cms x [rhzm-ER-%S (FC712 x 9931)F3]	05-FC1019H50	05-FC1019H50 = C790-15cms x rzm-ER-%S 20031019; FC20031019 = (FC712 x 9931)F3; 32 MR selected for resistance to rzm, CLS, Erwinia, %S, size, shape (see above). MR averaged 18.0% sugar. C790-15cms = mm, Rz1Rz1, ♀ tester, cms

2005 2R Rhizoctonia root rot resistance evaluation of Beta PIs

Seed Source	Subspecies*	Donor's ID	DI**	% 0-1	% 0-3	AP 0-1	AP 0-3
941025	vulgaris	(FC901/C817)//413 – 'SusCheck'	4.3	12.4	24.2	18.1	25.7
831083	vulgaris	FC705/1 – 'Highly Resistant Check'...	2.8	51.4	58.0	45.8	52.9
991017	vulgaris	FC703 – 'Resistant Check'	2.7	36.4	66.2	36.5	57.8
		LSD (P=0.05)	1.4			17.1	24.5
		Trial Mean	5.5	10.1	20.1	10.6	21.5
PI 504182	maritima	Wild beet, Italy	6.0	0.0	20.8	0.0	20.0
PI 504183	maritima	Wild beet, Italy	6.5	2.0	8.4	3.7	10.9
PI 504184	maritima	Wild beet, Italy	6.4	0.0	10.6	0.0	12.3
PI 504190	maritima	Wild beet, Italy	5.8	9.5	18.0	12.8	20.9
PI 504193	maritima	Wild beet, Italy	5.7	2.8	15.2	4.4	15.2
PI 504199	maritima	Wild beet, Italy	6.2	0.0	12.4	0.0	18.3
PI 504202	maritima	Wild beet, Italy	6.7	0.0	0.0	0.0	0.0
PI 504206	maritima	Wild beet, Italy	7.0	0.0	0.0	0.0	0.0
PI 504223	maritima	Wild beet, Italy	4.0	35.7	55.0	31.4	53.1
PI 504235	maritima	Wild beet, Italy	7.0	0.0	0.0	0.0	0.0
PI 504237	maritima	Wild beet, Italy	6.3	0.0	0.0	0.0	0.0
PI 504238	maritima	Wild beet, Italy	nr				
PI 504239	maritima	Wild beet, Italy	5.3	0.0	29.2	0.0	29.2
Ames 4436	maritima	Wild beet, Italy	4.8	11.0	28.0	13.8	28.2
PI 504248	maritima	Wild beet, Italy	5.5	4.0	14.0	5.3	14.3
PI 504253	maritima	Wild beet, Italy	5.8	11.6	11.6	13.0	13.0
PI 504264	maritima	IDBBNR 5798, UK.....	6.6	0.0	5.8	0.0	6.5
PI 518304	maritima	IDBBNR 5814, UK.....	5.9	5.0	17.5	6.6	17.9
PI 518320	maritima	IDBBNR 5836, UK.....	5.5	9.5	18.3	12.4	24.8
PI 518342	maritima	IDBBNR 5927, UK.....	5.5	6.6	23.0	7.0	24.7
PI 518433	maritima	WB 817, France.....	6.0	5.0	9.6	6.0	11.7
PI 540566	maritima	WB 886, France.....	nr				
PI 540632	maritima	IDBBNR 5600, UK.....	4.5	25.0	34.5	22.5	32.0
PI 546403	maritima	IDBBNR 5637, UK.....	4.2	17.0	42.0	17.7	40.2
PI 546407	maritima	IDBBNR 5644, Greece.....	5.3	12.8	23.6	13.4	27.9
PI 546428	maritima	IDBBNR 3863, Ireland	6.8	0.0	5.6	0.0	8.8
PI 604031	maritima	IDBBNR 9685, Greece, Aegean	6.1	3.6	15.6	7.0	20.0
PI 546518	maritima	IDBBNR 9675, Greece	6.6	2.8	7.2	4.4	10.0
PI 546508	maritima	Wild beet, Italy	5.4	12.5	25.0	11.3	22.5
PI 504220	maritima	4.1	42.3	47.3	40.1	46.7

43–□ Shown are the subspecies of *Beta vulgaris* examined.

** DI = Disease Index on a scale of 0 (no damage) to 7 (plant death), % 0-1= percent roots in class 0 and 1 combined, % 0-3 = percent roots in class 0 to 3 combined, AP is the arcsine-square root transformation of percentages of roots in classes 0-1 and 0-3 to normalize the data for analyses.

Nr = not rated. These two lines had very poor emergence and not enough beets emerged for a meaningful rating. All analyses were performed without these two lines.

**7R 2005 – Rhizoctonia Resistance Evaluation of USDA-ARS Fort Collins, CO (Lee Panella).
FC710(4X) 1019 removed due to poor plant stand.**

Entry	Seed Source	Release Description	DI ¹	% Hlthy ²	% 0 – 3 ³	Z% ⁴ Hlthy	Z% 0 – 3 ⁴
LSD ⁵			1.25			22.2	25.5
CV			28.7			68.9	44.9
Susceptible Check ⁶			3.8	16	39	18.2	35.4
Experiment Mean			3.5	24	51	25.5	45.0
1021	20041010HO	FC712/MonoHy A4	2.4	45	68	41.7	56.1
1023	2004A008	EL51	2.4	40	76	35.9	61.7
1018	20041007	FC709-2	2.7	29	70	31.4	57.2
1022	20041010HO1	FC712/MonoHy A4 – CMS equivalent	2.8	32	64	34.0	53.3
1016	19961014	FC724 New Release 2003	2.9	35	63	34.8	53.6
1020	20011007	F3 (907 x 709-2) for RhzcR – hs 10A-1775	2.9	27	75	31.0	60.5
1011	19921019	FC729 – FC712/A4, 3 cycles Rhizoc, MM	2.9	35	59	35.7	53.2
1012	19951016HO	FC723 – EL44/FC708 mm	2.9	36	64	36.6	53.3
1015	19961010HO	FC722 – C718/FC708 New Release 2005	3.5	9	56	11.3	48.7
1014	19961010HO1	FC722CMS – C718/FC708CMS Release 2005	3.7	14	44	14.4	41.3
1013	19951016HO1	FC723CMS – EL44/FC708 CMS	3.9	12	44	13.4	38.2
1024	2004A029	04-FC1028; (9933rr x FC709-2)F3	4.1	10	37	16.8	37.1
1017	20001017	FC720 – C718/(C718/FC708) Release 2005	4.2	23	36	25.7	33.8
1026	20051011HO1	03-124CMS FC123 derivative	5.2	15	22	14.1	21.5
1025	20051011PF	03-124 FC123 derivative	5.7	5	15	9.6	20.0

¹Disease Index is based on a scale of 0 (=healthy) to 7 (= plant dead).

²Percent of healthy roots (disease classes 0 and 1 combined).

³Percent of diseased roots likely to be taken for processing (disease classes 0 through 3 combined).

⁴Percentages were transformed to arcsine-square roots to normalize the data for analyzes.

⁵P=0.05; There were 6 missing plots, however LSD was estimated as if all plots were present.

⁶FC901/C817 – susceptible check

⁷FC703 – resistant check

⁸FC705/1 – highly resistant check

8R 2005 – Rhizoctonia Resistance Evaluation of USDA-ARS Salinas germplasm, CA (Bob Lewellen). Highly resistant control removed due to poor plant stand.

Entry	Seed Source	Release Description	DI ¹	% Hlthy ²	% 0 – 3 ³	Z% ⁴ Hlthy	Z% 0 – 3 ⁴
(<4.11 significantly better than susceptible check) LSD ⁵			1.19			17.7	21.4
CV			20.8			81.4	60.2
Susceptible Check ⁶			5.3	3	7	4.4	10.0
Experiment Mean			4.5	14	28	17.0	28.7
Resistant Check ⁷			4.0	18	38	21.3	37.7
1069	03-FC1030-16	Inc.01-FC1030-16; Iso40	3.2	27	59	28.0	50.9
1068	03-FC1030-15	Inc.01-FC1030-15; Iso39	3.3	37	53	36.1	47.0
1064	CR411	RZM CR311, CR311AA x A; Sp10	4.1	22	38	22.5	34.0
1062	R421	RZM-ER-% R221; Iso9	4.1	20	34	24.0	32.2
1071	CR311-88	Inc.CR111-88(A,aa); Iso38	4.2	25	36	27.1	33.3
1073	03-FC1030-15H50	C790-15CMS x 01-FC1030-15	4.3	8	28	12.6	27.7
1067	04-FC1038	RZM-% FC20021038; Iso12	4.3	12	28	19.4	31.5
1074	03-FC1030-16H50	C790-15CMS x 01-FC1030-16	4.4	15	23	20.3	27.9
1076	Y491H74	03-FC1015HI x Y391	4.5	11	34	17.0	33.7
1066	04-FC1037	RZM-% FC20021037; Iso11	4.6	7	22	9.3	24.3
1061	Y475	RZM-ER-% Y275; Iso7	4.9	12	20	16.0	23.5
1065	04-FC1028	RZM-% FC20021028; Iso10	4.9	14	25	18.9	27.1
1063	4931	RZM 3931,3931aa x A; Sp8	5.1	8	21	10.1	24.9
1072	03-F1014-22	Inc. 01-FC1014-22(A,aa); Iso39	5.1	4	14	8.7	19.3
1075	Y491H76	03-FC1014-22HS x Y391	5.3	5	12	10.4	17.8
1070	4933-14	2933-14 aa xA; Sp4	6.3	2	2	3.7	3.7

¹Disease Index is based on a scale of 0 (=healthy) to 7 (= plant dead).

²Percent of healthy roots (disease classes 0 and 1 combined).

³Percent of diseased roots likely to be taken for processing (disease classes 0 through 3 combined).

⁴Percentages were transformed to arcsine-square roots to normalize the data for analyzes.

⁵P=0.05; There were 6 missing plots, however LSD was estimated as if all plots were present.

⁶FC901/C817 – susceptible check

⁷FC703 – resistant check

5R 2005 – Rhizoctonia Resistance Evaluation of USDA-ARS Fort Collins Released Rhizoctonia Resistant Lines, CO (Lee Panella). Analyzed with PROC GLM and LSD values were calculated using 5 replications, although some plot values were lost. FC702, FC704, and FC705/1 were not analyzed because 3 or more of the 5 replications were lost.

		DI ¹	% Hlthy ²	% 0 – 3 ³	Z% ⁴ Hlthy	Z% 0 – 3
	LSD.	1.24			20.8	23.1
	CV.	30.2			56.6	38.2
FC201	2003A025	4.4	16	22	18.3	22.4
FC701	19931024	3.8	42	42	40.2	40.2
FC701-4	20021016	2.5	44	68	41.0	58.8
FC701-5	19721056	3.5	22	59	18.3	54.8

5R 2005 – Rhizoctonia Resistance Evaluation of USDA-ARS Fort Collins Released Rhizoctonia Resistant Lines, CO (Lee Panella). Analyzed with PROC GLM and LSD values were calculated using 5 replications, although some plot values were lost. FC702, FC704, and FC705/1 were not analyzed because 3 or more of the 5 replications were lost.

		DI ¹	% Hlthy ²	% 0 – 3 ³	Z% ⁴ Hlthy	Z% 0 – 3
	LSD.	1.24			20.8	23.1
	CV.	30.2			56.6	38.2
FC701-6	19801059H	2.5	44	74	41.4	60.1
FC702/2	19991016	3.4	21	49	24.0	44.4
FC702-4(4X)	20011009	3.7	20	52	23.9	49.3
FC702-6	19811055H	2.2	53	78	46.5	62.7
FC703	19991017	3.1	42	57	39.4	49.1
FC705	20001019	2.8	36	70	36.8	57.9
FC706	20001020	3.2	22	55	26.8	48.5
FC707	20001021	3.8	22	36	24.8	33.6
FC708	19831085HO	3.6	13	47	13.9	40.4
FC709	19991018	2.6	48	68	43.6	55.9
FC709-2	20041003	2.5	35	77	32.8	64.4
FC710	19941024	2.4	40	78	38.6	62.9
FC710(4X)	19971017	3.5	13	58	11.3	53.8
FC711	19821087	3.9	15	51	18.0	45.4
FC712	19881032H	2.3	41	83	36.7	74.0
FC712(4X)	19971018	3.1	36	51	33.8	46.0
FC715	19911026HO	2.8	39	66	35.4	55.0
FC716	19971019	3.3	26	52	29.7	46.3
FC717	19981025	5.4	6	13	7.5	11.3
FC718	19911032	3.0	27	63	25.2	53.5
FC719	19911037	2.9	41	59	39.1	51.2
FC720	19961015	2.3	45	82	42.1	68.1
FC721	19931005HO	3.5	15	52	19.2	46.2
FC721CMS	19931005HO1	3.4	21	55	24.4	48.2
FC722	19961010HO	4.0	8	44	7.9	40.7
FC722CMS	19961010HO1	3.5	27	55	25.0	50.9
FC723	19951016HO	3.1	26	64	27.8	53.9
FC723CMS	19951016HO1	2.6	35	73	33.3	59.5

5R 2005 – Rhizoctonia Resistance Evaluation of USDA-ARS Fort Collins Released Rhizoctonia Resistant Lines, CO (Lee Panella). Analyzed with PROC GLM and LSD values were calculated using 5 replications, although some plot values were lost. FC702, FC704, and FC705/1 were not analyzed because 3 or more of the 5 replications were lost.

		DI ¹	% Hlthy ²	% 0 – 3 ³	Z% ⁴ Hlthy	Z% 0 – 3
	LSD.	1.24			20.8	23.1
	CV.	30.2			56.6	38.2
FC724	19961014	2.7	42	61	40.3	51.9
FC725	19921008	1.9	65	79	56.8	66.3
FC726	19931010	3.2	41	57	36.4	46.8
FC727	19951017	2.6	37	73	37.5	59.5
FC728	19921025	2.6	47	63	43.0	53.1
Susc. Check	19941025	5.7	2	4	3.5	7.2
FC703	19991017	3.4	27	47	30.6	43.4

¹Disease Index is based on a scale of 0 (=healthy) to 7 (= plant dead).

²Percent of healthy roots (disease classes 0 and 1 combined).

³Percent of diseased roots likely to be taken for processing (disease classes 0 through 3 combined).

⁴Percentages were transformed to arcsine-square roots to normalize the data for analyzes.

FINAL REPORT ON BSDF PROJECT 441 CERCOSPORA LEAF SPOT RESEARCH AND BREEDING FOR CERCOSPORA AND CURLY TOP RESISTANCE

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2005 Field Research on Cercospora Leaf Spot of Sugar Beet

The breeding program in Fort Collins has created an annual artificial epiphytotic through inoculation with *Cercospora beticola* for over forty years. This epiphytotic has been used to evaluate and select for resistance to leaf spot caused by *C. beticola*. We have been pleased to participate in and lead this cooperative research project between the ARS, Colorado State University, and the BSDF. Because of the difficulty in getting good epiphytotics in our semi-arid climate, we are working with Mitch McGrath to relocate the Cercospora screening nursery to Michigan this summer (2006).

This year we lost the nursery in Akron, due to herbicide carry over from previous crops. The results for some of the experiments in Yuma, CO are included, but they were marginal at best, with significant differences in some of the experiments but not enough spread between resistant and susceptible genotypes to get good separation in others. Yuma, in 2005, had high temperatures, and Cercospora was late to develop. We did not have conditions conducive to Cercospora leaf spot development until late August and started rating in September. Four ratings were taken in September, but disease was not particularly high. The highest rating in the Cercospora field was a 6 (scale of 0-10).

Cercospora/Curly Top-Resistant Populations with Resistance to Multiple Sugar Beet Diseases and Superior Agronomic Characteristics

Germplasm under Development:

Cercospora Leaf Spot/Curly Top Resistant (LSR/CTR) Breeding Populations Currently Under Development.

FC301 population and sib lines

- 6) Cercospora leaf spot and curly top resistant monogerm base population from a polycross of FC607 and FC604 with two Salinas germplasms 2859 and 2890 (**Tested in Salinas as FC123**).
- a) 2890 (sp) = 0790 *mm aa* x 1890 (Salinas); is seed from *aa* plants open pollinated by A-plants. 0790 = population-790 cycle 5 synthetic by S₁ progeny, *aa*, *mm*, O-type, good combining ability, adapted to California, S^f. 1890 = BC population to population 790 to get Rz equivalent, remains variable for M-:*mm*, Rz-:*rzrz*, etc.

- b) 2859 m (sp) = 1859, 1859R aa x A- (Salinas); Released in 1992 as C859. S^f, similar to 2890, but should have higher curly top resistance. Segregates and variable for M-:mm, Rz-:rzz, A-:aa, predominant background is lines like C563.
- 7) Cercospora leaf spot and curly top resistant multigerm base population from a polycross of FC902 with two Salinas germplasms 278 and 4918.
 - a) 278 (Iso 83) = RZM R078; R278 is Rz (segregates Rz-:rzz) version of C46. It should be S^sS^s, MM.
 - b) 4918 (sp) = RZM 3918aa X A-, 142 aa plants; This is an increase of released material C918. It should be Multigerm, over 75% S^f and segregating for A-, R-, Rz-, VY, CT, Erw, & PM.
- 8) 20021037; (Best FC LSR x Best EL LSR) x CR011 (Salinas LSR/RhzmR) [(20011001 x 2001A031)blk F₂] – tested in Salinas as 04-FC1037
 - a) Salinas CR9110 = more broad based rhizomania and leaf spot resistant population, will segregate A- and S^f-
 - b) 20011001 = (Best Fort Collins leaf spot resistant x Best East Lansing leaf spot resistant), population cross and bulk made using hypocotyl color
- 9) 20021038; (Best FC LSR and EL LSR) x CR910 – [(20011001 x 2001A032)blk F₂] – tested in Salinas as 04-FC1038.
 - a) Salinas CR910 = fairly inbred rhizomania and leaf spot resistant population, will segregate A- and S^f-
 - b) 20011001 = (Best Fort Collins leaf spot resistant x Best East Lansing leaf spot resistant), population cross and bulk made using hypocotyl color.
- 10) Seed from FC709-2 x FC907 was sent to Larry Campbell at Fargo to cross to Sugar beet root maggot resistant germplasm to develop a population that will produce pollinators with resistance to Rhizoctonia, Cercospora, and Root maggot.

Progress in 2005

We were unable to obtain good data on advanced breeding lines of *Cercospora* resistant germplasms in the ARS leaf spot nursery at Yuma. These lines will be replanted this year, either in Fort Collins, Shakopee, or East Lansing. They are part of the resistant germplasm development effort in which a new germplasm should be released from the "pipeline" every two to four years. The above populations currently are in different stages of development.

- 1) FC301 was released from this population; other selections from ½ sib progeny rows based on combined leaf spot and curly top resistance (FC607&FC604/2859&2890) of the monogerm (FC123mm) and multigerm (FC123MM) population were planted in the 2003 mother root nursery for increase. Material sent to Salinas, CA and showed good rhizomania resistance and progeny families have been selected sucrose. Sib-lines to FC301 that have undergone reselection for resistance to Cercospora leaf spot are being increased for release in 2006 or 2007. Selected material from Salinas has been returned to Fort Collins for evaluation, crossing and selection (see table in 440 report).

- 2) Plants (F₂) from the CTR/LSR multigerm cross (2 above – FC902/278/4918) were tested for resistance to Rhizoctonia and Cercospora and recombined.

Variety and/or description						
20041013-xhs – EL & FC LSR polycross – monogerm				MEANS		
Seed Number	Plot No.	Plot No.	Entry No.	9/14/05	9/21/05	9/28/05
20041013-14	2474	2672	544	0.5	1.0	1.0
20041013-20	2478	2676	548	1.0	1.0	1.0
20041013-3	2487	2685	557	0.5	1.0	1.5
20041013-48	2502	2700	572	0.5	1.0	1.5
20041013-62	2511	2709	581	1.0	1.0	1.0
20041013-68	2518	2716	588	1.0	1.5	1.5
20041013-75	2525	2723	595	1.0	1.0	1.5

- 3) Seed of 04-FC1037 was received from R.T. Lewellen in Salinas after selection for sucrose and rhizomania and will be evaluated for Cercospora resistance. Half-sib families of (Best FC LSR x Best EL LSR) were grown in the cercospora nursery and selections were made and recombined for further testing (see table).
- 4) Seed of 04-FC1038 was received from R.T. Lewellen in Salinas after selection for sucrose and rhizomania and will be evaluated for Cercospora resistance.
- 5) Seed from (FC709-2 x FC907)F₂ has been sent to Larry Campbell at Fargo to cross to Sugar beet root maggot resistant germplasm and be selected for Cercospora resistance. Sib lines were selected this year for Cercospora resistance and recombined. The seed is being sent to Fargo for root maggot screening. The resulting population will provide pollinators with resistance to Rhizoctonia root rot and the sugar beet root maggot.

2005 LEAF SPOT FIELD PLANTING PLAN

Experiment 7A, 2005

Selections from Cercospora Nursery in Yuma, CO

20041014-xhs – EL & FC LSR polycross – multiger				MEANS		
Seed Number	Plot No.	Plot No.	Entry No.	9/14/05	9/21/05	9/28/05
20041014-01	2556	2754	626	0.5	2.0	1.5
20041014-07	2563	2761	633	1.0	1.0	1.0
20041014-17	2572	2770	642	1.0	1.0	1.0
20041014-21	2576	2774	646	1.0	1.5	1.0
20041014-38	2592	2790	662	1.0	1.5	1.0
20041014-54	2607	2805	677	1.5	1.5	1.0
20041014-57	2610	2808	680	1.0	1.0	2.0
20041014-62	2614	2812	684	1.0	1.0	1.5
20041014-71	2625	2823	695	1.5	1.0	1.5
20041014-74	2628	2826	698	1.0	1.0	2.0

2005 Curly Top Nursery in Kimberly, ID- USDA-ARS Plant Introductions						
Entry	Seed	ID			23-Aug	13-Sep
						p
					LSD _{0.05} CV	ns 16.1
31	1996A008	Beta G6040	<i>vulgaris</i>	Resistant Check		
1	Ames 4436		<i>maritima</i>		annual	
4	PI 504184		<i>maritima</i>	Italy	annual	
20	PI 518433	IDBBNR 5927	<i>maritima</i>	UK, England	annual	
8	PI 504200		<i>maritima</i>	Italy	annual	
21	PI 540566	WB 817	<i>maritima</i>	France	annual	
17	PI 504253		<i>maritima</i>	Italy	annual	
19	PI 518304	IDBBNR 5798	<i>maritima</i>	UK, England	annual	
2	PI 504182		<i>maritima</i>	Italy	annual	
3	PI 504183		<i>maritima</i>	Italy	annual	
15	PI 504238		<i>maritima</i>	Italy	annual	
12	PI 504223		<i>maritima</i>	Italy	annual	
14	PI 504237		<i>maritima</i>	Italy	annual	
7	PI 504197		<i>maritima</i>	Italy	annual	
18	PI 504264		<i>maritima</i>	Italy	annual	
13	PI 504235		<i>maritima</i>	Italy	annual	
10	PI 504213		<i>maritima</i>	Italy	annual	
9	PI 504202		<i>maritima</i>	Italy	annual	
16	PI 504239		<i>maritima</i>	Italy	annual	
11	PI 504220		<i>maritima</i>	Italy	annual	
29	PI 562601	IDBBNR 9750	<i>maritima</i>	Egypt, Matruh	annual	
22	PI 540632	WB886	<i>maritima</i>	UK, England	annual	
23	PI 546403	IDBBNR 5600	<i>maritima</i>	UK, England	annual	
28	PI 562600	IDBBNR 9749	<i>maritima</i>	Egypt, Matruh	annual	
27	PI 562591	IDBBNR 9742	<i>maritima</i>	Egypt, Matruh	annual	
25	PI 546508	IDBBNR 9687	<i>maritima</i>	Greece,	annual	
5	PI 504190		<i>maritima</i>	Italy	annual	
6	PI 504193		<i>maritima</i>	Italy	annual	
30	PI 562604	IDBBNR 9753	<i>maritima</i>	Egypt, Matruh	annual	
32	19911032	FC718	<i>vulgaris</i>	Suscep. check		
24	PI 546508	IDBBNR 9675	<i>maritima</i>	Greece	annual	
26	PI 562586	IDBBNR 9737	<i>maritima</i>	Egypt, Matruh	annual	

Experiment 4A, 2005. Leaf Spot Evaluation of USDA-ARS Salinas contributed lines.					
Entry	Identification	Disease Index ¹			
		September 14th	September 21st	September 28th	
	LSD _{0.05}	1.25	1.47	1.07	
449	LSS ² (931002)	3.0	3.0	4.0	
450	LSR ³ (821051H2)	1.0	1.8	3.3	
Trial Mean		1.9	2.5	3.2	
421	Monohikari	2.7	3.0	4.3	

Experiment 4A, 2005. Leaf Spot Evaluation of USDA-ARS Salinas contributed lines.

Entry	Identification	Disease Index ¹		
		September 14th	September 21st	September 28th
	LSD _{0.05}	1.25	1.47	1.07
449	LSS ² (931002)	3.0	3.0	4.0
450	LSR ³ (821051H2)	1.0	1.8	3.3
Trial Mean		1.9	2.5	3.2
422	Beta 4430R	5.0	5.8	6.3
423	03-SP 22-0	1.7	2.3	2.7
424	Y 475	2.3	3.2	3.7
425	R 421	3.3	3.5	3.7
426	Z 425	1.7	2.7	4.2
427	4 931	2.0	3.2	4.0
428	4 941	2.7	4.3	4.3
429	CR 411	1.7	2.7	2.7
430	N 412(sp)	1.7	2.2	2.7
431	N 472(sp)	2.2	2.7	3.0
432	04- FC1028	1.3	2.0	3.0
433	04- FC1037	1.3	2.0	2.7
434	04- FC1038	1.3	1.3	3.0
435	4951 -210	1.5	2.0	2.3
436	03-FC 1030-15	1.8	2.7	3.7
437	03-FC 1030-16	2.0	2.0	2.8
438	CR410 -203	1.7	2.0	2.7
439	4933 -14	1.0	2.0	2.0
440	4933 -14H50	2.3	2.7	3.3
441	CR410 -231	1.0	2.0	2.7
442	CR412 -211	2.5	3.0	4.3
443	CR412 -5	2.2	3.0	3.2
444	CR311 -88	1.7	1.7	3.0
445	CR311 -6	1.3	1.5	2.0
446	CR311 -41	1.3	1.7	2.3
447	03-F1014 -22	1.3	2.0	2.3
448	03-FC123 -31	1.3	2.0	3.0

¹ Disease Index is based on a scale of 0 (=healthy) to 10 (=dead).

² The Leafspot Susceptible Check is SP351069-0.

³ The Leafspot Resistant Check is ((FC504CMS x FC502/2) x SP6322-0).

Means and LSD values were calculated with missing data. Lines 335, 340, and 342 were two reps rather than three.

LSD and experimental mean values also were calculated with an additional nine entries

Experiment 6A, 2005. Leaf Spot Evaluation of USDA-ARS Fargo, ND contributed lines.

Entry	Identification	Disease Index ¹			
		September 7th	September 14th	September 21st	September 28th
	LSD _{0.05}	0.79	N.S.	N.S.	1.28
532	LSS ² (941027)	1.5	1.7	3.7	4.0
533	LSR ³ (821051H2)	0.8	1.2	1.5	1.8

Trial Mean		0.8	1.3	1.9	2.5
521	01 N0060	0.5	1.2	2.3	2.0
522	99 N0043	1.0	1.0	2.2	2.8
523	97 N0035	0.3	1.0	1.3	2.0
524	03 N0039	0.5	1.3	1.8	2.7
525	02 N0024	1.5	1.3	2.0	2.0
526	03 N0030	0.3	1.2	1.2	2.3
527	03 N0032	0.8	1.0	1.7	3.5
528	03 N0033	0.7	1.3	1.7	2.0
529	03 N0036	1.0	1.5	1.8	2.7
530	03 N0105	0.7	1.3	2.0	2.0
531	03 N0106	1.3	1.7	1.7	2.5
¹ Disease Index is based on a scale of 0 (=healthy) to 10 (=dead).					
² The Leafspot Susceptible Check is SP351069-0.					
³ The Leafspot Resistant Check is ((FC504CMS x FC502/2) x SP6322-0).					
N.S. - not significantly different, $\alpha=0.05$					

FINAL REPORT FOR BSDF PROJECT 443
PRE-BREEDING: THE INTROGRESSION OF NEW SOURCES
OF CERCOSPORA LEAF SPOT RESISTANCE FROM *BETA*
***VULGARIS* SSP. *MARITIMA* AND OTHER EXOTIC SOURCES**
INTO SUGAR BEET-TYPE POPULATIONS

L. Panella
USDA-ARS, Fort Collins, Colorado

Research Progress 2005

We are working with the eighteen populations listed below (Table) and have increased or made crosses in these populations. All of the male parents are germplasm that have been identified as having resistance to *Cercospora beticola* (causal agent of Cercospora leaf spot). The female parents are from a population developed to have high sucrose yield potential. These sucrose populations are based on old commercial varieties – i.e., MonoHy T6, A7, A4 and breeding lines from American Crystal Sugar Co. and Seedex, Inc. – and USDA-ARS developed germplasm such as L-19 (WC9127OM) and East Lansing smooth root germplasm, SR87. Other parents include high sucrose germplasm from Poland and other Eastern European countries. Salinas parent '3859' was used to produce populations that are self-fertile (S^f) and segregating for nuclear male sterility ($A:-aa$). The families from various crosses are in different stages of development and evaluation. At the F_3 stage, when sufficient seed is available, we are beginning field screening and selection. Seed of these families has been bulk increased and is beginning to be evaluated. All of the early generation populations show some annual plants in our environment.

We are re-crossing some of those from which we obtained insufficient F_1 seed. Plants from those populations producing some biennial plants are being vernalized for 90 days and the populations are being increased (i.e., random mated using the genetic male sterility where possible). The annuals will be handled in a similar fashion once the F_1 populations have been increased. All will be cycled through at least three cycles of random mating.

Half-sib progeny families were created for 20051002, 20051003, 20051004 and 20051005. These families will be selected in an artificial epiphytotic this summer and recombined and tested for release in 2007. 20051001 and 20051006 were planted in the mother root nursery in 2005 and bulk increased. They will be replanted in the 2006 mother root nursery to produce roots for half-sib family selection. The seed sources of these lines will be planted in both the Cercospora nursery (either in Fort Collins, East Lansing or Shakopee) and curly top nursery. Those lines in the shaded areas of the table below will be increased in either the greenhouse or mother root nursery.

Table 3. List of germplasm used in developing *Cercospora* leaf spot resistant populations and the stage of each of the populations. Those populations highlighted in yellow have been increased in 2004 and those in green in 2005 and those in green will be increased in 2005.

♀ parent	Donor (σ) Designation	Name or Origin (σ)	% Bolting (σ) no induction 1996 FC, CO	F ₁ Population	F ₂ Population	F ₃ Population	F ₄ Population	F ₅ Population	F ₆ Population
961005	PI 535826	Giant Poly	20%	971021H2	981031	991026	20011027MS	20031013	<u>20051002</u>
961005 19991024H2	PI 535833	Saturn	0%	---					
				20031001H2					
961005	PI 540593	WB 847	0%	971023H2	20021026	<u>20051001</u>			
961005	PI 540596	WB 850	70%	971024H2	981032	20011002bbPF 20011002bbMS 20011002B-	<u>20051004</u>		
961005	PI 540605	WB 859	25%	971025H2	20011054	20031014	<u>20051005</u>		
961005	PI 535843	PN MONO 1	100%	971026H2 ¹					
961005	PI 540575	WB 829	100%	971027H2 ²					
961005	PI 540599	WB 853	50%	971028H2	981033	20011045bbPF 20011045bbMS	<u>20051003</u>		
961005	BGRC #32375 (<i>B. v. maritima</i>)	Greece	annual	971029H2	20011036				
961005	BGRC #36538 (<i>B. v. maritima</i>)	Greece	annual	971030H2 ³	20011037				
851046HO	BGRC #45511 (<i>B. v. maritima</i>)	Greece	annual	981001H3	20011038B_ 20011038bb	shelved – use 20051006			
961005 19991024H2	BGRC #45511 (<i>B. v. maritima</i>)	Greece	annual	---	20021036B_ 20021036bb	<u>20051006</u>			
851046HO	BGRC #45516 (<i>B. v. maritima</i>)	Greece	annual	981002H3	20011039B_ 20011039bbPF 20011039bbMS				

Table 3. List of germplasm used in developing Cercospora leaf spot resistant populations and the stage of each of the populations. Those populations highlighted in yellow have been increased in 2004 and those in green will be increased in 2005.

♀ parent	Donor (♂) Designation	Name or Origin (♂)	% Bolting (♂) no induction 1996 FC, CO	F ₁ Population	F ₂ Population	F ₃ Population	F ₄ Population	F ₅ Population	F ₆ Population
961005 19991024H2	BGRC #45516 (<i>B. v. maritima</i>)	Greece	annual	---	20021033H2				
961005	BGRC #48810 (<i>B. v. maritima</i>)	Tunisia	annual	19981003H2	20011040B_ 20011040bb	20021030B_ 20021030bb	20031038bb		
851046HO	BGRC #48810 (<i>B. v. maritima</i>)	Tunisia	annual	981003H3	200110141B_ 200110141bb				
961005	BGRC #48819 (<i>B. v. maritima</i>)	Tunisia	annual	981004H2	20011042B_ 20011042bb	20021031B_ 20021031bb	20031039B_ 20031039bb		
961005 19991024H2	BGRC #48819 (<i>B. v. maritima</i>)	Tunisia	annual	---					
961005 19991024H2	BGRC #51430 (<i>B. v. maritima</i>)	Greece	annual	20021034H2					
961005 19991024H2	BGRC #51430 (<i>B. v. maritima</i>)	Greece	annual	---	20021035H2				
¹ Only 16 seed balls produced. ² Only 10 seed balls produced. ³ Only 60 seed balls produced. Light shading into GH/mother root nursery in 2006/07 Underlined seed productions produced in 2005 – into testing in 2006.									

BSDF PROJECT 446 -CHANGES IN SUGARBEET GENE EXPRESSION FOLLOWING CHALLENGE BY *CERCOSPORA BETICOLA*

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Justification for Research:

Cercospora leaf spot (CLS), caused by the fungus *Cercospora beticola* Sacc., is the most widespread foliar disease of sugar beet, and is a serious problem in many sugar beet production areas throughout the U.S. and world-wide. Disease-tolerant germplasm has been developed over the last 50 years by the USDA-ARS Sugarbeet Research Unit at Fort Collins, CO, and by public and private plant breeders at other locations. The identification of this germplasm requires an extensive field screening program with a corresponding commitment of time and labor. However, there is substantial variability in results, with an estimated 44 to 62% of the variability due to environmental factors. An effective method of marker-assisted selection, which could decrease the extensive field work to identify resistant lines, would be extremely beneficial, if also cost-effective.

Summary of Literature Review:

The mode of resistance in sugarbeet to CLS has been difficult to elucidate. Smith and Gaskill (1970) estimated that 4 or 5 major genes were responsible for CLS resistance, and, more recently, Schafer-Pregl *et al.* (1999) and Nilsson *et al.* (1999) estimated similar numbers of major genes using QTL mapping for resistance to *C. beticola* in sugarbeet. But due to the low heritability and difficulty in generating mapping populations in sugar beet, marker assisted selection has not been developed into a useful breeding technology to select for CLS resistance. The best markers of CLS resistance would be those genes activated by the disease defense response of the sugar beet plant.

Rapid alterations in gene expression are associated with defense response induction. Identification of host genes involved in defense responses is one of the most critical steps in the elucidation of disease resistance mechanisms in plants. Suppressive subtractive hybridization (SSH) will be employed to determine which genes are specifically expressed during defense in sugar beet against CLS. In this method, "driver" RNA, representing uninfected tissue, is physically subtracted from "tester" RNA, representing infected tissue, leaving only the mRNA which is unique to the plant after challenge by the fungus and, in much smaller quantities, from the fungus itself. Subtractive hybridization may utilize a normalization step as well as an enrichment step for differentially expressed transcripts (Diatchenko, 1996). As part of the subtractive hybridization procedure, this messenger RNA is converted to cDNA which is transformed into *E. coli* to create an expression library. SSH makes it possible to identify both highly expressed and low abundance genes related to defense. Additionally, all sequences found to be induced, regardless of known function, can be evaluated for use as biomarkers in marker-assisted selection.

SSH has been employed to identify a wide array of physiological conditions. Plant defense in rice (Lu *et al.*, 2004), cocoa (Verica *et al.*, 2004), wheat (Kong *et al.*, 2005) and *Arabidopsis* (Mahalingam *et al.*, 2003) have been characterized with this technique. SSH has effectively been applied to examine to sugar beet defense against root maggot (Puthoff and Smigocki, 2006). Most SSH analyses of plant defense have shown a majority of induced sequence are defense response-related proteins and antioxidants (Meng *et al.*, 2002; Ryang *et al.*, 2002). Gingras and Margolin (2000) used the results of SSH to develop six molecular markers for cell differentiation

and Quan and Lu (2003) identified two sequences that appear to function as tumor suppressors for breast cancer. Both situations demonstrate downstream applications of SSH results: molecular marker identification and greater understanding of cellular processes.

Long-term Objectives:

1. Determine gene expression associated with resistance using *C. beticola* challenged and mock-inoculated germplasm [(FC504CMS X FC502/2) X SP6322-0, MM].
2. Determine what genes are induced in CLS susceptible germplasm (FC403) following successful infection by *C. beticola*.
3. Characterize a subset of induced genes for use as biomarkers in marker-assisted selection.

Materials and Methods:

Plant treatment.

Plants (FC403, susceptible) will be maintained in glasshouses at $22 \pm 5^\circ\text{C}$, watered daily and kept under 16 h of daylight to maintain vigorous growth. At six weeks post emergence, beets will be inoculated with *C. beticola* (isolate HC-13 – from Gary Franc, U of WY) by spraying a spore suspension of 1×10^5 conidia ml^{-1} in distilled water. A mock inoculation will consist of spraying distilled water onto the plant leaf surface. All inoculations will include 10 plants per treatment. Following inoculation, plants will be transferred to growth chambers and maintained at 22°C , 95% relative humidity, for 72 hours to promote infection. At 72 hours the leaves from each treatment will be independently harvested and pooled before grinding in liquid nitrogen in preparation for RNA extraction.

Suppressive Subtractive Hybridization. RNA will be extracted using RNeasy™ kit (Qiagen, Valencia, CA) what kit and SSH will be performed using previously employed methods from the Panella lab using a subtractive hybridization kit (Clontech, Mountain View ,CA).

Long term storage and PCR. All *E. coli* bacterial colonies harboring plasmids representing individual expressed gene products derived from the SSH procedure will be prepared for long term storage. Each colony will be transferred to an individual well in a 96-well plate containing LB and $100 \mu\text{g ml}^{-1}$ carbenicillin for positive selection. Following an overnight incubation at 37°C (with rigorous shaking), the well contents will be diluted 1:1 with sterile 10% glycerol. In preparation for PCR, each plate will be replicated and fresh overnight cultures prepared. The fresh cultures will serve as template for the amplification of the sugarbeet gene sequence contained within each plasmid. The purity and concentration of the resultant PCR product will be verified by agarose electrophoresis. MacroGen USA (Rockville, MD) will do all sequencing.

Data analysis: Induced sequences will be identified by BLAST comparison using the *Beta vulgaris* gene index (TIGR database) and homology-based searches in NCBI. Identified genes will be classified according to physiological function. Comparisons between results from susceptibility- and resistance-associated gene sequences will be performed to identify spurious gene expression and genotypic differences between the germplasm.

Biomarker selection: Following SSH analysis, genes will be analyzed for use as biomarkers for marker-assisted selection. Genes will be selected based on the following criteria: 1) low copy

number gene (i.e. not a member of a large gene family with many alleles), 2) biologically relevant to resistance, and 3) overlap with resistance responses to other pathogens. Low copy number will ensure there is no cross-reactivity with biologically unassociated alleles. Biological relevance will increase the likelihood of reliably and reproducibly detecting expression differences between resistant and susceptible populations. Lastly, overlap with other resistance responses may identify molecular markers for use in breeding against more than one major pathogen.

Copy number will be determined by Southern blotting. Total DNA will be extracted using a DNeasy DNA extraction kit (Qiagen, Valencia, CA), then quantified spectrophotometrically (A_{260}/A_{280}). Approximately 10 µg of each DNA will be digested with appropriate restriction enzymes. The restriction fragments will be separated by agarose gel electrophoresis then transferred onto a positively charged nylon membrane (Roche, Indianapolis, IN). Hybridization will be carried out using a DIG-labeled (Roche, Indianapolis, IN) PCR product probe. The immunological detection will be performed using the CDP Star (ready to use, Roche).

Once the gene copy number has been determined, for those gene that are single copy, qualitative RT-PCR will be performed to determine relative expression in resistant and susceptible germplasm. RNA will be extracted at 0, 6, 12, 24, 48, 72, and 96 hours post *C. beticola* inoculation using an RNeasy extraction kit (Qiagen, Valencia, CA). The RNA will be quantified spectrophotometrically then standardized concentrations will be used as template in RT-PCR using an OneStep RT-PCR kit (Qiagen, Valencia, CA). Relative abundance of each transcript will be visualized following separation by agarose gel electrophoresis.

Progress to date

With BSDF support, significant progress has been made characterizing gene expression unique to CLS resistance, showing similar results to other SSH studies of plant defense (Table below).

SSH results: *C.beticola* infected CLS resistant germplasm

Gene Identification	Accession #	# of clones
Resistance-related		
jacalin lectin	gi 0686497	1
jacalin lectin	gi 1170595	1
auxin-induced SAUR-like protein	gi 20149052	1
catalase 2	gi 22656382	1
Drm3	gi 2688824	1
mevalonate kinase-like protein	gi 28558789	1
auxin-induced beta-glucosidase	gi 32481073	1
resistance protein candidate	gi 38045738	1
glycerol kinase	gi 40457263	1
Putative pathogenesis-related protein	gi 45124837	1
unkn. Protein, jacalin -like lectin domain	gi 50932275	1
flavanone 3-hydroxylase	gi 54306626	1
glucosyltransferase	gi 5918023	1
myo-inositol-1-phosphatase synthase	gi 84468400	1
Disease resistance protein; Heat shock protein	gi 92887648	1
Stress Related		
S-adenosylmethionine decarboxylase	gi 1155242	1
salt tolerance protein 4 (B. vulgaris)	gi 30524687	1
salt-induced protein	gi 31879434	10
UVB repressible protein	gi 33520421	1
adenosylmethionine decarboxylase	gi 547472	1
Ntdin, senescence assoc protein	gi 7594903	1
lipid binding protein	gi 79495992	1
Regulation of gene expression and protein modification		
homolog to 26s ribosomal RNA	gi AF223066	1
RPS15AB; structural constituent (ribosomal)	gi 15224834	1
ATHB-12; transcription factor	gi 15228625	1
ATPG4 ubiquitin domain Arabidopsis	gi 15234839	1
Bare-1 retrotransposon	gi 2598547	1
pol protein	gi 28558781	1
translation initiation factor	gi 30696543	1
polyubiquitin	gi 3126967	1
ATGP4 Arabidopsis	gi 4097567	1
Yabby-like transcription factor	gi 41745642	1
ubiquitin-conjugating enzyme family	gi 46577794	1
zinc finger	gi 51535585	1
zinc finger-like protein	gi 53791927	1
polyubiquitin	gi 602076	1
Cys2/His2 zinc-finger transcription	gi 63259075	1
splicing factor Prp8	gi 71534916	1
DNA-directed RNA polymerase	gi 81501	1
peptide chain release factor	gi 83283955	1
rRNA intron-encoded endonuclease	gi 13171103	1

SSH results: *C.betica* infected CLS resistant germplasm

Gene Identification	Accession #	# of clones
zinc finger	gi 92894858	1
Primary metabolism and respiration		
phosphoribosylaminoimidazolecarboxamide formyltransferase	gi 11878280	1
nitrate reductase	gi 128198	1
o-acetyl transferase related protein	gi 15026102	1
DNA binding	gi 15223502	1
calmodulin binding [Arabidopsis	gi 15226852	1
UXS5; catalytic (Arabidopsis)	gi 15231432	1
Formate--tetrahydrofolate ligase	gi 2507455	2
NADP-dependent glyceraldehydephosphate dehydrogenase	gi 2529370	1
3-hydroxyisobutyl-coenzyme A	gi 30679729	1
oxidoreductase (Arabidopsis)	gi 30695050	1
serine decarboxylase	gi 4996105	1
UDP-D-glucuronate decarboxylase	gi 50659026	1
copper amine oxidase	gi 50922251	1
flavonol 6-hydroxylase	gi 51475558	2
protein/phosphatidylethanol--	gi 62149620	1
putative NADPH-cytochrome P450 reductase	gi 6503253	1
carboxyphosphoenolpyruvate	gi 6831519	1
pyruvate kinase	gi 73811195	1
fructokinase 2-like protein/constans protein	gi 76160970	1
ycf5 protein	gi 7636161	1
NADH dehydrogenase ND1 subunit	gi 7636167	1
ATP synthase	gi 11497510	1
Cell wall modification		
cinnamoyl coA reductase	gi 25140436	1
triacylglycerol lipase	gi 30679836	1
Pectinacetylesterase	gi 87241323	1
WAX2	gi 30696940	1
Membrane proteins/receptors		
pto-like kinase	gi 14010487	1
permease/ transporter	gi 18399065	1
ATP binding	gi 18416540	1
ethylene responsive transcription factor	gi 21553721	1
ATP binding/adenylate kinase	gi 22327339	1
hydrolase/protein serine/threonine	gi 22331208	1
vacuolar membrane protein	gi 23197608	1
C2 domain containing protein	gi 25412005	1
Ki1 protein (B. vulgaris)	gi 29824930	1
ATP binding	gi 30681308	1
membrane protein	gi 6996562	1
G-protein; guanyl nucleotide binding	gi 7270389	1
ids-4 protein, signal trans.	gi 7671502	1

SSH results: *C.beticola* infected CLS resistant germplasm

Gene Identification	Accession #	# of clones
NTK-1 --like;ser/thr protein kinase)	gi 62857014	1
Disease resistance protein; NBS-LRR	gi 92887648	1
Photosynthesis		
photosystem II CP43	gi 108802639	2
photosystem II M protein	gi 109156586	3
Photosystem I reaction centre subunit	gi 92876000	1
photosystem I subunit VIII	gi 94502501	1
magnesium chelatase	gi14861035	1
light harvesting protein	gi 309673	1
photosystem II M protein	gi 42795478	1
PsaB, photosystem I apoprotein	gi 56122494	1
phytoene synthase	gi 56122551	1
photosystem I P700 apoprotein	gi 5738994	6
photosystem I P700 apoprotein	gi 11497524	1
photosystem I P700 apoprotein	gi 32480842	1
dihydroxyacid dehydratase	gi 14532594	1
Oxidative Response		
thioredoxin	gi 18159032	1
thioredoxin H1	gi 33621082	1
thioredoxin	gi 308906	1
maganese superoxide dismutase	gi 33186704	1
oxygen evolving complex	gi 9229957	1
Cell growth and development		
microtubule assoc protein	gi 21615419	1
actin	gi 34541966	1
profilin (actin-binding protein)	gi 57021112	1
cell cycle control protein	gi 92872088	1
CENP-C	gi 51477411	1
Hypothetical Proteins		
unknown protein	gi 109130369	1
hypothetical protein	gi 12324282	1
hypothetical protein	gi 13544020	1
unknown protein	gi 15228878	2
conserved hypo. protein	gi 15234570	1
hypothetical protein	gi 15236949	2
hypothetical protein	gi 16660290	1
putative protein	gi 17473759	1
predicted protein	gi 18402409	2
unknown protein (Arabidopsis)	gi 18415091	1
Hypothetical protein (poss same as C10)	gi 20259856	1
unknown protein rice	gi 23307431	1
unknown protein rice	gi 29367513	1
unknown protein (Arabidopsis)	gi 30682825	1

SSH results: *C.beticola* infected CLS resistant germplasm

Gene Identification	Accession #	# of clones
unknown protein [Arabidopsis]	gi 30696086	1
unknown protein Arabidopsis	gi 39585444	1
At1g78800	gi 50058919	1
unknown protein	gi 50924111	1
unknown protein [Arabidopsis]	gi 50937813	1
unknown protein [Arabidopsis thaliana] >...	gi 53850559	1
unknown protein rice	gi 72004298	1
unknown protein	gi 76155239	1
hypothetical protein rice	gi 7630051	1
putative protein	gi 88183399	1
unknown protein (Arabidopsis)	gi 88186114	1
Hypothetical protein	gi 92868431	1
At5g27860 (Medicago)	gi 92895847	1

The induced sequences have been categorized according to predicted protein function. The resistance-related proteins include pathogenesis-related proteins such as β -glucanase, that has antifungal activity (Zareie *et al.*, 2002). Drm3 is a DNA methyltransferase induced in *Arabidopsis* upon viroid infection (Cao and Jacobsen, 2002). Lastly, jacalin lectins recognize foreign glycans from invading microorganisms during defense (Jiang *et al.*, 2006). Of the stress-related proteins induced, most were associated with salt stress, including adenosylmethionine decarboxylase which is also induced during cold stress (Hao *et al.*, 2005). A fair number of genes pertaining to oxidative stress, such as superoxide dismutase, thioredoxin, and the oxygen evolving complex were all induced. Since *Cercospora beticola* produces free radical-generating toxins (Daub and Ehrenshaft, 2000), these oxidative stress-related proteins could function in the oxidative burst, the earliest response of defense induction, or in free radical scavenging as a mode of defense. Others have found over expression of superoxide dismutase in sugar beet confers greater resistance to *C. beticola* (Tertivanidis *et al.*, 2004). Modifiers of proteins, transcription factors and peptide chain release factors were all classified as being involved in the regulation of gene expression and protein modification. Ubiquitin and its associated proteins all are involved in protein turnover, but also play a major role in plant defense (Takai *et al.*, 2002; Gonzalez-Lamothe *et al.*, 2006). Several proteins associated with normal growth and developmental processes, such as primary and secondary metabolism, respiration, photosynthesis and the cell cycle have changes in expression following pathogen inoculation suggesting a shift in resources within the plant. Cell wall modifying proteins, including those involved in cell strengthening were induced in resistant sugarbeet germplasm with *C. beticola* inoculation suggesting changes in cell wall structure during defense. This is not uncommon since physical barriers are crucial in fungal defense (Vogel *et al.*, 2004). Lastly, since many gene products have not been annotated with regards to function, a large number of significant matches were for hypothetical or predicted proteins. These genes are usually not characterized in a biological format, but rather predicted using computer algorithms that look for start and stop codons within genomic sequence. One benefit of a screen like SSH, is that gene function does not have to be known in order to use a sequence as a molecular marker. Downstream analyses may also provide clues regarding the function of these genes.

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BSDF PROJECT 903 - EVALUATION OF CONTRIBUTED LINES FOR RESISTANCE TO *RHIZOCTONIA SOLANI*, A CAUSAL FUNGUS OF SUGAR BEET ROOT ROT

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Annually, for over thirty years, the sugar beet program in Fort Collins has included the production of an artificial epiphytotic through inoculation with *Rhizoctonia solani* to evaluate and select for resistance to *Rhizoctonia* root rot. We have been pleased to participate and lead this cooperative research project between the ARS, Colorado State University, and the BSDF.

In 2006 the project involved field studies conducted at the Crops Research Lab-Fort Collins Research Farm near Wellington, CO. Randomized, complete-block designs with five replicates were used to evaluate ARS breeding germplasm and Plant Introduction accessions. *Rhizoctonia*-resistant line FC703, highly resistant FC705-1, and susceptible FC901/C817 were included as internal controls. The field was treated with Telone II April 11.

One-row plots, planted May 24th, were 14 feet long with 22 inches between rows and 8-10 inches within-row spacing. The field was sprayed once with Betamix Progress, Upbeet, and Stinger (July 20) to control weeds. The field was thinned by hand and irrigated as necessary. Inoculation with dry, ground, barley-grain inoculum of *Rhizoctonia solani* AG2-2 isolate R-9 was performed on July 13th; immediately after inoculation, a cultivation was performed so as to throw soil into the beet crowns. Beets were harvested Sept. 19 through 21. Each root was rated for rot on a scale of 0 to 7 (dead) as previously described. ANOVAs were performed on disease indices (DIs), percent healthy roots (classes 0 and 1 combined), and percentage of roots in classes 0 thru 3. Percentages were transformed to arcsin-square roots to normalize the data for analyses. LSDs are provided for comparing entries with those of our internal checks.

The high daytime temperatures in the summer of 2005, combined with a moderate inoculum load, contributed to a mild root rot epidemic. Due to water restrictions, sprinkler irrigation could not be applied immediately after applying inoculum which reduced severity. In addition, timing of irrigation could not be regulated sufficiently to provide moderate water stress at desired intervals. Mild disease developed by mid-September. Mean DIs across all tests for highly resistant FC705-1, resistant FC703, and susceptible FC901/C817 controls were 1.7, 1.8, and 3.5 respectively. Mean DIs for these controls in 2005 were 2.7, 3.1 and 4.9 respectively. Percentages of healthy roots were 51.5, 43.7, and 21.3% for these controls. Percentages of roots in disease classes zero thru three were 97.4, 91.5, and 50.9% respectively. The highest and lowest DIs for the evaluated lines were 5.8 and 1.0, respectively.

Table 1. Summary data of the 2006 *Rhizoctonia* root rot nursery. The experiment mean, the mean of the susceptible check, the mean of the resistant check, and the mean of the highly resistant check are given for each of the experiments in the nursery. LSD is at the $t=0.05$ level.

Exp.	Disease Index					Percent Healthy (classes 0&1)					Percent in Classes 0 to 3				
	Mean	Sus.	Res.	H. Res.	LSD	Mean	Sus.	Res.	H. Res.	LSD	Mean	Sus.	Res.	H. Res.	LSD
1R	3.4	3.0	1.6	1.8	1.0	29.6	34.0	63.0	48.9	15.7	55.9	57.8	95.7	93.3	16.8
2R	4.1	3.2	1.7	1.6	1.6	8.9	17.4	40.3	52.1	16.8	49.8	54.5	98.5	100.0	29.8

Exp.	Disease Index					Percent Healthy (classes 0&1)					Percent in Classes 0 to 3				
	Mean	Sus.	Res.	H. Res.	LSD	Mean	Sus.	Res.	H. Res.	LSD	Mean	Sus.	Res.	H. Res.	LSD
3R	3.1	3.8	2.6	1.8	0.9	20.5	9.9	13.2	50.4	14.6	64.7	45.1	81.6	92.5	17.7
4R	2.9	3.7	1.0	1.1	1.2	53.9	32.7	96.3	93.8	17.8	66.4	45.9	100.0	98.6	18.8
5R	3.5	4.2	1.8	2.2	1.2	16.4	10.0	31.9	32.0	19.5	53.1	33.4	80.6	97.5	20.1
6R	3.4	3.3	1.8	1.8	1.4	28.8	34.5	50.5	52.2	16.0	56.6	59.3	91.5	96.7	23.1
7R	2.3	3.0	1.9	1.4	0.7	34.2	13.2	20.2	57.7	19.6	81.9	67.5	97.0	100.0	12.2
8R	3.4	4.3	2.2	1.6	1.2	18.2	18.1	35.4	45.0	19.2	55.6	34.5	83.5	100.0	22.6
11R	2.5	3.4	1.8	1.9	1.0	3.2	20.3	42.3	31.1	17.8	80.7	56.9	95.5	98.0	19.0

Percent in Classes is the transformed value (arcsin-square root)

Mean = Experiment Mean;

Sus. = Susceptible Check (FC901/C817);

H. Res. = Highly Resistant Check (FC703);

SUGARBEET RESEARCH

2006 Report

SECTION C

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**This research was supported in part by funds provided through
the Beet Sugar Development Foundation (Projects 650 and 660)**

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PUBLICATIONS

Abstract of Papers Presented or Published

Campbell, L.G., Klotz, K.L. 2006. Postharvest storage losses associated with *Aphanomyces* root rot in sugarbeet. *Journal of Sugar Beet Research*. 43:113-127.

Because of its persistence in the soil and the ineffectiveness of control measures, *Aphanomyces* root rot (caused by *Aphanomyces cochlidioides* Drechal.) is one of the more problematic fungal root rots attacking sugarbeet (*Beta vulgaris* L.). As the prevalence of *Aphanomyces* increases, the proportion of diseased roots placed in storage piles increases. This report provides guidance for determining the *Aphanomyces* root rot severity that would justify not harvesting a field or if roots from diseased fields should be processed early in the campaign. Roots from six commercial fields with chronic root rot problems were divided into groups based upon root rot severity. Prior to measuring storage respiration rate, sucrose concentration, and extractable sucrose concentration, a root rot index (0 = no rot to 100 = completely rotted) was determined for each sample. Regression analyses were used to characterize relationships among root rot index, postharvest respiration rate, and extractable sucrose losses during storage for 120 days. Below rot indices of 35, *Aphanomyces* had little, or no effect on respiration rate or extractable sucrose loss during storage. Sucrose losses associated with rot indices of 65 and 80 were 1.8 and 2.8 times those associated with a rot index of 35, respectively. *Aphanomyces* root rot has the potential to significantly increase losses during storage; however, field by *Aphanomyces* severity interactions and variability in the observed response patterns indicate that accurately predicting these losses prior to harvest will be difficult.

Haagenson, D.M., Klotz, K.L., Campbell, L.G., Khan, M.F. 2006. Relationships between root size and postharvest respiration rate. *Journal of Sugar Beet Research*. 43:129-144.

Sugarbeet root size is dependent on genetics, environmental conditions, and cultural factors. To evaluate the effect of root size on respiration rate and explore possible physiological mechanisms that regulate respiration in sugarbeet roots, the relationship of root mass, surface area, and the ratio of surface area to mass (specific surface area) with respiration rate and the relationship between surface area and total respiration were determined using three field-grown sugarbeet varieties. Root mass, surface area, and specific surface area were significantly associated to respiration rate by a sigmoidal relationship. The variation in respiration rate among KW 2249, VDH 46177, and Beta 4818 was best explained by root mass alone ($R^2 = 0.55, 0.40, \text{ and } 0.43$), or the specific surface area ($R^2 = 0.57, 0.34, \text{ and } 0.33$). For each variety, there was a critical root size above which size had little impact on respiration. Below this critical size, root respiration increased dramatically as root mass or surface area decreased. This critical beet size, determined by the inflection point was 0.68, 0.50, and 0.92 kg for KW 2249,

VDH 46177, and Beta 4818, respectively. Total respiration, i.e. respiration per beet, was linearly associated with surface area for KW 2249 ($R^2 = 0.70$) and VDH 46177 ($R^2 = 0.46$), but not for Beta 4818 ($R^2 = 0.11$). The relationships observed are consistent with the theories that root respiration occurs largely at the root surface and that root respiration is limited by gas diffusion through the bulky taproot. However, the low coefficient of determinations present in this study suggest other unknown physiological mechanisms may contribute to respiratory regulation.

Klotz, K.L., Finger, F.L., Anderson, M.C. 2006. Wounding increases glycolytic but not soluble sucrolytic activities in stored sugarbeet root. *Postharvest Biology and Technology*. 41:48-55.

The wounding of sugarbeet (*Beta vulgaris* L.) roots by harvesting and piling operations increases the demand for sucrolytic and glycolytic products for wound-healing processes. To determine if sucrolytic and glycolytic enzyme expression increases to meet this demand and to identify the enzymes that may be induced, the activities of the major sucrolytic enzymes and the major regulatory enzymes of the glycolytic pathway were determined in wounded and unwounded sugarbeet roots during thirteen days of storage at 10° C. Activities of the enzymes responsible for catalysis of the first two reactions of the glycolytic pathway, hexokinase, fructokinase and phosphofructokinase, were elevated in wounded roots. The sucrolytic enzymes, sucrose synthase, alkaline invertase, and soluble acid invertase, and the glycolytic enzyme, pyruvate kinase, did not increase in wounded roots. The activities of the early glycolytic enzymes peaked 24 to 48 h after wounding when the demand for substrates for wound-healing processes was expected to be maximal. Fructokinase exhibited the greatest and most persistent increase in activity, increasing by 150% 24 h after wounding and remaining elevated for the duration of the study. The increase in hexokinase, fructokinase, and phosphofructokinase activities suggests that expression of these early glycolytic enzymes may be up-regulated to meet the demand for glycolytic intermediates and products for wound-healing processes. The lack of an increase in any sucrolytic activities in response to wounding suggests that sucrolytic flux is determined by a mechanism other than protein expression.

Campbell, L.G., Klotz, K.L. 2007. Characterizing sugarbeet varieties for postharvest storage losses complicated by environmental effects and genotype x environment interactions. *Canadian Journal Plant Science*. 87:121-127.

Each year millions of tons of sugarbeet (*Beta vulgaris* L.) roots await processing in large exposed piles. During postharvest storage, respiration and invert sugar formation consume sucrose and even a small reduction in these losses would have substantial economic impact. This study investigated the relative importance of hybrid, environment, and hybrid X environment interactions and examined their

implications in characterizing hybrids for sucrose loss during storage or developing hybrids with improved storage properties. Glucose, fructose, and extractable sucrose concentrations and respiration rate were measured 30 and 120 days after harvest (DAH) on five hybrids produced in six environments. Environment effects were significant on both dates for all traits except fructose 30 DAH. Significant hybrid X environment interactions were observed for respiration rate 30 and 120 DAH, for extractable sucrose 120 DAH, and for glucose concentration 30 DAH. The only trait with a significant hybrid main effect was extractable sucrose 30 DAH. For the 90 days between measurements, extractable sucrose losses for individual hybrid-environment combinations ranged from 2% to 63% of the sucrose available 30 DAH. It appeared that large environmental impacts and hybrid X environment interactions, compared to the relatively small hybrid influences, would complicate selecting parental lines with all or most of the storage traits desired. Furthermore, a comprehensive evaluation of commercial hybrids or breeding lines for storage traits would require considerable resources. Efforts to understand the impact of production practices and growing season environment on storage properties would probably be more productive than attempting to produce commercial hybrids with improved storage characteristics.

Campbell, L.G., Klotz, K.L. 2007. Impact of rhizomania on storage respiration rate and sugar loss. 2006 Sugarbeet Research Extension Report, Coop Extension Service, North Dakota State University. 37:107-109.

Rhizomania, (beet necrotic yellow vein virus) is a serious threat to sugarbeet (*Beta vulgaris*) production in Minnesota and eastern North Dakota. As the prevalence and severity of the disease has increased, the proportion of diseased roots placed in postharvest storage piles also has increased. This report provides information on the storability of diseased roots that will assist in making decisions that will minimize postharvest sugar losses. Roots with and without the diseases were stored for up to 120 days after harvest during which time storage respiration rate and sugar loss were measured. The sugar loss attributable to rhizomania varied considerably from year to year but it was apparent that the potential loss from storing diseased roots is substantial. In one year of the 3-year trial, diseased roots lost more than half of the sugar they had at harvest; healthy roots lost less than 10% of their sugar during 120 days in storage. Rhizomania resistant varieties are the most effective method of reducing these losses and if diseased roots are harvested they should be processed as soon as possible.

ROLE OF SUCROSE METABOLIZING ENZYMES IN SUGARBEET GROWTH, CARBOHYDRATE PARTITIONING AND POSTHARVEST SUCROSE LOSS

(Project 650)

Karen L. Klotz

Sucrose catabolism has been implicated as a major factor controlling whole plant carbon partitioning, root growth, sucrose accumulation, and postharvest sucrose loss (Wyse, 1974; Giaquinta, 1979; Sung *et al.*, 1989; Zrenner *et al.*, 1995; Berghall *et al.*, 1997). In sugarbeet root, sucrose catabolism is catalyzed by three enzyme activities: sucrose synthase, acid invertase and alkaline invertase. Although all three activities are found in sugarbeet root, sucrose synthase is the predominant activity during root development and accounts for more than 90% of the total soluble sucrolytic activity during postharvest storage (Klotz and Finger, 2002; 2004). The enzyme is involved in sucrose utilization during development (Xu *et al.*, 1989; Amor *et al.*, 1995), has been implicated in sucrose partitioning to storage organs (Sung *et al.*, 1989; Zrenner *et al.*, 1995) and is believed to be the enzyme largely responsible for postharvest sucrose degradation in sugarbeet (Echeverría and Gonzalez, 2003).

Two sucrose synthase genes have been identified in sugarbeet, sugarbeet sucrose synthase 1 (SBSS1; Hesse and Willmitzer, 1996) and sugarbeet sucrose synthase 2 (SBSS2; Haagenson *et al.*, 2006). Previous research has demonstrated that both genes are highly expressed in roots, developmentally regulated, and relatively unresponsive to typical postharvest stresses including harvest, wounding, cold temperature, and anaerobic conditions (Haagenson *et al.*, 2006; Klotz and Haagenson, *in press*). During the past year, research was conducted to determine the tissue-specificity of sucrose synthase gene expression, since this knowledge may provide clues to the individual function of sucrose synthase genes. Plasmids were also constructed to allow sucrose synthase gene expression to be altered *in planta*. The generation of plants with altered sucrose synthase expression will provide the means to directly probe the function of individual sucrose synthase genes and determine the influence of each sucrose synthase gene on root yield, sucrose content and postharvest loss. In addition, research was conducted to refine and validate a high-throughput, enzyme-based assay developed for the quantification of sucrose, glucose, fructose and raffinose. The assay provides a rapid method to quantify sucrose and common carbohydrate impurities in sugarbeet roots, and may prove useful for screening germplasm for sucrose and carbohydrate impurity content and for monitoring carbohydrate changes during postharvest storage.

Tissue Specificity of Sucrose Synthase Gene Expression

The tissue specificity of SBSS1 and SBSS2 expression was determined by *in situ* hybridization using sugarbeet root tissue from plants six to seven weeks after planting. Digoxigenin-labelled RNA probes were made by *in vitro* transcription of the 3' end of the two genes in a region where the genes share little homology. Probes were gene-specific and did not hybridize with mRNA from the nontargeted sucrose synthase gene as determined by dot blot hybridizations with *in vitro* transcribed SBSS1 and SBSS2 RNA of varying concentrations.

Both sugarbeet sucrose synthase genes were expressed in storage and ray parenchyma but not in the dividing and expanding cells in and surrounding cambial tissue, in phloem or in the parenchyma cells surrounding xylem elements (Fig. 1). Both genes were also expressed in the cortex peripheral to the outermost vascular ring, although expression of SBSS2 in this tissue was more pronounced than SBSS1. Generally, SBSS1 expression was greatest in the storage parenchyma of older, central rings, while SBSS2 expression was greatest in the storage parenchyma of younger, peripheral rings. The expression patterns observed suggest that sucrose synthase has little role in phloem unloading as has been suggested in other plant species (Nolte and Koch, 1993) and appears to have no role in supporting growth of dividing and expanding cells, even though a role for sucrose synthase in cell wall biosynthesis has been demonstrated in other plant species (Amor et al., 1982). Rather, sucrose synthase expression was observed only in the sucrose-storing cells of the root. The enzyme's function in these cells is unclear. Although capable of both synthesis and degradation of sucrose, the enzyme is believed to function primarily as a sucrose-degrading enzyme in most plant species. Little sucrose degradation, however, would be expected in these cells.

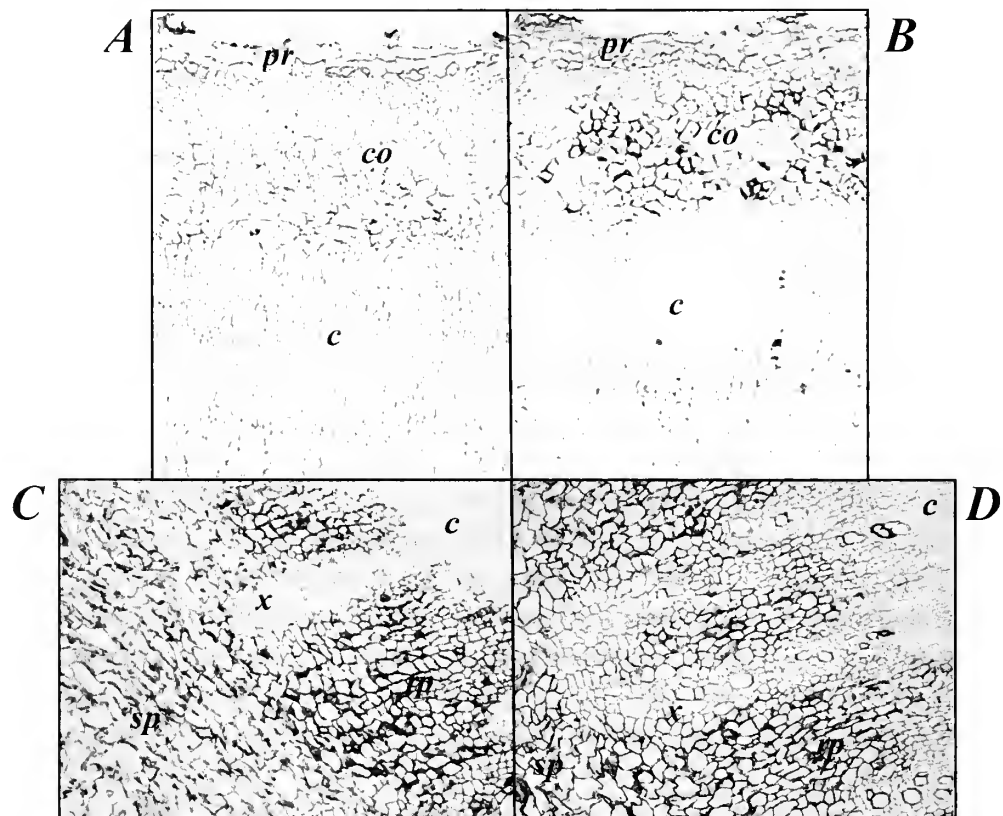
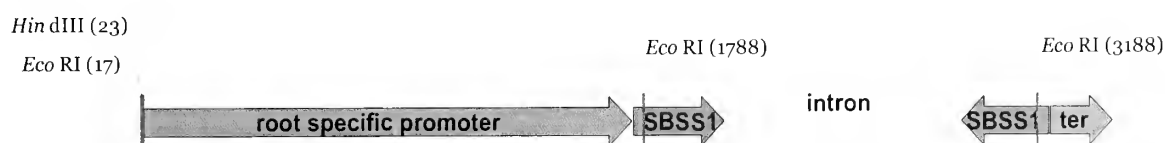


Figure 1: Localization of SBSS1 and SBSS2 expression in six to seven week old sugarbeet root. Root cross-sections at the peripheral regions (A and B) and interior regions (C and D) of the root were hybridized with digoxigenin-labeled probes for SBSS1 (A and C) and SBSS2 (B and D). Blue staining denotes regions of sucrose synthase expression. c, cambium; co, cortex; pr, periderm; rp, ray parenchyma; sp, storage parenchyma; x, xylem. Magnification = 100x.

Construction of Plasmids for Sugarbeet Transformation

As the initial step in generating plants with altered sucrose synthase activity, plasmids were constructed for use in the creation of stably transformed sugarbeet plants. Plasmids were constructed to decrease SBSS1 expression, decrease SBSS2 expression, and increase SBSS1 expression (Fig. 2). No construct was made to increase SBSS2 expression, since the SBSS2 gene product is abundant throughout development. Gene constructs designed for reducing sucrose synthase expression utilized RNA interference technology (Smith et al., 2000) and incorporated fragments of the SBSS1 or SBSS2 gene in sense and antisense orientations behind a root specific promoter, separated by an intron, and preceding a terminator. SBSS1 and SBSS2 gene fragments were 300 to 400 bp in length and were from a cDNA terminus where the two genes share little homology. A gene construct to increase expression was synthesized by ligation of the entire SBSS1 coding region to a root specific promoter and a terminator.

SBSS1 RNAi



SBSS2 RNAi



SBSS1 sense

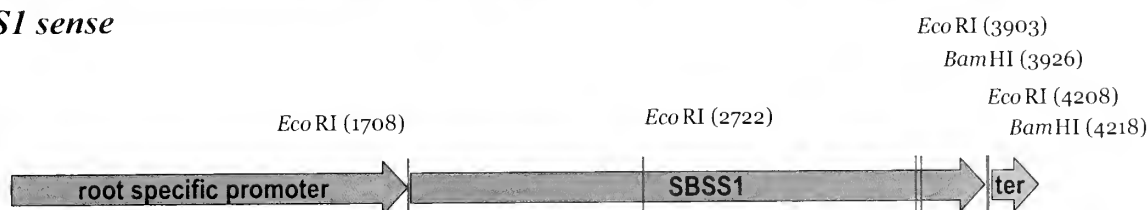


Figure 2: SBSS1 RNAi, SBSS2 RNAi, and SBSS1 sense gene constructs to be used to alter sucrose synthase expression in sugarbeet plants. ter = terminator.

Development of an Enzyme-Based Microtiter Plate Assay for Sucrose, Glucose, Fructose and Raffinose

Research was initiated during the last reporting cycle to develop a simple, rapid, accurate and cost-efficient assay for quantification of sucrose, glucose, fructose, and raffinose in sugarbeet root extracts in response to limitations of commonly used carbohydrate assay methods. Presently carbohydrates are quantified by polarimetry, refractometry, HPLC, GC or near-infrared (NIR)

spectroscopy. Current methods, however, are inaccurate for the analysis of deteriorated roots (polarimetry, refractometry), time-consuming (HPLC, GC), and/or require costly instrumentation (HPLC, NIR). In last year's report (Klotz, 2006), modifications to an enzyme-based microtiter plate assay designed for the analysis of sucrose, glucose and fructose (Spackman and Cobb, 2001) were described. The original assay accurately quantified sucrose, glucose and fructose, but its use was limited by time-consuming sample preparation steps, long assay times, and a narrow linear range. Modifications were made during the past two years to (1) reduce sample preparation times by adapting the method to use clarified beet extracts, (2) reduce reaction times from 60 min to 10 to 15 min, (3) increase the linear range of the assay 8-fold, and (4) expand it to quantify raffinose in addition to sucrose, glucose and fructose.

The microplate assay uses sucrose, glucose, fructose and raffinose as substrates for a series of enzyme catalyzed reactions to form products whose concentrations can be easily determined spectrophotometrically using a microtiter plate reader (Fig. 3). Assays for sucrose, glucose and fructose determinations use a commercially available diagnostic reagent that couples glucose to the reduction of NAD^+ using the enzymes hexokinase and glucose 6-phosphate dehydrogenase. In these assays, the concentration of NADH produced is indicative of the initial concentration of carbohydrate. For determination of glucose concentration, the reagent is used without modification (equation 1). For determination of fructose concentration, phosphoglucose isomerase is added to the reagent allowing NAD^+ to be reduced by fructose as well as glucose (equation 2). For determination of sucrose concentration, sucrose is first cleaved to glucose and fructose by the enzyme, invertase (equation 3), and the glucose formed in this reaction is determined. A new assay was developed for quantification of raffinose which utilizes galactose oxidase and peroxidase to couple the oxidation of raffinose to the oxidation of guaiacol (equation 4). In this assay, the concentration of biphenoloquinone, the oxidized form of guaiacol, is indicative of the initial raffinose concentration.

Carbohydrate standards were used to determine the linear range of the assays. Assays were linear for sucrose concentrations of 4 to 200 mM, glucose and fructose concentrations of 0.4 to 20 mM, and raffinose concentrations of 0.03 to 3 mM (Fig. 4).

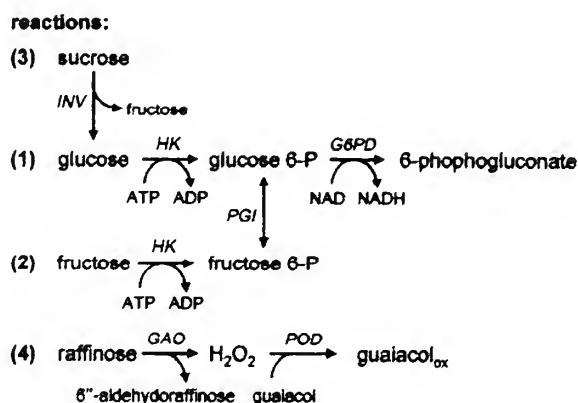


Figure 3: Enzyme catalyzed reactions used to determine sucrose, glucose, fructose and raffinose concentrations. Assays for sucrose, glucose and fructose measure NADH formation at 340 nm; raffinose assay measures the formation of oxidized guaiacol at 470 nm.

Enzyme abbreviations: G6PD, glucose 6-phosphate dehydrogenase; GAO, galactose oxidase; HK, hexokinase; INV, invertase; PGI, phosphoglucose isomerase; POD, peroxidase.

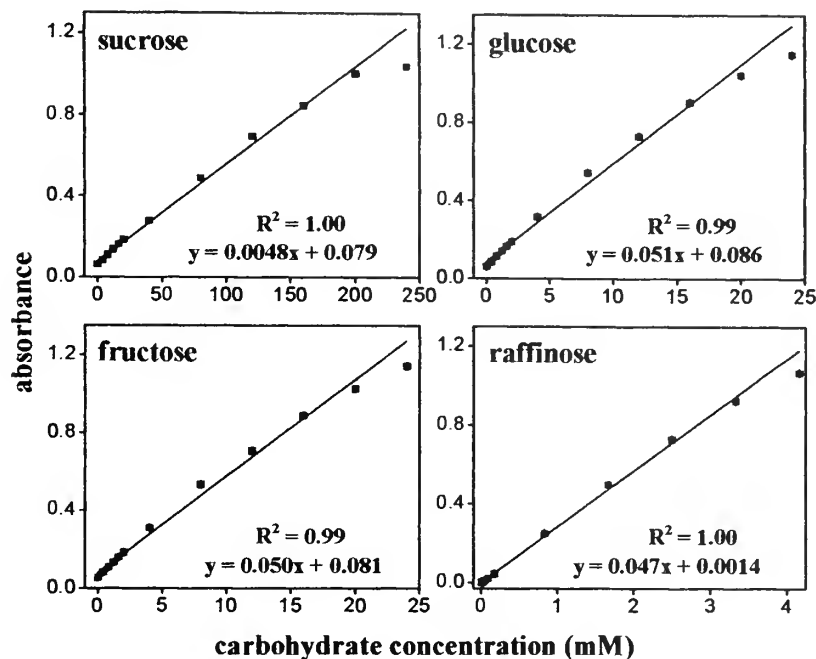


Figure 4: Absorbance as a function of carbohydrate concentration for sucrose, glucose, fructose and raffinose using the developed assay. Absorbance for sucrose, glucose and fructose was determined at 340 nm. Absorbance for raffinose was determined at 470 nm.

Accuracy of the microtiter plate assay was determined by comparing carbohydrate quantifications of clarified extracts from healthy, stored, rotted and frost-damaged roots using the modified microplate assay and HPLC. Correlation coefficients for sucrose, glucose and fructose concentrations determined by the two assay methods were 0.96, 0.98 and 0.94, respectively (Fig. 5). Because fructose concentrations determined with the microplate assay were, on average, 30% lower than fructose concentrations determined by HPLC, the microplate assay was also compared to the Nelson-Somogyi spectrophotometric assay which measures total invert sugar concentration (glucose + fructose; Fig. 6). Invert sugar concentrations determined using the Nelson-Somogyi assay were similar to those obtained with the modified microplate assay, but

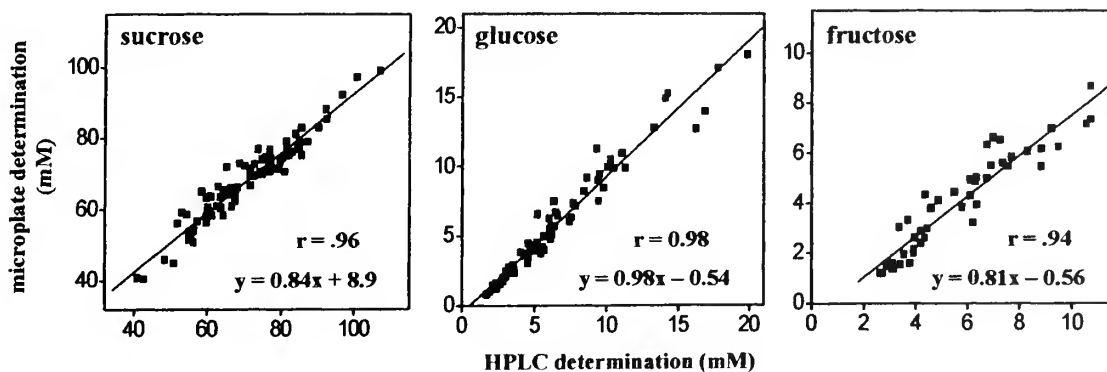


Figure 5: Correlation between sucrose, glucose, and fructose concentrations in clarified root extracts determined by the modified microplate method and HPLC.

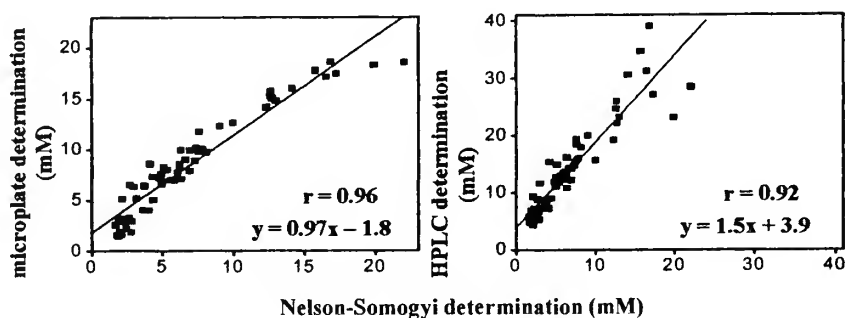


Figure 6: Correlation between invert sugar concentrations in clarified root extracts determined by the modified microplate assay and the Nelson-Somogyi spectrophotometric assay, and by HPLC and the Nelson-Somogyi spectrophotometric assay.

were approximately 50% lower than those obtained by HPLC. Comparison of raffinose concentrations determined by the modified microplate assay and HPLC remains to be done.

CONCLUSIONS:

- Sugarbeet sucrose synthase 1 (SBSS1) and sugarbeet sucrose synthase 2 (SBSS2) are expressed in the sucrose-storing cells of roots, but are not expressed in vascular tissue or in the dividing and expanding cells in and adjacent to cambial tissue. The expression patterns observed for SBSS1 and SBSS2 suggest that they have no role in phloem unloading or in supporting growth of dividing and expanding cells. Sucrose synthase's function in sucrose-storing cells remains to be determined.
- Plasmids were constructed that will allow sugarbeet plants to be generated that have (1) increased SBSS1 expression, (2) decreased SBSS1 expression, or (3) decreased SBSS2 expression.
- The accuracy of an enzyme-based microtiter plate assay developed for rapid quantification of sucrose and the common carbohydrate impurities found in sugarbeet roots was confirmed for sucrose, glucose, and fructose. The accuracy of the assay for quantification of raffinose remains to be determined.

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CHARACTERIZATION OF RESPIRATORY PROCESSES DURING SUGARBEET ROOT STORAGE

(Project 660)

Karen L. Klotz

Sucrose losses during storage have been estimated at 200 g per day per ton of roots--approximately equivalent to the daily loss of 0.1% of the sucrose present in the root at harvest (Tungland et al., 1998). Sucrose loss occurs due to respiration, storage diseases, and conversion of sucrose to other carbohydrates. Respiration, however, is the principal cause of postharvest sucrose loss with 60 to 80% of the sucrose lost during storage attributed to this process (Wyse and Dexter, 1971). Although many studies have examined the effect of environmental factors including temperature (Oldfield et al., 1971; Wyse, 1978a), injury (Wyse 1978b; Wyse and Peterson, 1979), and carbon dioxide or oxygen concentration (Stout, 1954; Wyse, 1973) on root respiration rate, little information is available regarding the endogenous factors that influence and control sugarbeet root respiration. Research conducted under this project seeks to determine these internal factors.

Previous research conducted in this project has focused on identifying the metabolic reactions, products or pathways that limit respiration rate, and this research continues. During the past year, however, most research was directed toward understanding the influence of the plant hormone, ethylene, on wound-induced and maintenance respiration rate, and the effect of leaf regrowth on storage respiration rate.

Ethylene Production And Its Effect On Respiration

Ethylene is a natural plant hormone that induces respiration in most plant tissues and organs. Endogenous ethylene production is controlled by developmental cues and, in many plant tissues, is strongly stimulated by mechanical injury and other stresses including chilling and low oxygen conditions (Yang and Hoffman, 1984). Experiments were conducted to (1) quantify ethylene production in wounded, unwounded and conventionally harvested sugarbeet roots, (2) determine the effect of ethylene on storage respiration rate, and (3) determine the effect of ethylene synthesis and response inhibitors on basal and wound-induced respiration.

Unwounded sugarbeet roots produce very little ethylene (Fig. 1a). During the four days after harvest, gently hand-harvested roots produced, on average, $0.17 \text{ nmol kg}^{-1} \text{ h}^{-1}$ ethylene. Severe injury to roots, however, induced ethylene production by 4 to 6-fold in the four days following wounding. Concurrent with the increase in ethylene in wounded roots, root respiration rate was elevated (Fig 1b). Respiration rate in wounded roots was elevated 1.5 and 2.0-fold 72 and 96 h after wounding, relative to unwounded roots.

In commercial sugarbeet piles, ethylene concentrations were less than 2 ppb during the first 21 d after piling in both a ventilated and a nonventilated pile (Fig. 2). Despite root injury by harvest and piling operations, conventionally harvested and piled roots produced ethylene at a rate similar to the unwounded roots described above (data not shown). Beginning 31 and 67 d after

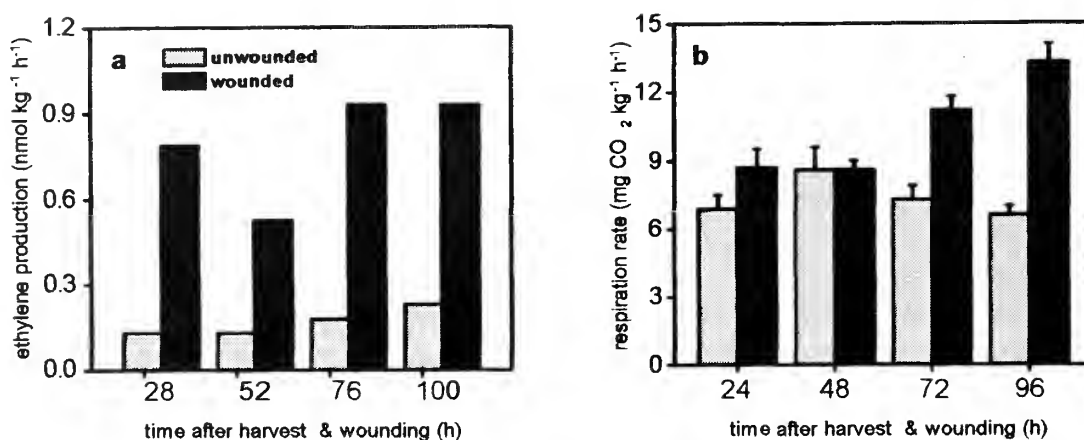


Figure 1. Ethylene production (a) and respiration (b) of greenhouse-grown roots, harvested 17 wk after planting, at 10°C. Following harvest, roots were severely wounded by tumbling 30 min in a pilot scale beet washer, causing bruising and surface abrasions. Error bars = SE of the mean. $n = 2$ and $n = 6$ for ethylene and respiration measurements, respectively.

piling, ethylene concentrations increased in nonventilated and ventilated piles, respectively. The source of elevated ethylene levels after storage for 1-2 months is unknown, but may be due to ethylene induction by cold temperatures or ethylene production by pathogens.

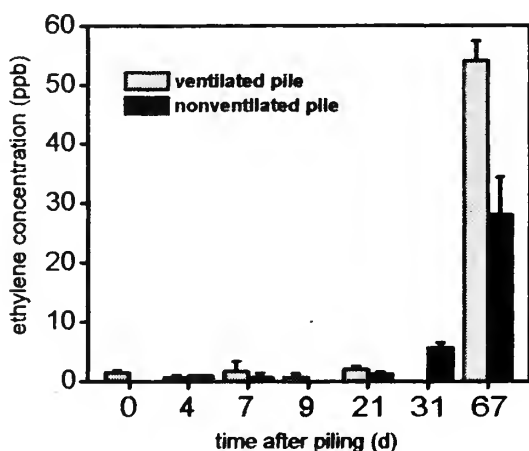


Figure 2. Ethylene concentrations in air samples collected at a depth of 1.5 m from a ventilated, 32 ft (9.8 m) pile and a nonventilated 18 ft (5.5 m) pile in Moorhead, MN. No data was collected for the nonventilated pile 0 and 9 d after piling. Ethylene concentrations in the ventilated pile 31 d after piling were below limits of detection. Data are mean \pm SE of the mean ($n = 3$).

Ethylene was found to induce respiration in stored roots (Fig. 3). Ethylene concentrations of 0.02 and 0.1 ppm caused a transient, 60% increase in respiration rate after 24 and 48 h of exposure to ethylene. Ethylene concentrations of 1.4 and 14 ppm elevated root respiration rate for at least 4 d. On average, respiration rate was elevated 73% by 1.4 ppm ethylene and 100% by 14 ppm ethylene.

Ethylene synthesis and response inhibitors demonstrated ethylene's role in wound-induced respiration. In a series of experiments, respiration rates were determined in wounded and unwounded roots after treatment with ethylene synthesis and response inhibitors, and compared

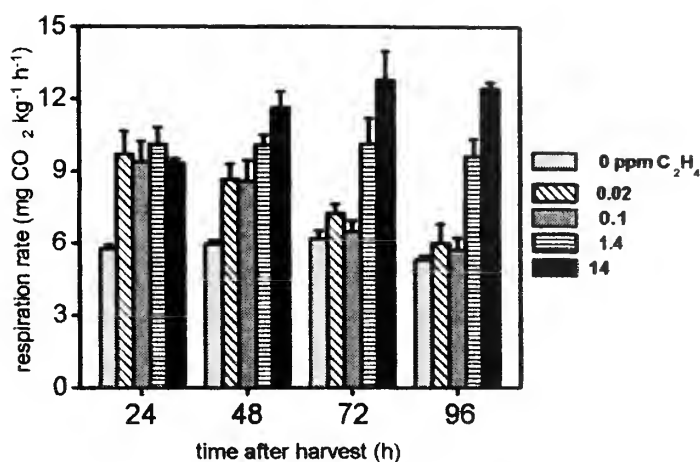


Figure 3. Respiration rate of greenhouse-grown roots exposed to varying concentrations of ethylene, at 10°C. Roots were harvested 18 wks after planting. Roots were exposed to ethylene throughout the 4 d experiment. Data are mean \pm SE of the mean ($n = 3$).

to that of untreated wounded and unwounded roots. The ethylene synthesis inhibitor, aminoethoxyvinylglycine (AVG) prevented ethylene production in wounded roots (Fig. 4a) and attenuated the increase in wound-induced respiration by 38, 54 and 58% after 48, 72, and 96 hours after harvest and wounding (Fig. 4b). The reduction, but not the elimination of a respiratory increase due to wounding, indicates that ethylene has a role in the increase in respiration due to wounding, but is not solely responsible for the respiratory increase.

Similar to AVG, the ethylene response inhibitor, silver thiosulfate (STS), attenuated the increase in respiration due to wounding (Fig. 5). Wound-induced respiration was reduced 60% by STS treatment 72 and 96 h after harvest and wounding. Similar experiments were conducted with the ethylene response inhibitor, 1-methylcyclopropene (MCP). However, no consistent results could be obtained with this compound, despite repeated efforts.

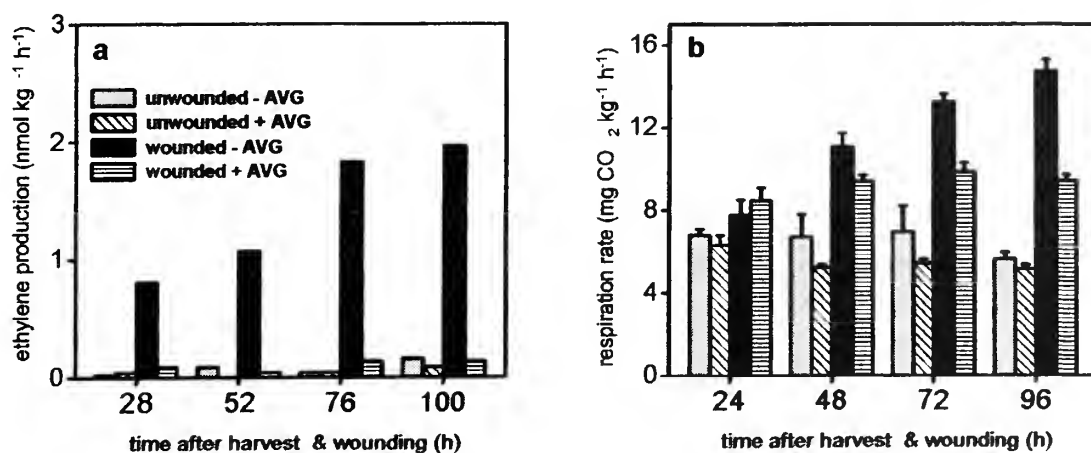


Figure 4. Ethylene production (a) and respiration rate (b) at 10°C of wounded and unwounded greenhouse-grown roots, 18 wk after planting, with and without treatment with 50 μ M aminoethoxyvinylglycine (AVG). Wounded roots were severely bruised and abraded by tumbling 30 min in a pilot scale beet washer. Inhibitor treatments were administered after wounding by submerging roots for 1 h in aerated water or AVG solution. Error bars = SE of the mean. $n = 2$ and $n = 3$ for ethylene and respiration measurements, respectively.

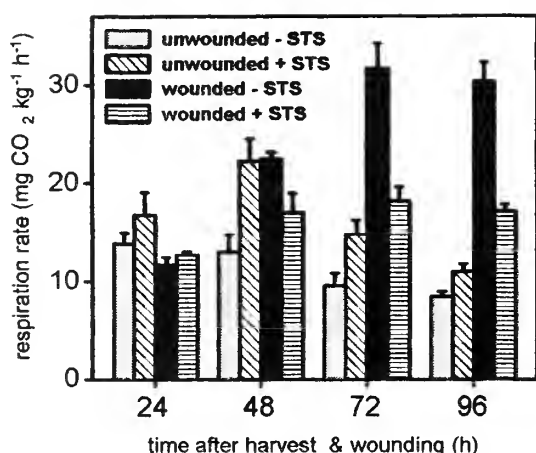


Figure 5. Respiration rates of wounded and unwounded greenhouse-grown roots, 18 wk after planting, with and without treatment with 4 mM silver thiosulfate (STS) at 10°C. Wounded roots were severely bruised and abraded by tumbling 30 min in a pilot scale beet washer. STS treatment was administered after wounding by briefly immersing root tissue in STS solution. Data are mean \pm SE of the mean ($n = 3$).

Effect of leaf regrowth on storage respiration rate

Leaf regrowth is common in storage piles, yet information regarding the environmental conditions that promote leaf regrowth and quantification of the effect of regrowth on storage properties is lacking. During the past year, research was conducted to determine (1) the effect of temperature on the extent of leaf regrowth and (2) the effect of leaf regrowth on storage respiration rate. Mechanically flailed, hand-harvested roots of four varieties (ACH 817, Beta 2084, VDH 46177, and Horizon) were stored for up to 25 days at 4, 8, 12, 16, or 20°C. Leaf regrowth at these storage temperatures was evaluated after 7, 14 and 25 days in storage. Roots from this study exhibited varying degrees of leaf regrowth and were subsequently used to determine the effect of leaf growth on root respiration rate. After the initial 25 days in storage at different temperatures, roots were transferred to a 6°C cold room and allowed to equilibrate and acclimate to this storage temperature for 8 days. Respiration rate was then measured on these roots before and after removal of the regrown leaves.

Leaf regrowth was influenced by storage temperature, storage duration and variety. Both the number of leaves per root (Fig. 6) and the total length of leaves per root (Fig. 7), a measure of the amount of leaf material produced per root, increased with storage temperature and time in storage. Both number and total leaf length were exponentially related to storage temperature, as the relationships between storage temperature and the logarithm of the number of leaves per root (Fig. 8a) and the logarithm of the total leaf length per root (Fig. 8b) were linear. Varietal

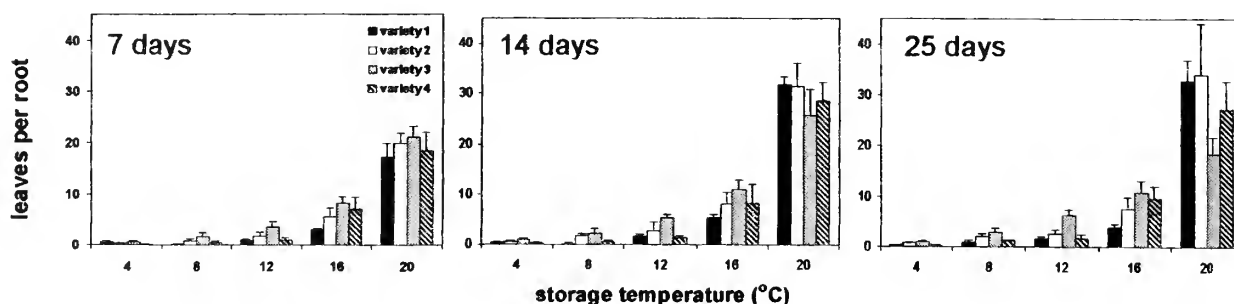


Figure 6. Number of leaves produced per root after storage at 4, 8, 12, 16 or 20°C for 7, 14, or 25 days for four sugarbeet varieties. Data are the mean \pm SE.

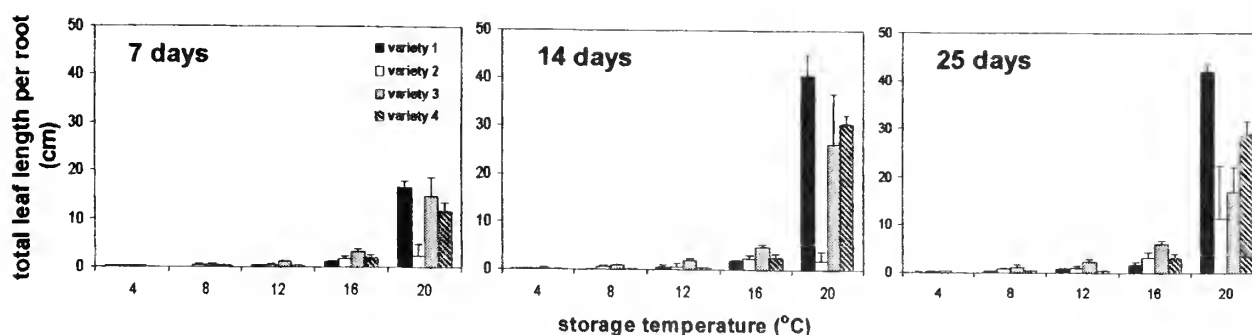


Figure 7. Total length of leaves produced per root after storage at 4, 8, 12, 16 or 20°C for 7, 14, or 25 days for four sugarbeet varieties. Total leaf length was the sum of the leaf length of all leaves present on a root. Data are the mean \pm SE.

differences were also noted in both the number of leaves produced per root and total leaf length per root.

Root respiration rate was significantly greater for roots with regrown leaves (Table 1). Removal of regrown leaves reduced respiration rate by 15%, on average. The increase in respiration due to the presence of leaves, however, was unrelated to the surface area or weight of the removed leaves (data not shown).

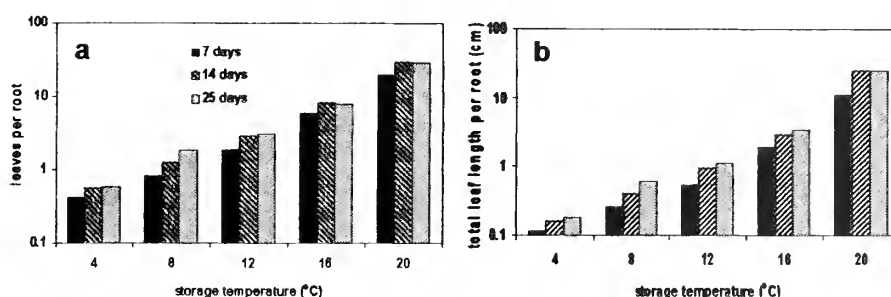


Figure 8. Exponential relationships between number of leaves produced per root (a) and total length of leaves produced per root (b) as a function of storage temperature. Leaves per root (a) and total leaf length per root are graphed on the y-axis using a logarithmic scale. Data is averaged over the four varieties.

Table 1. Respiration rate of roots of four sugarbeet varieties exhibiting leaf regrowth before and after removal of the leaves. All differences due to presence or absence of leaves are significant at $P \leq 0.05$. Data are mean of four replicates, with each replicate composed of ten roots.

variety	respiration rate (mg CO ₂ kg ⁻¹ h ⁻¹)	
	with leaves	leaves removed
1	5.9	5.2
2	5.3	4.7
3	6.4	5.2
4	5.9	4.8
mean	5.9	5.0
LSD _(0.05) = 0.38		

CONCLUSIONS:

- Sugarbeet roots produce low levels of ethylene. Although ethylene production is induced by injury, the injury required to significantly increase ethylene production is greater than that which typically occurs during conventional harvesting and piling operations.
- Ethylene, if present in sufficient concentrations, induces sugarbeet root respiration. However, the ethylene concentrations detected in commercial storage piles would be expected to have no or only a transient effect on storage respiration rate.
- Ethylene has a role in the respiratory increase that occurs after severe root injury. Ethylene was responsible for approximately 60% of the increase in respiration that occurred after severe injury.
- Regrowth of leaves is temperature dependent with the number and size of leaves regrown during storage exponentially related to storage temperature.
- Respiration rate was elevated by the presence of regrown leaves. Removal of these leaves reduced respiration rate by 15%, on average. The increase in respiration rate due to the presence of regrown leaves, however, was unrelated to the amount of regrown leaf material.

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**SUGARBEET RESEARCH
USDA-ARS SUGARBEET AND BEAN RESEARCH UNIT
EAST LANSING, MICHIGAN**

2006 REPORT

SECTION D

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***This research was supported in part by funds provided through the Beet
Sugar Development Foundation (Project 740)***

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INTRODUCTION

The Sugarbeet and Bean Research Unit at East Lansing, MI has projects involved with sugarbeet, dry bean, apple, and cucumber. The sugarbeet program has three primary areas of investigation. First is breeding enhanced germplasm for adaptation to the Eastern US growing areas, with a priority on high sucrose, smooth root, and seedling disease resistance. Second is determining genetics of agronomic traits including sucrose accumulation, inheritance of seedling disease resistance, developing recombinant inbred lines, and constructing and characterizing molecular tools for the community (genetic maps, expressed sequence tags, bacterial artificial chromosome libraries). Third is the investigation of seedling vigor, including field emergence and stand establishment, stand persistence, development of in vitro germination and vigor tests, and molecular characterization of early plant development.

PUBLICATIONS IN 2006:

- McGrath, J.M., Trebbi, D., Fenwick, A. Panella, L., Schulz, B., Laurent, V., Barnes, S., Murray, S.C. (2007) An open-source first-generation molecular genetic map from a sugarbeet x table beet cross and its extension to physical mapping. Published online 1 January 2007; doi:10.2135/cropsci2006-05-0339tpg. *Crop Science* 47: S-27-S-44.
- McGrath, J.M. (2006) Registration of EL53 sugarbeet germplasm with smooth-root and moderate resistance to *Rhizoctonia* crown and root rot. *Crop Science* 46: 2334-2335.
- McGrath, J.M., Trebbi, D. (2006) Notice of release of TBEL-1 table beet germplasm with high sweetness and cylindrical shape. USDA-ARS Germplasm Release, February, 2006.
- Haagenson, D.M., Klotz, K.L., McGrath, J.M. (2006) Sugarbeet sucrose synthase genes differ in structure and organ-specific and differential expression. *J. Plant Physiology* 163: 102-106.
- Nagendran, S. (2006) *Rhizoctonia* disease in sugar beet: Disease screening and cytopathology of the sugar beet – *Rhizoctonia solani* interaction. Ph.D. Dissertation. Michigan State University. 107 pages.

SUGAR BEET ACTIVITIES OF THE USDA-ARS EAST LANSING CONDUCTED IN COOPERATION WITH SAGINAW VALLEY BEAN AND BEET FARM DURING 2006

J. Mitchell McGrath, Tim M. Duckert, Teresa Koppin and Scott Shaw
USDA – ARS, East Lansing, Michigan

Four evaluation plots were planted at the Saginaw Valley Bean and Beet Research Farm in 2006; two agronomic trials, one *Cercospora* leaf spot evaluation trial conducted in conjunction with Beet Sugar Development Foundation, and another with USDA-ARS cooperators. All seed planted in the agronomic trials was untreated to maximize stand and seedling vigor traits inherent in the breeding germplasm. Agronomic trials (Tests 06BB01 & 06BB02) were planted into Range 11 west of the drainage ditch on April 18, 2006, following normal fall tillage and seedbed preparations. Blocking and thinning was completed by June 20th for all trials. Harvest of agronomic trials was completed by October 10th, and sucrose determinations were done on brei samples taken one day later, frozen, and sucrose content was analyzed by HPLC in the USDA-ARS lab on the Michigan State University campus. Statistical analyses were done using the JMP statistical package (SAS Institute, Cary, NC).

Test 06BB01: This test was conducted to re-evaluate promising populations as identified in the 2005 Saginaw Valley Bean and Beet Farm agronomic trial and to examine performance of new populations derived from a number of source materials. Thirty-eight entries (Tables 1 & 2) were tested in a completely randomized block design with four two-row plot replications 24 feet long (entries 542, 544 – 546 were duplicated, to give a 42 entry test). Commercial check varieties were Beta 5736 and Hilleshög E17. Hilleshög E17 out-performed all other entries for traditional stand (Table 1) and agronomic measures (Table 2).

A new quantity for measuring stand persistence is proposed here, that is the Stand Index, simply expressed as the stand at harvest divided by the maximum stand (Table 1). Although these fields were blocked and thinned, this value may be useful in that very high (>0.8) or very low (<0.2) may indicate severe problems with the seedlots, although the significance of this measure over multiple seasons needs to be ascertained. Emergence of planted seed historically is about 60%, and the Stand Index values appear to approximate this mean as well, for unknown reasons. Stand Index seems to be inversely related to harvest spacing and average beet weight, and may be able to factor into a quality measure as desired for future grower payments. Seven of the top 10 entries for maximal stand on May 9, 2006 were also among the top 10 agronomic performers at harvest, and these also had higher plant densities as well as smaller and presumably sweeter beets at harvest. Two of these top 10 (Entries 522 and 508) will be released to industry as improved germplasm in 2007. Other top 10 stand performers except E17 and SR97 are part of a group of intercrosses made in 2003 between SR96, SR97, EL0204 and a few other elite East Lansing germplasm lines, and will be released to industry following another round of intercrossing.

Yields were very high this season expressed as tons per acre (T/A; Table 2), but somewhat lower in sucrose content (SucFW) than historical for these and similar breeding materials. Commercial checks out performed germplasm entries for all measured traits except T/A for four entries (518, 528, 530, and 535). Sucrose content (SucFW) was determined exclusively by HPLC this year, and is perhaps the most accurate measure available. Refractometry was also determined (BRIX, Table 2), and in general better reflects but slightly overestimates traditionally

reported polarimetry data. These physiological values are given as percent in Table 2, including Water, Dry Matter (DM), and the sucrose proportion of the dry matter (SucDM). Interestingly, water content again appeared to be a significant variable for agronomic performance, since commercial materials have significantly less moisture than most of the breeding germplasm. However, the low moisture trait was detected in three breeding lines (Entries 515, 517, and 519; Figure 1) for the first time in 2006 and efforts are underway to follow the genetics and select for this trait in future years. It appears to be independent of other genes, and gene interactions, contributing a higher sucrose content in the commercial materials since the experimental hybrid Entry 529 did not appear to receive the benefit of heterosis for high sucrose content.

Test 05BB02: This test was conducted to evaluate entries for possible inclusion into the germplasm release stream. This test had high genetic diversity and a wide range in stand and yield components (Table 3). Most of this germplasm was field tested for the first time in 2006, and many derive from crosses with wild and unadapted germplasm. Stand Index (defined above) showed a wider range of values than Test 06BB01, perhaps reflecting the influence of this genetic diversity. Much of this germplasm is targeted at acceptable sucrose per acre yield contributed by recent smooth-root germplasm releases with moderate to high resistance to *Aphanomyces* and *Rhizoctonia* contributed by wild and unadapted germplasm. Root yields were exceptionally high. Harvest conditions were very muddy, and some of this yield difference reflects soil tare. This was not a problem in test 06BB01, which was harvested one week later.

Other Trials and Evaluations: In addition to seven field seed increase plots on the MSU campus, beets were grown for evaluation in East Lansing. One trial was at the Plant Pathology Farm, traditionally used for *Rhizoctonia* crown and root rot evaluation and selection. This nursery was changed by inoculating five weeks earlier than normal to evaluate for seedling *Rhizoctonia* resistance (see report in 2007 ASSBT Proceedings). Results suggest a low frequency of seedling resistance in many materials, and selections have been made. A selection nursery was planted using all materials in the **Test 06BB01** trial for both reduced water content of roots as well as combining Smooth-Root with rhizomania and other agronomic traits, and another nursery to evaluate inbreeding lines.

CERCOSPORA NURSERY

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The need continues within the sugarbeet industry for objective evaluations of company breeding lines for their reaction to *Cercospora beticola*, the cause of leaf spot of sugar beet. Historically, the *Cercospora* nursery has been conducted at the ARS Ft. Collins, CO location, in large part due to the unique conditions where *Cercospora* leaf spot could be incited in the absence of other disease pressures. In 2003, the original site was lost to a housing development and alternate sites were sought. The new site selected was not assured of regular water supply and in 2004 the Ft. Collins nursery received severe hail five times. Only a part of the Western Sugar Co. trial and USDA-ARS breeding material from Salinas, CA remained. In 2005, a site at the Irrigation Research Foundation of Yuma, Colorado was planted to *Cercospora* leaf spot nursery for two major reasons: 1) water was assured because the center-pivots pump from the Ogallala aquifer, and 2) night time temperatures and higher relative humidity in Eastern Colorado would favor the development of *Cercospora* leaf spot. The bulk of the trial was planted

in Yuma, and Western Sugar Co. lines were duplicated in Akron, CO, at the USDA-ARS station there. Unfortunately, the trial in Akron was lost due to herbicide carry-over. Although the Yuma trial got off to a good start, problems were encountered and the test was abandoned. Residential encroachment, dwindling field staff, and relocating the Ft. Collins nursery have each taken a toll on the ability to incite an epiphytotic in Colorado, and epiphytotics seem to come naturally in Michigan.

2006 Cercospora Field Evaluation: After considerable discussion, the cooperative BSDF Cercospora leaf spot nursery was moved from the historic Ft. Collins, CO ARS site to the East Lansing, MI ARS location, and conducted at the Saginaw Valley Bean and Beet Farm. Cercospora trials (06USDAcerc & 06COMcerc) were planted on April 26th and 27th, respectively, in Range 6 on prior year sugarbeet ground, but which had been sown with winter wheat since the decision to plant the nursery in Michigan did not occur until March 2006. Commercial entries (96 lines) were planted in 2-row plots, each 15 feet in length, replicated four times in a randomized complete-block design in 30-inch rows. A susceptible 'spreader row' hybrid, kindly provided by Betaseed, Inc., was placed between each 2-row experimental entry. At least 150 seeds per plot were planted with a cone planter, and seeds were treated by cooperators to control early seedling diseases. All seed was planted and no other use or distribution of seed or plants was allowed. USDA-ARS seed (117 entries) was similarly planted with the exception that the experimental design was single rows with three replications, and all but East Lansing seed was treated to minimize the impact of seedling disease. Emergence was very good to excellent, and plots were blocked to 4-inch spacing and doubles were removed where necessary by the third week of June. Plots were inoculated with a spore suspension spray by Michigan Sugar in the third week of July, shortly before complete row closure (in the commercial entries). The assistance of Michigan Sugar in conducting the Cercospora trials is gratefully acknowledged.

Cercospora ratings began a weekly rating schedule on August 9th. Plots were initially viewed for evidence of disease on July 27, at which time a few lesions could be observed in the spreader rows and some of the more susceptible entries, but complete data was not collected, and similar observations were noted on August 1. By August 9, the disease had dramatically spread due to the high night temperatures and humidity. In general, most of the commercial materials submitted were susceptible or highly susceptible (Table 4), and a range of reaction was observed among the breeding materials submitted by USDA cooperators in Salinas (Bob Lewellen), Fargo (Larry Campbell), Ft. Collins (Lee Panella), and East Lansing (Mitch McGrath) (Table 5). We propose that this cooperative project be continued in Saginaw for 2007.

The first rating (Mean M1; Tables 4 and 5) was taken using the visual scoring given at <http://www.sbreb.org/brochures/cercospora/figureB.pdf>. Ratings are summarized for reference but the specific varieties have not been disclosed by the cooperators. The second rating followed the scheme followed by the National Plant Germplasm System (Mean M2, Tables 4 and 5; similar to the KWS system) given at <http://www.ars-grin.gov/cgi-bin/npgs/html/codes.pl?49073> in order to better conform to previous years scores. The M1 system relies on the number or coverage of spots per leaf while the M2 system rates primarily the number of 'flag' leaves per plot. This latter system is perhaps more conservative in rating resistant lines (i.e., the M1 data have a rough cut-off score for resistance at a rating of 6-7, where the M2 system has a cut-off value for resistance at 3-4). Both systems yielded similar conclusions.

Table 1: Stand establishment and persistence of germplasm tested in Test 06BB01.

Entry	Accession	Description	Stand (5/2)	Stand (5/9)	Harvest Stand	Stand Index ¹	Harvest Spacing (in)	Lbs / Beet
505	EL-A011867	E17	243.8	287.5	88.5	0.3	6.38	1.88
523	EL-A013700	02B097	154.5	192.0	86.5	0.5	6.65	1.52
522	EL-A013698	WC030246 (EL55 TBA)	170.8	187.0	76.0	0.4	7.56	2.02
515	EL-A013501	03B051-a	176.0	184.0	91.0	0.5	6.29	1.76
507	EL-A012174	WC970311 (SR97)	159.3	176.0	82.5	0.5	6.90	1.80
514	EL-A013499	03B046	153.8	175.0	91.8	0.5	6.25	1.56
525	EL-A013705	02B103	165.0	174.8	75.5	0.4	7.70	2.08
516	EL-A013503	03B056 (OB-SR97smrIP)	160.8	173.5	83.0	0.5	6.84	1.38
510	EL-A013478	03B051-b	165.3	168.3	78.3	0.5	7.48	2.13
508	EL-A012176	WC970457 (release TBA)	144.0	167.3	76.0	0.5	7.46	2.03
528	EL-A014964	EL0204 Sel	149.0	157.5	78.5	0.5	7.30	2.18
524	EL-A013704	02B096	133.3	152.8	68.5	0.4	8.63	2.10
526	EL-A014205	EL54 TBA (Hero)	129.8	150.5	79.3	0.5	7.24	1.96
518	EL-A013507	03B050 (OS-EL0204smrIP)	149.0	148.0	76.8	0.5	7.49	2.27
538	EL-A014990	03B263 (EL50/2 TBA)	118.8	137.8	69.8	0.5	8.22	2.12
513	EL-A013495	03B056 (MF-SR97smrIP)	126.3	137.3	73.5	0.5	7.78	2.04
541	EL-A014987	SR Comp F3	115.8	133.8	71.5	0.5	7.92	2.08
519	EL-A013508	03B051-c	120.8	133.3	70.0	0.5	8.34	2.02
534	EL-A014974	EL40	120.0	122.3	66.8	0.5	8.81	2.38
531	EL-A014971	EL0204 Sel	112.0	120.3	59.8	0.5	9.79	2.47
530	EL-A014970	SR97 Sel	104.5	113.0	67.8	0.6	8.56	2.55
509	EL-A013475	03B046	113.5	112.8	78.5	0.7	7.40	1.92
511	EL-A013481	03B062	112.8	111.8	65.3	0.6	8.89	2.20
521	EL-A013514	03B023 (RA-01B006smrIP)	98.5	111.5	71.3	0.6	8.21	1.95
506	EL-A011964	B5736	107.0	110.0	73.3	0.7	8.04	2.33
532	EL-A014972	SR94 Sel	101.0	107.5	69.8	0.6	8.55	2.18
533	EL-A014973	EL50	84.8	103.5	60.5	0.6	9.88	2.74
520	EL-A013510	03B057	97.3	102.3	66.3	0.6	8.60	2.25
542	EL-A014988-2	Gamish from Rhizoc/sel	89.0	99.0	60.3	0.6	9.49	2.43
537	EL-A014988-1	Gamish from Rhizoc/sel	93.3	97.3	59.8	0.6	9.51	2.63
535	EL-A014975	USH20	83.3	94.8	58.0	0.6	10.34	3.22
543	EL-A013486-1	03B061	83.0	90.3	58.5	0.6	9.95	1.70
517	EL-A013506	03B030	81.3	86.0	63.5	0.7	9.17	2.29
512	EL-A013492	03B051-d	71.5	80.0	51.3	0.6	11.04	2.47
546	EL-A013486-2	03B061	79.0	79.5	49.3	0.6	11.52	2.38
536	EL-A014981	EL50 Sel	62.8	67.5	50.3	0.7	11.73	3.08
529	EL-A014966	WC960451Sel (85657CMSxSR)	61.3	63.0	48.3	0.8	11.83	2.39
544	EL-A019278-2	2005 Group A-mix of 04 roots	46.8	47.3	32.8	0.7	17.57	3.50
527	EL-A014963	EL51 Sel	39.8	47.0	37.5	0.8	16.46	2.57
545	EL-A019297-2	2005 Range A mix	45.0	41.5	30.5	0.7	19.49	3.89
539	EL-A019278-1	2005 Group A-mix of 04 roots	35.5	41.3	44.3	1.1	13.91	2.57
540	EL-A019297-1	2005 Range A mix	23.3	24.3	25.3	1.0	27.46	3.43
Grand Mean			111.5	121.6	65.8	-	9.73	2.29
LSD (0.05)			29.1	23.2	16.8	-	3.38	0.70
CV (%)			43.4	43.8	29.0	-	50.66	34.77
F value			20.89***	43.00***	7.96***	-	5.86***	2.03**

¹ Stand Index = Harvest Stand / Maximum Early Stand (here on May 9, 2006)

Table 2: Agronomic results from germplasm entered into Test 06BB01.

Entry	Seedlot	Description	SucFW	T/A	Suc/A	Suc/T	DM	Water	SucDM	BRIX
505	EL-A011867	E17	18.20	32.9	11,886	364.1	23.27	76.73	78.19	20.38
506	EL-A011964	B5736	18.12	32.2	11,649	362.4	24.59	75.41	73.71	21.27
518	EL-A013507	03B050	15.02	34.2	10,273	300.4	22.10	77.90	67.94	18.67
513	EL-A013495	03B056	15.24	29.4	10,114	304.7	22.43	77.57	67.50	18.59
515	EL-A013501	03B051	16.04	30.9	9,961	320.9	22.79	77.21	70.42	19.46
507	EL-A012174	WC970311 (SR97)	16.09	29.4	9,483	321.7	22.31	77.69	72.21	19.17
517	EL-A013506	03B030	15.84	28.6	9,456	316.7	22.83	77.17	69.01	19.51
508	EL-A012176	WC970457 (release)	15.61	30.2	9,450	312.2	21.41	78.59	72.93	18.25
516	EL-A013503	03B056	15.73	30.1	9,294	314.7	22.45	77.55	70.04	19.49
510	EL-A013478	03B051	14.31	32.1	9,177	286.3	21.12	78.88	67.77	18.15
509	EL-A013475	03B046	15.69	29.2	9,174	313.9	21.80	78.20	72.02	18.71
528	EL-A014964	EL0204 Sel	13.00	33.9	8,802	260.0	21.15	78.85	61.48	18.03
530	EL-A014970	SR97 Sel	13.18	33.3	8,715	263.7	21.30	78.70	62.17	18.56
520	EL-A013510	03B057	14.80	29.2	8,659	296.0	21.94	78.06	67.52	18.96
519	EL-A013508	03B051	15.58	27.3	8,499	311.6	22.72	77.28	68.59	19.80
535	EL-A014975	USH20	12.39	34.3	8,484	247.7	21.62	78.38	57.27	18.64
514	EL-A013499	03B046	14.63	28.4	8,196	292.6	21.63	78.37	66.77	18.85
511	EL-A013481	03B062	15.05	27.2	8,184	301.1	21.34	78.66	70.59	18.55
533	EL-A014973	EL50	13.16	30.5	8,005	263.2	22.09	77.91	59.54	18.93
542	EL-A014988-2	Gamish from Rhizoc/se	13.76	29.2	7,984	275.3	21.73	78.27	63.38	18.50
537	EL-A014988-1	Gamish from Rhizoc/se	12.77	31.1	7,956	255.3	20.99	79.01	60.76	17.59
525	EL-A013705	02B103	12.98	30.1	7,830	259.6	21.07	78.93	61.52	17.92
541	EL-A014987	SR Comp F3	13.52	29.1	7,820	270.3	21.27	78.73	63.57	17.90
522	EL-A013698	WC030246 (EL55)	12.62	30.4	7,700	252.3	19.86	80.14	63.52	16.75
512	EL-A013492	03B051	15.47	24.9	7,654	309.4	21.44	78.56	72.16	18.24
536	EL-A014981	EL50 Sel	12.84	29.4	7,534	256.8	21.70	78.30	59.23	18.76
534	EL-A014974	EL40	12.87	29.3	7,518	257.4	21.52	78.48	59.82	18.88
526	EL-A014205	EL54 TBA (Hero)	12.52	30.0	7,481	250.4	20.94	79.06	59.82	17.58
532	EL-A014972	SR94 Sel	13.00	28.8	7,462	259.9	21.37	78.63	60.74	18.68
538	EL-A014990	03B263 (EL50/2)	12.92	28.6	7,351	258.4	22.03	77.97	58.98	19.19
531	EL-A014971	EL0204 Sel	12.71	27.8	7,077	254.2	21.41	78.59	59.34	18.60
521	EL-A013514	03B023	13.06	26.4	6,881	261.2	20.49	79.51	63.67	17.39
523	EL-A013700	02B097	12.20	25.2	6,250	243.9	19.10	80.90	63.67	16.54
545	EL-A019297-2	2005 Range A mix	13.58	22.5	6,102	271.6	21.12	78.88	64.30	17.95
544	EL-A019278-2	2005 Group A mix	13.25	22.7	6,038	265.1	21.37	78.63	62.05	18.12
524	EL-A013704	02B096	10.90	27.5	6,024	218.0	18.56	81.44	59.48	17.90
546	EL-A013486-2	03B061	12.92	22.9	5,958	258.5	21.39	78.61	60.30	18.09
529	EL-A014966	SP85657CMSxSR97	13.10	22.6	5,930	261.9	21.14	78.86	61.94	17.56
527	EL-A014963	EL51 Sel	12.07	19.3	4,798	241.4	20.17	79.83	59.70	17.42
543	EL-A013486-1	03B061	12.53	19.2	4,764	250.6	21.34	78.66	58.53	16.74
540	EL-A019297-1	2005 Range A mix	12.27	14.6	3,577	245.3	21.12	78.88	58.09	17.87
539	EL-A019278-1	2005 Group A mix	12.81	19.5	3,561	256.2	21.58	78.42	58.70	18.12
Grand Mean			13.91	28.0	7,862	278.2	21.51	78.49	64.58	18.43
LSD (0.05)			1.51	6.9	2,037	30.1	1.93	1.93	4.33	1.52
CV (%)			13.60	21.8	27.4	13.6	7.36	2.02	9.15	7.10
F value			9.72***	3.37***	6.01***	9.72***	2.42***	2.42***	12.11***	3.10***

Table 3: Agronomic evalutaion of Test 06BB02

Entry	Accession	Description	Stand (5/9)	Harvest Stand	Stand Index	T/A
487	EL-A019306	EL51 Rhiz sln (border row)	84.7	56.7	0.7	42.1
450	EL-A013475	EL0204 IC-A	53.0	46.7	0.9	41.7
479	EL-A014979	mixer: EL0204,EL40,EL50,USH20	35.0	38.7	1.1	40.0
436	EL-A014207	(SP6822-4 X 625-4)	104.3	42.3	0.4	38.6
435	EL-A014204	(SP6822-4 X 625-4)	106.3	46.0	0.5	37.9
481	EL-A014974	mixer: EL0204,EL40,EL50,USH20	53.3	36.7	0.7	37.3
495	EL-A014964	mixer: EL51,EL0204	18.7	59.3	3.2	36.7
497	EL-A013491	mixer: EL51,EL0204,SR94,SR97	65.0	37.3	0.6	36.4
468	EL-A013499	EL0204/ag sel	82.7	40.0	0.5	36.2
442	EL-A014215	(SP6822-4 X 625-4)	121.0	40.0	0.3	36.1
443	EL-A014216	(SP6822-4 X 625-4)	107.3	46.7	0.4	35.9
480	EL-A014975	mixer: EL0204,EL40,EL50,USH20	49.3	26.3	0.6	35.4
465	EL-A013700	Broad Mix group C	16.7	53.0	3.2	35.3
482	EL-A014981	mixer: EL51,EL0204,SR94,SR97	48.3	38.0	0.8	35.0
464	EL-A013704	WC980435=EL51=96RR	85.7	45.3	0.6	35.0
498	EL-A014971	mixer: EL51,EL0204,SR94,SR97	69.7	53.7	0.8	34.9
492	EL-A013489	01B002-01B010 sel	52.3	39.7	0.7	34.8
489	EL-A019304	Mix: O-Type	48.0	46.0	1.0	34.8
472	EL-A013503	95HS2/sel	33.7	45.0	1.5	34.7
473	EL-A013501	EL0204/sel	59.0	41.7	0.7	34.4
467	EL-A013698	00B041 = 61G1X03,77B2-01, etc.	109.0	44.3	0.4	34.4
474	EL-A013508	SR96/sel	65.0	35.3	0.5	34.1
503	EL-A019310	96RM13-02	40.0	44.3	1.2	34.0
451	EL-A013476	EL0204 IC-B	47.0	26.7	0.6	34.0
494	EL-A014970	MIX 01 RHIZOC	46.7	49.3	1.1	33.2
437	EL-A014208	(SP6822-4 X 625-4)	62.0	39.7	0.6	32.8
499	EL-A014972	mixer: EL51,EL0204,SR94,SR97	52.7	42.3	0.8	32.6
469	EL-A013500	EL0204/pyt sel	63.3	39.3	0.6	32.3
458	EL-A013514	01B006/sel	57.3	33.0	0.6	32.0
459	EL-A013521	EL0204/sel	53.7	40.3	0.8	31.9
441	EL-A014209	(SP6822 X 625-4) ms OP	80.0	38.7	0.5	31.8
475	EL-A013510	SR97/sel	45.7	31.3	0.7	31.2
466	EL-A019297	EI Rhizoc. EL0204, SR96/97	28.0	21.0	0.8	30.8
439	EL-A014211	(SP6822-4 X 625-4)	76.3	45.0	0.6	30.2
477	EL-A014973	mixer: EL0204,EL40,EL50,USH20	56.0	36.7	0.7	29.3
483	EL-A015023	93EL657CMS	78.0	49.0	0.7	29.0
457	EL-A013479	USH20 IC-C	43.7	22.7	0.6	29.0
491	EL-A013488	WC010218/00J12-01	29.3	26.0	0.9	28.9
455	EL-A013481	SR97	22.0	30.0	1.6	28.8
463	EL-A013705	96RM14-01	71.7	47.7	0.7	28.6
470	EL-A013507	SR96/sel	64.7	39.7	0.6	28.4
471	EL-A013506	SR97/sel	63.7	30.0	0.5	28.3
490	EL-A019295	Mix: CMS	59.3	44.0	0.7	28.2
452	EL-A013477	EL0204 IC-C	42.7	24.3	0.6	28.2
504	EL-A019303	Nematode (cyst) R from Salinas	62.3	61.7	1.0	27.4
447	EL-A013472	USH20 IC-A	36.3	28.3	0.8	27.0
478	EL-A014980	mixer: EL0204,EL40,EL50,USH20	51.0	37.0	0.7	26.9
440	EL-A014210	(SP6822-4 X 625-4)	65.0	43.3	0.7	26.3
500	EL-A019277	SR, mm, Rhizoc	63.3	45.3	0.7	26.2
461	EL-A015022	F4 SR Comp mm 16-17%	123.0	42.0	0.4	25.9

Table 3: (con't)

446	EL-A013474	6869-1 X 409-7	8.0	36.3	4.8	25.7
453	EL-A013478	SR96 IC-A	62.0	36.0	0.6	25.6
476	EL-A014966	mixer: 91HS10,FC607CMSxSR94, etc.	29.0	19.3	0.7	25.2
460	EL-A014989	mm sel 2x Rhizoc SR	77.0	32.3	0.4	24.8
438	EL-A014214	(SP6822-4 X 625-4)	85.7	46.7	0.5	24.8
456	EL-A013480	USH20 IC-B	45.7	16.0	0.4	24.6
488	EL-A019305	EL0204 Rhiz sln (border row)	78.7	42.0	0.5	24.4
454	EL-A013482	SR96 IC-B	35.7	30.0	0.9	24.4
0	EL-A000000	HME17	125.0	32.0	0.5	23.6
493	EL-A013490	02B095-01, FC sel	39.3	34.0	0.9	23.6
496	EL-A014963	mixer: EL51,EL0204	65.7	21.0	0.3	23.5
484	EL-A019278	SR96/97, EL0204	23.7	18.0	0.8	23.5
502	EL-A019311	99J01-24	53.3	39.0	0.7	22.5
448	EL-A013486	96N7-00 IC	45.7	27.7	0.6	22.1
486	EL-A019294	Hero Rhiz sln	66.7	33.7	0.5	17.8
501	EL-A019309	95J11	65.0	21.3	0.4	17.4
462	EL-A019298	95HS3	95.0	16.3	0.2	16.7
485	EL-A019278	SR96/97, EL0204	21.0	18.0	0.8	15.9
444	EL-A014986	Y03-384- (6869x625)	37.7	25.0	0.7	14.0
445	EL-A019307	6869-1 X 409-7	58.7	22.3	0.4	10.4
434	EL-A013485	Y03-384-MIX	16.7	13.0	0.9	8.5
449	EL-A019308	SP6822 IC	68.3	9.0	0.1	6.7
Grand Mean			58.4	36.4	0.8	29.0
LSD (0.05)			15.8	11.2	0.4	7.0
CV (%)			45.4	34.2	89.6	28.1
F value			20.16***	7.62***	22.46***	8.82***

Table 4: Leaf spot ratings for commercial entries in the BSDF nursery

Entry	Contributor	ID	mean M1	sd M1	mean M2	sd M2
1	Western Sugar	WS 1	9.5	0.6	7.8	0.5
2	Western Sugar	WS 2	9.5	0.6	7.3	1.0
3	Western Sugar	WS 3	8.8	1.3	7.3	0.5
4	Western Sugar	WS 4	10.0	0.0	7.5	0.6
5	Western Sugar	WS 5	8.5	3.0	7.3	1.0
6	Western Sugar	WS 6	10.0	0.0	8.0	0.0
7	Western Sugar	WS 7	6.5	1.9	6.3	0.5
8	Western Sugar	WS 8	10.0	0.0	8.0	0.0
9	Western Sugar	WS 9	9.8	0.5	8.0	0.0
10	Western Sugar	WS 10	10.0	0.0	8.0	0.0
11	Western Sugar	WS 11	8.3	1.0	6.0	0.8
12	Western Sugar	WS 12	9.5	0.6	8.0	0.0
13	Western Sugar	WS 13	8.8	1.5	8.0	0.0
14	Western Sugar	WS 14	7.0	0.8	5.5	1.0
15	Western Sugar	WS 15	7.8	1.5	6.8	0.5
16	Western Sugar	WS 16	10.0	0.0	8.0	0.0
17	Western Sugar	WS 17	7.8	1.5	6.5	1.0
18	Western Sugar	WS 18	7.5	1.7	6.8	1.5
19	Western Sugar	WS 19	9.5	0.6	8.0	0.0
20	Western Sugar	WS 20	9.5	0.6	8.0	0.0
21	Western Sugar	WS 21	9.3	1.0	7.5	0.6
22	Western Sugar	WS 22	8.5	1.0	7.8	0.5
23	Western Sugar	WS 23	8.5	1.3	5.8	0.5
24	Western Sugar	WS 24	9.5	0.6	7.3	1.0
25	Western Sugar	WS 25	8.0	0.8	6.0	0.8
26	Western Sugar	WS 26	8.3	2.2	6.0	0.8
27	Western Sugar	WS 27	10.0	0.0	8.0	0.0
28	Western Sugar	WS 28	9.0	0.0	5.5	1.3
29	Western Sugar	WS 29	6.3	1.5	6.3	1.3
30	Western Sugar	WS 30	9.0	0.0	6.8	1.3
31	Western Sugar	WS 31	9.0	1.2	6.5	0.6
32	Western Sugar	WS 32	9.3	0.5	7.5	0.6
33	Western Sugar	WS 33	9.5	0.6	7.3	0.5
34	Western Sugar	WS 34	9.8	0.5	7.5	0.6
35	Western Sugar	WS 35	10.0	0.0	6.8	0.5
36	Western Sugar	WS 36	9.8	0.5	7.8	0.5
37	Western Sugar	WS 37	8.5	0.6	6.3	1.0
38	Western Sugar	WS 38	7.5	1.9	6.3	0.5
39	Western Sugar	WS 39	9.0	2.0	7.8	0.5
40	Western Sugar	WS 40	8.3	2.2	6.8	1.3
41	Western Sugar	WS 41	8.5	0.6	6.5	0.6
42	Western Sugar	WS 42	8.3	2.2	6.8	0.5
43	Western Sugar	WS 43	10.0	0.0	7.8	0.5
44	Western Sugar	WS 44	9.5	0.6	7.8	0.5
45	Western Sugar	WS 45	9.3	1.0	7.8	0.5
46	Western Sugar	WS 46	9.8	0.5	8.0	0.0
47	Western Sugar	WS 47	9.3	1.0	7.3	1.0
48	Western Sugar	WS 48	10.0	0.0	7.5	0.6
49	Western Sugar	WS 49	8.3	2.2	6.0	0.8
50	Western Sugar	WS 50	9.0	0.0	7.0	0.8
51	Western Sugar	WS 51	9.3	0.5	6.8	1.0

Table 4: (con't)

Entry	Contributor	ID	mean M1	sd M1	mean M2	sd M2
52	Western Sugar	WS 52	9.0	0.8	7.0	0.8
53	Western Sugar	WS 53	8.3	1.3	6.8	1.0
54	Western Sugar	WS 54	9.0	0.8	7.8	0.5
55	American Crystal	CS 1	9.5	0.6	7.3	0.6
56	American Crystal	CS 2	10.0	0.0	7.8	0.5
57	American Crystal	CS 3	9.8	0.5	7.8	0.5
58	American Crystal	CS 4	9.8	0.5	7.8	0.5
59	American Crystal	CS 5	9.3	1.0	8.0	0.0
60	American Crystal	CS 6	9.8	0.5	8.0	0.0
61	American Crystal	CS 7	9.5	0.6	8.0	0.0
62	American Crystal	CS 8	10.0	0.0	7.3	1.0
63	American Crystal	CS 9	9.8	0.5	8.0	0.0
64	American Crystal	CS 10	9.0	2.0	7.5	0.6
65	American Crystal	CS 11	7.0	2.4	4.5	1.0
66	American Crystal	CS 12	10.0	0.0	8.0	0.0
67	American Crystal	CS 13	9.5	0.6	8.0	0.0
68	American Crystal	CS 14	10.0	0.0	7.8	0.5
69	Southern Minnesota	SM 1	10.0	0.0	7.8	0.5
70	Southern Minnesota	SM 2	9.8	0.5	8.0	0.0
71	Southern Minnesota	SM 3	7.8	1.3	6.0	0.8
72	Southern Minnesota	SM 4	9.0	1.2	6.8	0.5
73	Southern Minnesota	SM 5	9.5	1.0	8.0	0.0
74	Southern Minnesota	SM 6	9.8	0.5	7.3	1.0
75	California Beet Growers	CA 1	10.0	0.0	7.8	0.5
76	California Beet Growers	CA 2	8.3	2.1	7.5	1.0
77	California Beet Growers	CA 3	10.0	0.0	8.0	0.0
78	California Beet Growers	CA 4	9.3	1.5	7.5	0.6
79	California Beet Growers	CA 5	9.5	1.0	8.0	0.0
80	California Beet Growers	CA 6	10.0	0.0	8.0	0.0
81	California Beet Growers	CA 7	10.0	0.0	7.8	0.5
82	California Beet Growers	CA 8	9.8	0.5	7.8	0.5
83	California Beet Growers	CA 9	10.0	0.0	7.8	0.5
84	California Beet Growers	CA 10	10.0	0.0	7.8	0.5
85	California Beet Growers	CA 11	9.8	0.5	8.0	0.0
86	California Beet Growers	CA 12	9.5	1.0	7.5	1.0
87	California Beet Growers	CA 13	9.8	0.5	7.5	0.6
88	California Beet Growers	CA 14	9.5	1.0	7.0	0.8
89	California Beet Growers	CA 15	8.0	1.2	6.3	1.5
90	California Beet Growers	CA 16	9.8	0.5	8.0	0.0
91	California Beet Growers	CA 17	9.3	1.5	7.5	0.6
92	California Beet Growers	CA 18	9.8	0.5	7.5	0.6
93	California Beet Growers	CA 19	9.5	0.6	7.5	0.6
94	California Beet Growers	CA 20	7.5	2.5	4.5	0.6
95	California Beet Growers	CA 21	9.8	0.5	7.8	0.5
96	California Beet Growers	CA 22	9.8	0.5	7.8	0.5
97	Resistant Check (c1)	LSR	5.0	2.2	4.8	0.5
98	Susceptible Check (c2)	LSS	10.0	0.0	7.8	0.5
99	Resistant Check (c3)	C355	2.5	0.6	3.5	0.6
0	Resistant Check (c4)	EL50/2	2.3	0.5	2.5	1.0
Grand Mean			8.99		7.17	
LSD (0.05)			1.49		0.92	
CV (%)			18.14		16.24	
F value			6.34***		9.46***	

LSS = Leaf Spot Susceptible = Ft. Collins USDA synthetic check 19941027

LSR = Leaf Spot Resistant = Ft. Collins Hybrid 821051H2

Table 5: Leaf spot ratings for USDA-ARS entries in the BSDF nursery

Entry	Contributor	Accession	Entry	mean M1	sd	mean M2	sd
1	Fargo, ND	05N0090	F1016	7.7	0.6	6.3	0.6
2	Fargo, ND	05N0101	F1016/961009H2 (Half-sib families)	4.3	2.5	5.0	1.7
3	Fargo, ND	05N0102	F1016/961009H2 (Half-sib families)	4.0	2.0	5.3	0.6
4	Fargo, ND	05N0103	F1016/961009H2 (Half-sib families)	3.0	2.6	4.5	2.1
5	Fargo, ND	05N0105	F1016/961009H2 (Half-sib families)	5.5	0.7	5.5	0.7
6	Fargo, ND	05N0106	F1016/961009H2 (Half-sib families)	5.3	1.2	6.3	1.2
7	Fargo, ND	05N0108	F1016/961009H2 (Half-sib families)	4.0	1.0	5.5	0.7
8	Fargo, ND	05N0109	F1016/961009H2 (Half-sib families)	7.3	2.9	7.0	1.0
9	Fargo, ND	05N0110	F1016/961009H2 (Half-sib families)	5.7	2.1	6.7	0.6
10	Fargo, ND	05N0111	F1016/961009H2 (Half-sib families)	6.0	1.0	6.3	1.5
11	Salinas, CA	-	HM-E17	4.3	1.5	4.7	1.2
12	Salinas, CA	-	EL-SP22-0	5.7	1.5	4.3	1.5
13	Salinas, CA	-	BETA 4430R	10.0	0.0	8.0	0.0
14	Salinas, CA	-	Y595	7.3	2.9	6.3	0.6
15	Salinas, CA	-	P531CT(sp)	6.7	2.3	6.0	1.0
16	Salinas, CA	-	R522	10.0	0.0	7.3	0.6
17	Salinas, CA	-	R521	6.3	4.6	6.0	1.0
18	Salinas, CA	-	R539	7.0	2.6	5.0	1.4
19	Salinas, CA	-	Z510	8.7	2.3	8.0	0.0
20	Salinas, CA	-	5944	5.7	2.5	6.7	1.5
21	Salinas, CA	-	5933	7.3	2.1	7.3	0.6
22	Salinas, CA	-	CR411	5.3	1.2	4.3	0.6
23	Salinas, CA	-	CR311-6	4.0	2.0	4.3	1.2
24	Salinas, CA	-	CR511-88	6.3	0.6	6.7	1.2
25	Salinas, CA	-	CR509-1-312	8.3	2.1	7.3	0.6
26	Salinas, CA	-	CR510-2-305	5.7	1.2	5.0	1.0
27	Salinas, CA	-	CR511-7-302	2.7	1.2	4.0	1.0
28	Salinas, CA	-	CR311-6H50	6.3	2.5	5.7	1.5
29	Salinas, CA	-	CR511-88H50	6.7	2.5	6.3	1.2
30	Salinas, CA	-	CR509-1-312H50	7.0	2.6	6.3	2.1
31	Salinas, CA	-	CR510-2-305H50	5.7	1.2	5.0	1.0
32	Salinas, CA	-	CR511-7-302H50	6.0	1.0	4.7	0.6
33	Salinas, CA	-	05-FC1036H50	6.3	1.5	5.7	0.6
34	Salinas, CA	-	04-FC1028	7.7	1.5	7.3	0.6
35	Salinas, CA	-	04-FC1037	6.3	1.5	6.7	0.6
36	Salinas, CA	-	04FC1038	6.5	0.7	6.3	1.5
37	Salinas, CA	-	05-FC1022	7.3	2.5	7.3	0.6
38	Salinas, CA	-	05-FC1018	4.0	1.0	4.0	1.7
39	Salinas, CA	-	05-FC1019	8.0	1.0	7.3	0.6
40	Salinas, CA	-	05-fc1030-15(sp)	6.0	3.0	5.7	1.5
41	Salinas, CA	-	05-FC1030-16(sp)	6.0	2.6	6.7	1.2
42	Salinas, CA	-	05-FC1023M(Iso)	8.0	1.0	6.7	0.6
43	Salinas, CA	-	05-FC1036H50	5.7	1.5	7.0	0.0
44	Salinas, CA	-	05-FC1030-15H50	9.0	1.0	7.7	0.6
45	Salinas, CA	-	051030-16H50	8.3	2.9	7.3	1.2
46	Salinas, CA	-	05-FC1023H50	8.7	1.5	7.7	0.6
47	Fort Collins, CO	19831085HO	FC708	2.7	1.5	5.3	2.1
48	Fort Collins, CO	19911026HO	FC715	3.0	1.7	5.3	1.5
49	Fort Collins, CO	19921021	FC703-5	5.3	2.1	4.7	1.5
50	Fort Collins, CO	19921022	FC702-7	4.7	1.2	6.0	1.0
51	Fort Collins, CO	19921025	FC728	6.0	1.0	6.0	1.7

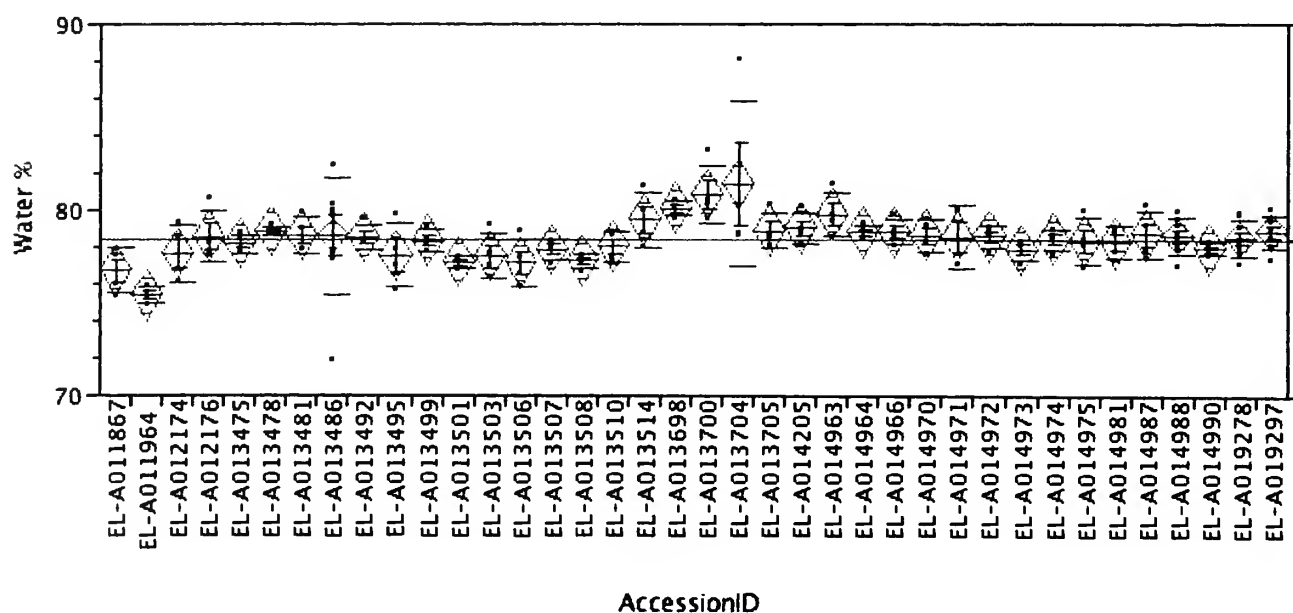
Table 5: (con't)

52	Fort Collins, CO	19951017	FC727	7.3	2.1	6.3	1.5
53	Fort Collins, CO	1997A050	FC607	3.7	1.2	3.0	1.0
54	Fort Collins, CO	19981025	FC717	5.0	1.0	5.7	1.2
55	Fort Collins, CO	19821052	FC709-2	8.3	0.6	7.7	0.6
56	Fort Collins, CO	19741026H	maritima backcross	4.7	1.5	4.7	0.6
57	Fort Collins, CO	19771082	LSR CTR population	7.0	2.0	5.3	0.6
58	Fort Collins, CO	19911043HO	FC403	9.0	1.0	8.0	0.0
59	Fort Collins, CO	19911043HO1	FC403CMS	8.3	2.1	7.7	0.6
60	Fort Collins, CO	19921019	FC729	4.7	2.1	5.7	1.2
61	Fort Collins, CO	19931007	FC720	5.7	1.5	7.0	0.0
62	Fort Collins, CO	19931012	FC901	7.3	3.1	7.3	1.2
63	Fort Collins, CO	19951016HO	FC723	8.0	1.0	8.0	0.0
64	Fort Collins, CO	19951016HO1	FC723 CMS	8.0	2.0	7.0	1.0
65	Fort Collins, CO	19961010HO	FC722	3.7	1.5	6.0	1.0
66	Fort Collins, CO	19961010HO1	FC722 CMS	5.3	3.2	6.0	1.4
67	Fort Collins, CO	19961014	FC724	5.3	1.5	6.7	0.6
68	Fort Collins, CO	19971017	FC710(4X)	4.0	1.0	4.3	1.2
69	Fort Collins, CO	20001007	LSR w/ Fargo	4.3	2.1	5.7	1.5
70	Fort Collins, CO	20001017	FC720	3.0	1.0	5.0	1.7
71	Fort Collins, CO	20051020	FC710(4X)	5.7	1.5	5.7	0.6
72	Fort Collins, CO	20011002bbPF	WB850 x SucroseMM	8.3	0.6	6.0	1.7
73	Fort Collins, CO	20011007	F3 LSR MM x RhzcR/LSR	5.7	2.1	6.3	1.5
74	Fort Collins, CO	20011045PF	(SucroseMM x PI540599)F2	7.7	1.5	6.3	0.6
75	Fort Collins, CO	20021018HO	FC712/Mono-Hy A4	6.0	4.4	6.7	1.2
76	Fort Collins, CO	20021018HO1	FC712/MonoHy A4 CMS	8.0	1.7	7.3	0.6
77	Fort Collins, CO	20031025	FC72	7.0	3.5	6.0	1.0
78	Fort Collins, CO	20041010HO	FC712/MonoHyA4	6.7	1.2	6.7	1.2
79	Fort Collins, CO	20041010HO1	FC712/MonoHyA4	5.0	1.7	5.0	1.7
80	Fort Collins, CO	20041012	FC123MM, ½ sib of FC301	7.0	3.0	6.0	1.0
81	Fort Collins, CO	20051007HOP	half sib selection within FC201	5.7	3.2	6.0	2.0
82	Fort Collins, CO	20051021	FC201	8.7	0.6	7.3	1.2
83	Fort Collins, CO	20051022	FC301	4.7	1.5	5.7	0.6
84	Fort Collins, CO	19941027	LSS = synthetic check	9.7	0.6	7.7	0.6
85	Fort Collins, CO	821051H2	LSR	3.3	2.1	3.7	0.6
86	East Lansing, MI	EL-A012160	SR97	5.3	0.6	6.0	1.0
87	East Lansing, MI	EL-A012172	SR94	7.3	1.5	6.3	0.6
88	East Lansing, MI	EL-A012176	(96RHS21-7)	8.0	1.0	7.0	1.0
89	East Lansing, MI	EL-A012189	SR96	8.3	1.5	6.7	0.6
90	East Lansing, MI	EL-A012194	EL50	1.7	1.2	1.7	1.2
91	East Lansing, MI	EL-A012858	EL0204	9.0	1.0	6.7	0.6
92	East Lansing, MI	EL-A013487	C869 CMS x 2003 Botany East	7.0	2.8	4.5	2.1
93	East Lansing, MI	EL-A013499	EL0204/ag sel	6.7	2.3	6.5	0.7
94	East Lansing, MI	EL-A013500	EL0204/pyt sel	7.3	2.5	6.0	2.0
95	East Lansing, MI	EL-A013501	SR96/sel	6.3	2.9	4.7	1.5
96	East Lansing, MI	EL-A013503	SR97/sel	7.0	1.4	4.0	1.7
97	East Lansing, MI	EL-A013507	EL0204/sel	8.3	1.2	6.7	0.6
98	East Lansing, MI	EL-A013514	01B006/sel	4.3	3.1	2.3	0.6
99	East Lansing, MI	EL-A013699	(fodder x sugar 89F2-2)	8.7	0.6	6.7	0.6
100	East Lansing, MI	EL-A013702	EL55 / TBA	2.0	1.0	3.3	2.5
101	East Lansing, MI	EL-A013474	IC w/ 03B031,36,41,46,48,50,51,52,57,6	7.7	2.3	6.3	2.1
102	East Lansing, MI	EL-A014963	mixer: EL51,EL0204	3.3	2.3	3.3	1.5
103	East Lansing, MI	EL-A014970	mixer: EL51,EL0204,SR94,SR97	8.3	1.2	6.7	0.6

Table 5: (con't)

104	East Lansing, MI	EL-A014972	mixer: EL51,EL0204,SR94,SR97	7.0	1.0	5.3	0.6
105	East Lansing, MI	EL-A014973	mixer: EL0204,EL40,EL50,USH20	4.3	1.2	3.0	2.0
106	East Lansing, MI	EL-A014981	mixer: EL51,EL0204,SR94,SR97	4.7	1.5	2.7	0.6
107	East Lansing, MI	EL-A014986	Y03-384- (6869x625)	9.0	1.0	6.7	0.6
108	East Lansing, MI	EL-A014990	EL50/2	2.3	1.5	1.0	0.0
109	East Lansing, MI	EL-A015020	SR Composite F4	5.7	2.5	4.0	2.0
110	East Lansing, MI	EL-A015028	C869	9.3	0.6	7.3	0.6
111	East Lansing, MI	EL-A015030	SP7322	5.3	1.5	5.3	1.2
112	East Lansing, MI	EL-A015032	USH20	7.3	2.5	6.3	0.6
113	East Lansing, MI	EL-A019294	Mix: O-Type	7.7	2.1	5.0	0.0
114	East Lansing, MI	EL-A019295	Mix: CMS	5.3	2.9	5.0	2.0
115	East Lansing, MI	EL-A019297	El Rhizoc. EL0204, SR96/97 (composite	5.0	2.0	5.0	1.0
116	East Lansing, MI	EL-A019298	2005 Botany Irr mix (composite)	4.7	1.2	3.0	1.0
117	East Lansing, MI	EL-A013493	IC w/ 03B16,18,19,49,51,54,55,56,59,60	6.3	2.1	5.7	2.3
118	Resistant Check	821051H2		3.7	0.6	3.3	1.2
119	Susceptible Check	19941027		9.7	0.6	8.0	0.0
120	Resistant Check	C355		2.7	0.6	2.0	1.0
Grand Mean				6.19		5.77	
LSD (0.05)				3.07		1.86	
CV (%)				39.69		30.11	
F value				2.97***		4.71***	

Table 1: Mean water content of roots harvested from Test 06BB01. Lower numbers are better.



UNDERSTANDING TRANSCRIPTION FACTORS IN SUGAR BEETS: GENETIC AND PHYSICAL MAPPING, DIFFERENTIAL EXPRESSION, AND CONSERVATION BETWEEN RELATED GERMPLASM

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Abstract

Transcription factors control all biological processes at the cellular level, but their role in sugar beets is still widely unknown. In order to develop a greater understanding, 47 primer pairs were designed around expressed tag sequences (ESTs) whose putative functions are various transcription factors. These primers were used to try and discover genetic and physical markers, examine expression in six cDNA libraries, and examine conservation between related germplasms. No genetic or physical markers were mapped on an existing map, but five primer pairs were linked to each other to form an island that can be placed on the genetic map as more markers are discovered. Expression data matched expected data for three transcription factors based on their known function in other organisms, indicating similar biological roles in sugar beet as their known functions in other plants. The conservation data also confirmed the existing phylogeny of the eight germplasm tested.

Introduction

Sugar beets (*Beta vulgaris* L.) represent one of two crops that are grown exclusively for sucrose production. They produce more than a third of the world's sucrose supply and are second only to the sugar cane, which until a few centuries ago was the only available source of pure sucrose. The sugar beet typically grows in temperate regions in the northern hemisphere and is grown on every populous continent except Australia (Cooke & Scott 1993).

There are four major groups of cultivated beets, each with a specific use. Leaf beets (e.g. Swiss Chard) are cultivated for their leaves, sugar beets for their sugar, garden beets for their roots, and fodder beets for feeding animals. All varieties of beets are ancestors of the wild maritime beet (*Beta vulgaris* ssp. *maritima*). Beets as a whole have also historically been grown for their leaves since the ancient Greeks and for their roots since the 1500s. It has only been a relatively recent invention in the history of beets to extract pure sugar from the roots of beets. Sucrose extraction from beets was not discovered until 1747 by Marggraf and was not conducted on a large scale until 1802 by Marggraf's student Achard. The major driving force behind the spread of the sugar beet industry was the shortage of British cane sugar during the Napoleonic wars (Winner 1993).

As with all major crops, farmers and scientists are constantly seeking to improve important agronomical traits through breeding. For sugar beets, some of these traits include higher sucrose content and root yield, pest resistance, and disease resistance. Current understanding of genetics and specifically genetic markers can assist in the selection and breeding of these favorable traits (Bosemark 1993).

Genetic markers have a number of applications and can be used to construct genetic linkage maps, fingerprint genotypes, marker-assisted selection, and to determine genetic diversity of germplasms (Bosemark 1993; Skaracis 2005). There are a number of types of markers including restriction fragment length polymorphisms (RFLPs), amplified fragment length polymorphisms

(AFLPs), random amplified polymorphic DNA (RAPDs), single nucleotide polymorphisms (SNPs), and simple sequence repeats (SSRs), also known as micro-satellites (Varshney 2005). These markers are commonly used to develop genetic maps, which place markers on linkage groups based on recombination. The construction of marker-saturated maps is important for studies on gene function, regulation, and expression and is vital for any work on breeding using marker-assisted selection (Skarcias 2005).

Physical markers can be identified from bacterial artificial chromosome (BAC) libraries, which are libraries of large genomic DNA fragments. Identified physical markers on a BAC library can be arranged into contigs, which are overlapping BAC clones (Luo 2003), and can be used to develop physical maps. Physical markers can also provide access to regulatory sequences surrounding traits with agronomic value and contigs with genetic markers can link the genetic map and physical map and assess the quality of integrated genetic maps (Lamoureux 2006). For sugar beets, a BAC library made from hybrid US H20 is publicly available (McGrath 2004).

Other than generating random genetic markers with unknown function, such as RFLPs, AFLPs, and RAPDs, markers with known or putative functions can be identified using expressed sequence tags (ESTs) by designing forward and reverse primers that flank the sequence. Essentially, ESTs are single-pass, roughly sequenced copies of cDNA, which are reverse transcribed from mRNA, which represents an expressed gene (McGrath 2005). These are important because they have actual function. Most importantly, they can be compared against other ESTs with known function and can be assigned putative functions based on how closely related they are. Multiple ESTs that share the same function can also be put together to form a Tentative Consensus (TC). A TC takes all of its ESTs and creates a nucleotide sequence for the putative function based on the most frequently appearing base pairs.

Transcription factors (TFs) are proteins in eukaryotes that bind to DNA and are necessary for RNA polymerase to recognize and attach to DNA. Thus, TFs are vital to all higher organisms and control many biological processes. They activate and repress transcription of genes (de Folter 2006) and can be activated and repressed themselves; expression of many TFs is regulated at the level of transcription (Chen 2002). Identifying their location and where they are expressed can be helpful in understanding their specific biological roles (Czechowski 2004). There are a number of families of TFs as well as different physical structures and they can be very specific or very diverse in what they regulate. The MADS-box family is one example and typically regulates floral organ development of the sepal, petal, stamen, and carpel. The family is also known to play a role in roots, vernalization, flowering time control, and in ovule and seed coat development (Leseberg 2006). Another family includes the AP2 family, which is unique to plants and has a role in the regulation of disease resistance pathways (Gutterson 2004). The WRKY family is another that, like the AP2 family, participates in resistance bacterial and fungal infection. It is also involved in the response to abiotic stresses including drought, cold, and wounding. WRKY TFs are also known to play a role in cell maturation of roots in *Arabidopsis*, fruit maturation in pepper, and in floral and embryonic tissue (Talker 2004). Participation of another family, MYB, is evident in secondary metabolism, cellular morphogenesis, and plant growth regulators (Martin 1997). Basic leucine zipper (bZIP) TFs are different from families of TFs because they are organized based on their DNA-binding domains and represent diverse roles including pathogen defense, light and stress signaling, seed maturation, and flower development in *Arabidopsis* (Jakoby 2002). Another group based on its domain are the basic helix-loop-helix (bHLH) TFs, which like the bZIP TFs, represent a functionally diverse group involved in anthocyanin biosynthesis, phytochrome signaling, fruit dehiscence, carpel and epidermal

development, and stress response (Kim 2006).

In sugar beet, very little is understood about transcription factors and what specific biological processes they are involved in such as development and stress-response. One way to better understand their general function and role is to search for expression in various copy DNA (cDNA) libraries, which are collections of DNA copies of messenger RNA from a specific part of a plant at a specific state or grown in a specific condition. Some available cDNA libraries for sugar beet include germination, stress germination, leaf, 3-week-old root, and 7-week-old root.

Searching for conservation between related germplasm can also provide a greater understanding of transcription factors as a gene class and their role in plant development and in responses to the environment. Conservation can also be used to verify or question existing phylogenetic trees and compare the role of transcription factors in closely related species with those in sugar beets. Transcription factors with known biological function in related germplasm may also have the same or similar biological functions in sugar beet as well.

Methodology

Using the TIGR Beet Gene Index, 33 TC sequences that are similar to transcription factors were identified using the keywords 'transcription factor'. Forward and reverse primers were then designed using the program PrimerSelect for a total of 47 ESTs from the TC sequences. The primers were chosen to meet specific criteria, such as a total length between 18 and 23 base pairs (bp) long, create a fragment length of 350 to 600 bp and have a melting temperature (T_m) between 44°C and 63°C. They also could not have primer pair dimers, primer self-dimers, or primer hairpins with a ΔG value of -3.1 or less. Primer sequences designed from TIGR Sugar Beet Gene Index are listed in Table 1.

TABLE 1: The TC annotations denote the putative functions for the TCs, the sequence IDs are the genbank accession numbers for the ESTs, and the primers flank a segment of its respective EST.

TC Annotation	Sequence ID	Forward Sequence 5' → 3'	Reverse Sequence 5' → 3'
TC107	CK136769	CCGGGGGCGCTCACACTACTTT	GTGCCCTGCTCTGGAAGTCTC
	BQ490452	GTCCGCACTGGTGGTAAGGGTAG	GAAGGTCTCGCCAGCAACAAG
TC140	BQ586687	TTCTCACCTCCCCCAAATCCA	GCGCGTGCTGCCTCGTCT
	BQ490272	TTCTCACCTCCCCCAAATCCA	GCGTGCTGCCTCGTCTTCTTC
TC265	BQ594674	GAAACCTCCGTACCCAAAAATC	GTATCCGGTGACGAAGAACATC
TC297	BQ594789	CAAAAACACGGCCCAAGAACTG	AAAACATGCGAACCAGGAATCACT
	BQ586690	GGATCTTAGCTTGTCGTTACCTG	ATTCTTCCGATCACATTCTTCTG
TC447	BQ589154	CTCATCCGCATCAAGTTCAA	GCTCTGTGCTCATGGTTATCA
TC603	BQ587373	GTAACCCTAACCTCCACAT	TCCATTCCCGAAGTATTG
TC675	CF543190	CACGCGTCCGAACAAGAAGAAAT	CCGGCATCGATCCAAAAGTC
TC837	BI543288	ATTCGGCGTCGTTTAGTATTCA	ATTGGTTTTTGGCCGTATTTTC
	BQ588384	AGAACACCGACACTCACCTG	ACTAAAACAACCTCCACCTCATT
TC924	CF543508	AGACAACGCTGAAAGGGAGTGAT	AAAGCAGCTGCAGTAGAAGAAGT
TC1017	BQ587699	ACTTGTTTTGATTTTGTTAGAA	TTGCAGTTGTAGATGTTGTAGAG
TC1127	CF543723	TCGGAAAATGATGGGTGAA	CATTGCGGATTGATCTTTTTGTC
TC1230	BQ592726	TTCTTCGCTTTAATGTCCTCCTT	AGCCCGAATTTACCAACCTCA
TC1281	BQ586152	GATGTCTCACCCACTCCAG	GTTCCATCACTCGTCTTATTGT

TC1332	BI543775	TCCCAAAGAAAGCAGTAGTGA	TTCTCCCAGCAAGTTCCTC
	BQ584393	TATGAGCTTTCTATTCTTTGTGA	TGATCCAGCATATGTTGACTC
TC2088	BQ592788	ATGGCGGAGAATGCGACTTT	ACTTCCCCACATGCTTATCAACC
TC2312	BQ587647	ATTATTTCCCCCTCCTTTTCTTT	TACGGAGTTGTTGATGGTGGTGA
TC2421	BQ582550	CACACCCTTCATAACTCTC	CATCCCCAACTTGACATTTTT
TC2741	CV301654	TGATGATGATGATGATGATGAGG	TTTAACAGTACGCGTAGGAGCAG
	CV301722	GCTGACCGCTGATTATTTGTG	GTTTTGTGGTGGTGGTGTGAGT
	CV301766	TAATCTCCGACTTCATACCC	AAATTCACCTTGGCCTTCTCAC
	BQ589058	TCCGCCAAGAGAAAGAGAAAGAA	CTCCCCAACCAAAATCAGAACAA
	BQ590424	CAGCACCACCACAAAACATAAAC	TGGGAATCAAAATCAGCATCAG
	BQ590625	GGAGATGCTGTACCTGCTGATAA	CTGCCCAACAAACACCACAAG
TC2855	BQ588656	TTCATCAAAAGCCATCTATTCAG	CACGGCCTTCTCCTCACTCCTC
TC2992	BI543353	TTGAAAATGGCGAAGGAAGTTAC	ACGACGACGACGATTGAGATTAC
TC3338	BQ583169	ATGACTTTTTACTGTTAGATTA	GATATGTGCCCTCCTCAA
TC3409	BQ586609	AGGGTGAGGTTTTTAAGATTGAT	AAGGCCGGTTTCCATTG
TC3460	BQ489149	TTCTCCTTTCTTCAACTTATTTT	AGGGGTGAGCTTGGGGATTAGAT
TC3511	BQ487701	GCTTAATTTGTGGGTTTTGATGT	AGAAGATGTAACCTCCCCAGGTG
TC3591	BQ590555	GGAAAAGTACCCACCAATCT	ATAACAAAATACCACCACATCAG
TC3614	BQ488221	CGTGCTCGAATGGTACTGACTTG	ATGGCATGCTGACTCTTGAA
	BQ593336	TGTTACAGGGAAGCATCGTT	TCTCCTTATTTATAGTTTTACCA
TC3664	BQ489638	CTCTTCTGCTTCACGTATTCTTC	GACTTTTAGCTCCAACCTCCA
	BQ585793	ATCGGCCGTCTCATCCTCTC	TCGCCTGTGCCATTCTAAG
TC3703	CV301701	CCTCTTACCACCACCATTTTACC	CACTGCCATTACCGTTACCT
TC3756	BQ594126	AGCGATGGCAGACACGACGAT	CAGGCTATGACCAGTTTCTTTGA
	BQ593897	GCGGCAGCGAGCAGTAAG	CCCCGTGCAAGGATTGTC
TC3808	BQ488901	GGTCCGGCGCCATTTTTG	TTACGACTCAGCTTTTCTATCT
TC3825	BQ588969	AATTCCTCGACAAAACTCC	AATTACAAGCCTCCATAGCATCC
	BQ593130	ATGCGGAAGAAAGCTACAATCAC	AAACCTTCGGCACCTCAATACTT
TC3880	BQ584750	TGGGGGACATTAGAGGAGT	TTTTTGGTGATTTCGTTGAGT
TC3999	CF543618	AAGGAGGGTGTGGAAGAAAAAG	TGTGCACACCGCTCATAAAG

The primers were then ordered from IDT in a 96-well format and put back into suspension overnight to make each one into a 100 μ M solution. 15 μ L of each solution was then be added to 135 μ L of nuclease-free water (ddH₂O) to create a 10 μ M working stock. These primers were then used to create individual reactions with DNA from the USH20 and F2 pools, which are genetic pools developed from a diverse hybrid and cross between a table beet and a sugar beet respectively. Each reaction contained 7.50 μ L ddH₂O, 10.00 μ L master mix (2xMM), 0.75 μ L of the forward primer from the working stock, 0.75 μ L of the reverse primer from the working stock, and 1.00 μ L of DNA from either of the pools. Polymerase Chain Reaction (PCR) was then be used to amplify the DNA with a program consisting of 94.0°C for 1.5 min, 12 cycles of 94.0°C for 30 s, 58.0°C 0.8°C per cycle for 30 s, 72.0°C for 1 min, 30 cycles of 94.0°C for 1 min, 47.0°C for 30 s, 72.0°C for 30 s, and a final extension at 72.0°C for 10 min. The reactions were then loaded into a pre-made 4% agarose 1xTAE, 6(16+2) wells with EtBr gel by EmbiTec and run with a 1xTAE buffer at 100 volts for 30 minutes and examined under a UV light to determine which primer pairs amplified (Figure 1).

The ones that did amplify the F2 or USH20 pools of DNA were then used to create 16 individual reactions using randomly selected F2 individuals from the F2 pool. Just like the

amplification test for the F2 and USH20 pool, the same procedure was used to examine amplification within the 16 individuals. The gels were also exposed to UV light and examined for an amplification pattern that appeared polymorphic. The primer pairs that did appear polymorphic were then tested using the full F2 population individuals with the same procedure. Those that appeared polymorphic for the full F2 population were quantified for Mendelian segregation using the program JoinMap 3.0 with a minimum log of odds (LOD) score of 3.5.

All the primer pairs were also tested for expression in six cDNA libraries: 10 week old, stress germinated, developmental, inflorescence, leaf, and 1 month cold storage. These libraries were provided by the Sugar Beet and Bean Research Unit located at Michigan State University and differed in the type of tissue or plant stage. For the stress-germinated library, seedlings germinated in pure water were used. Leaves were used for the leaf library, flowers for the inflorescence library, and 10-week-old plants for the 10-week-old library. 18-week-old roots stored at 1°C for five weeks were used for the cold storage library and the developmental library was a composite of multiple plants at different ages. The plants were three to seven weeks old sugar beets harvested weekly. The six cDNA libraries were tested with each primer pair using the identical procedure used for the amplification test of the USH20 and F2 pools.

Along with expression in multiple cDNA libraries, the primer pairs were also used to check for expression in genomic libraries of related organisms. These organisms included ice plant, spinach, quinoa, Swiss chard, wild beat, and three varieties of sugar beet: EL51, F2, and USH20. The genomic libraries were provided by the Sugar Beet and Bean Research Unit located at Michigan State University. The same procedure to test for amplification was used with the exception of the individual PCR reactions. In order to conserve 2xMM and thereby lowering the cost of the experiment, a smaller volume of 15 µL was created using the same concentration, so each reaction contained 5.6250 µL ddH₂O, 7.5000 µL 2xMM, 0.5625 µL FP, 0.5625 µL RP, and 0.7500 µL DNA.

Discussion

Through the mapping experiment, there were a total of 34 out of 47 primer pairs that were expressed in the F2 or USH20 pools. From those, 16 of primer pairs appeared polymorphic with 16 individuals. Out of those, only six looked scoreable. Those six were scored and input into the genetic linkage program JoinMap Version 3.0. Five of those linked with each other to create an island with a LOD score of 3.5. The gels were also scored twice, and the first time lead to a weak linkage of all six transcription factor genes to chromosome six. However, upon rescoring the F2 population, one dropped out of the island and it was no longer weakly linked to the sixth chromosome.

In the cDNA libraries, the transcription factor genes were most heavily expressed within the stress germination, 10-week-old, and developmental libraries. In the inflorescence and leaf libraries, the genes were expressed to a lesser degree and even less in the 1-month cold storage library.

At the individual transcription factor gene level, expression did not follow a specific pattern and was largely distributed. This was especially true for groups of transcription families, which were expected to have at least some degree of consistency.

However, there were individual transcription factors that were differentially expressed as expected. Transcription Factor MADS1 is known to play a role in flower organ identity in rice (Kumar 2005) and in shoot induction and development in *Paulownia kawakamii* (Prakash 2002)

and two different ESTs encoding for MADS1 were expressed in the inflorescence and leaf cDNA libraries. ATB2, a member of the bZIP family, and is known to be expressed in the presence of light and is thought to be involved in the transport and use of metabolites including sucrose (Rook 2002). An EST encoding for ATB2 was expressed in all the libraries, five of which have light exposed tissue and in the root, where sucrose is stored. Another member of the bZIP family, bZIP3, is known to be involved in responding to stress and was expressed in the stress germination, 1 month cold, and developmental libraries.

FIGURE 1: This is the island that contains the five markers that were linked to each other. The island covers a large distance and the markers are spaced far apart. That fact could contribute to the reason why the markers are not strongly linked to any mapped chromosomes.

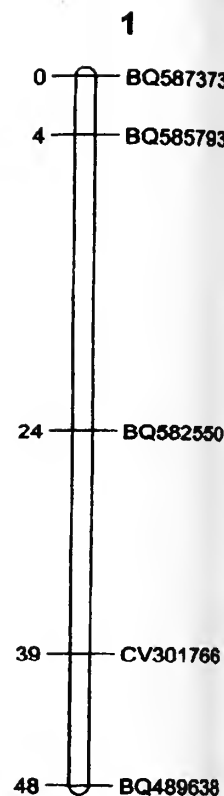


TABLE 2: This table shows the differential expression data from the cDNA libraries. A zero represents an absence of DNA while a one represents a presence of DNA. Many of the putative functions are very general and most only reference a family for the transcription factor. A = 10-week, B = Stress, C = 1-month cold, D = Inflorescence, E = Leaf.

A	B	C	D	E	F	Sequence ID	Putative Function
1	1	1	1	1	0	CK136769	Transcription factor
1	1	1	1	0	1	BQ490452	
0	1	1	1	1	1	BQ586687	AP2 domain transcription factor
1	1	1	1	1	1	BQ490272	
0	1	1	1	1	0	BQ594674	Transcription factor like protein
0	1	1	1	1	0	BQ594789	Myb-related transcription factor-like
0	1	1	1	1	1	BQ586690	
0	1	1	0	1	0	BQ589154	MYB transcription factor-like
1	1	1	1	1	1	BQ587373	Transcription factor AtVOZ1
0	0	1	0	0	0	CF543190	Myb family transcription factor-like
0	1	1	1	1	1	BI543288	WRKY transcription factor 68
0	1	1	1	1	1	BQ588384	
0	1	1	1	1	0	CF543508	Oligodendrocyte transcription factor 2
0	0	0	0	0	0	BQ587699	WRKY transcription factor NtEIG-D48
1	1	1	0	1	0	CF543723	Transcription factor MADS27
1	1	1	0	1	1	BQ592726	Heat shock transcription factor 8
1	1	1	1	1	1	BQ586152	AtbZIP transcription factor
0	0	0	1	0	1	BI543775	MADS box transcription factor MADS1
0	0	0	1	0	1	BQ584393	
1	1	1	1	1	1	BQ592788	BZIP family transcription factor
0	1	0	0	1	0	BQ587647	Transcription factor PCF3-like

0	0	1	0	1	0	BQ582550	Transcription factor AtVOZ1
1	1	1	1	1	1	CV301654	Ethylene transcription factor
1	1	1	1	1	1	CV301722	
1	1	1	1	1	1	CV301766	
1	1	1	1	1	1	BQ589058	
1	1	1	1	1	1	BQ590424	
1	1	1	1	1	1	BQ590625	
0	1	0	0	1	1	BQ588656	AP2 transcription factor
0	1	1	1	1	1	BI543353	Transcription factor Myb1
0	0	0	0	0	0	BQ583169	MYB transcription factor
0	1	1	1	1	1	BQ586609	Zinc finger transcription factor-like protein
0	1	1	0	1	0	BQ489149	BZIP transcription factor 3
1	1	1	1	1	1	BQ487701	BZIP transcription factor ATB2
0	1	1	0	1	0	BQ590555	Basic leucine zipper transcription factor
0	1	1	0	1	1	BQ488221	bHLH transcription factor
0	1	1	0	1	1	BQ593336	
0	1	1	0	1	1	BQ489638	AtbZIP transcription factor
0	1	1	0	1	1	BQ585793	
0	1	1	1	1	0	CV301701	Transcription factor LIM
0	0	1	1	1	0	BQ594126	Transcription factor IID
1	1	1	1	1	0	BQ593897	
0	1	1	0	1	0	BQ488901	Heat shock transcription factor like protein
1	0	0	0	0	0	BQ588969	MYB transcription factor
0	1	1	0	1	0	BQ593130	
0	0	1	0	0	0	BQ584750	Forkhead-related transcription factor 2
0	1	0	0	0	0	CF543618	Transcription factor CA150b
36.1	80.9	83.0	57.4	80.9	55.3		

For the conservation experiment, the amount of transcription factor genes shared between the organisms decreased as they became less related for the most part. However, the EL51 variety had only 29.8% expression of the genes. Another interesting finding was that although spinach and quinoa were very close in the amount of transcription factor genes expressed, only half of the genes were shared between the two species. There are also a number of cases that go against the classification where spinach, quinoa or ice plant have transcription factor genes that wild beet and swiss chard do not.

TABLE 3: This table shows the presence and absence of DNA with a one and a zero respectively and shows a general trend of less expression with organisms that are more distantly related to sugar beets.

US H20	F2	EL51	Wild Beet	Swiss Chard	Quinoa	Spinach	Ice Plant	Sequence ID	Putative Function
0	1	0	0	0	0	0	0	CK136769	Transcription factor
1	1	0	0	0	1	1	1	BQ490452	
1	1	1	1	1	1	1	1	BQ586687	AP2 domain transcription factor

1	1	1	1	1	1	1	1	BQ490272	
1	1	0	1	1	0	1	0	BQ594674	transcription factor like protein
1	1	1	1	1	1	1	1	BQ594789	Myb-related transcription factor-like
1	1	0	1	1	0	0	0	BQ586690	
1	1	1	1	1	0	1	0	BQ589154	MYB transcription factor-like
1	1	0	0	0	0	1	0	BQ587373	Transcription factor AtVOZ1
1	1	0	0	0	0	0	0	CF543190	Myb family transcription factor-like
1	1	1	1	1	1	0	0	BI543288	WRKY transcription factor 68
1	1	0	1	1	0	0	1	BQ588384	
1	1	1	1	1	1	0	1	CF543508	Oligodendrocyte transcription factor 2
1	0	1	1	0	0	0	0	BQ587699	WRKY transcription factor NtEIG-D48
1	1	0	1	1	0	1	0	CF543723	Transcription factor MADS27
1	1	0	0	0	0	0	0	BQ592726	Heat shock transcription factor 8
1	1	0	1	1	1	0	0	BQ586152	AtbZIP transcription factor MADS box transcription factor MADS1
0	0	0	0	0	0	0	0	BI543775	
0	0	0	0	0	0	0	0	BQ584393	
1	1	0	1	1	1	1	0	BQ592788	BZIP family transcription factor
1	0	0	1	0	0	0	0	BQ587647	Transcription factor PCF3-like
1	1	0	1	1	0	0	0	BQ582550	Transcription factor AtVOZ1
1	1	0	1	0	0	0	0	CV301654	Ethylene transcription factor
1	1	0	1	0	0	0	0	CV301722	
1	0	0	0	0	0	0	0	CV301766	
1	1	0	1	1	1	1	1	BQ589058	
1	1	1	1	1	0	1	0	BQ590424	
1	1	1	1	1	0	0	1	BQ590625	
1	1	0	1	0	0	0	0	BQ588656	AP2 transcription factor
1	0	0	0	0	0	0	0	BI543353	Transcription factor Myb1
1	0	1	1	0	1	1	1	BQ583169	MYB transcription factor
1	1	0	1	1	1	0	0	BQ586609	Zinc finger transcription factor-like protein
1	1	0	1	0	0	0	0	BQ489149	BZIP transcription factor 3
1	1	1	1	1	1	0	1	BQ487701	BZIP transcription factor ATB2
1	1	0	1	1	0	0	0	BQ590555	Basic leucine zipper transcription factor
1	0	0	0	0	0	0	0	BQ488221	bHLH transcription factor
1	1	0	0	0	0	0	0	BQ593336	
1	1	0	1	1	1	1	0	BQ489638	AtbZIP transcription factor
1	1	0	1	0	1	0	0	BQ585793	
1	0	0	0	0	0	1	0	CV301701	Transcription factor LIM

0	0	0	0	0	1	0	0	BQ594126	transcription factor IID
0	0	1	0	0	0	0	0	BQ593897	
1	0	1	1	1	1	0	1	BQ488901	Heat shock transcription factor like protein
1	1	0	0	0	0	0	0	BQ588969	MYB transcription factor
1	0	1	1	0	0	0	0	BQ593130	
1	1	0	1	0	0	1	0	BQ584750	Forkhead-related transcription factor 2
0	0	0	0	0	0	0	0	CF543618	transcription factor CA150b
87.2	70.2	29.8	66.0	44.7	34.0	31.9	23.4		

Conclusions

It was interesting that the markers were linked with each other and not distributed evenly. Currently, five markers are not enough to determine anything and there is still a great likelihood that it was all just chance. However, with 10 or more markers, there could be a few reasons why they link together. The island could be associated with a chromosome that is under represented by genetic markers and be too far away to be significantly linked to those markers or there could be pipetting errors and scoring errors that could result in an artifact. The latter is more reasonable at this point because all of the gels were scored with difficulty; many of the bands were subjective and open to interpretation by the person scoring the gel.

The differential expression data suggests that there is increased expression of transcription factors during times of high biological activity, less transcription factors in specialized tissue, and even less in dormant tissue. Three transcription factors: MADS1, ATB2, and bZIP3 met their expectations of expression based on their known function. They may also take part in similar biological processes for sugar beets as their known functions in other organisms. It also confirms that this procedure is working and that differential expression is dependant on the type of tissue used and the environment under which it was grown in.

As expected, the conservation fell more or less into line with the known phylogeny of the organisms with the exception of the EL51 variety. One probable cause for this could be due to the fact that it is very resistant to *Rhizoctonia* and therefore has a bottleneck due to breeding. Quinoa, beet, and spinach may also have separated from their common ancestor around the same time because of how few of the transcription factors they share with each other. Quinoa may also be more closely related to sugar beet than spinach, but this is not definite because it had only one more transcription factor gene that it shared with sugar beet than spinach did.

Future Research

For the mapping project, more primers could be developed and tested for the ESTs where the primers failed. More ESTs could be tested and the TCs themselves could be tested as well. A backward approach could also be attempted in which the primers would be used to check for amplification within the BAC library. The Sugar Beet and Bean Research Unit at Michigan State University is currently in the process of getting its BAC library's end sequences sequenced, so the end sequences from the wells in which the primers amplify could be examined for possible polymorphisms and tested.

In terms of differential expression, new primers could be designed for the ones that failed and tested again. As new cDNA libraries get developed, the same primers could be tested on those for expression to uncover more about where they are expressed in and what possible role they

may play in the plant. Also, ESTs whose exact transcription factors are known would be better candidates for studying differential expression because their expression could be compared against known function in other organisms.

With the conservation project, new primer pairs could be designed for the ESTs that did not amplify on any of the genomic libraries and more ESTs could be tested in order to gain a greater understanding in related germplasm. Other related organisms could also be tested to verify or challenge the existing phylogenetic tree. And finally, transcription factors from other organisms could be tested as well.

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SEGREGATION FOR SALT TOLERANT GERMINATION AMONG PROGENY OF AMES 3051 SELECTED UNDER SALT GERMINATION CONDITIONS

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Improved germination of seeds under abiotic stress appears to be one means by which improved stand establishment can be accomplished. Salinity is one such stress that may serve a dual purpose by allowing selection for improved stand establishment as well as obtaining a profitable stand in saline soils, which are becoming more prevalent in some parts of the world. The objective of this study was to examine whether improvement in emergence can be achieved through stress selection. In testing, emergence of seven inter-pollinated progeny was compared to that of the parent Ames 3051 when germinated under stress in the lab. Ames 3051 was chosen based from previous experimental results done in collaboration with Egypt's Agricultural Genetic Engineering Institute. In that study, some wild germplasm including Ames 3051 had greater NaCl germination than did cultivated sugarbeet germplasm.

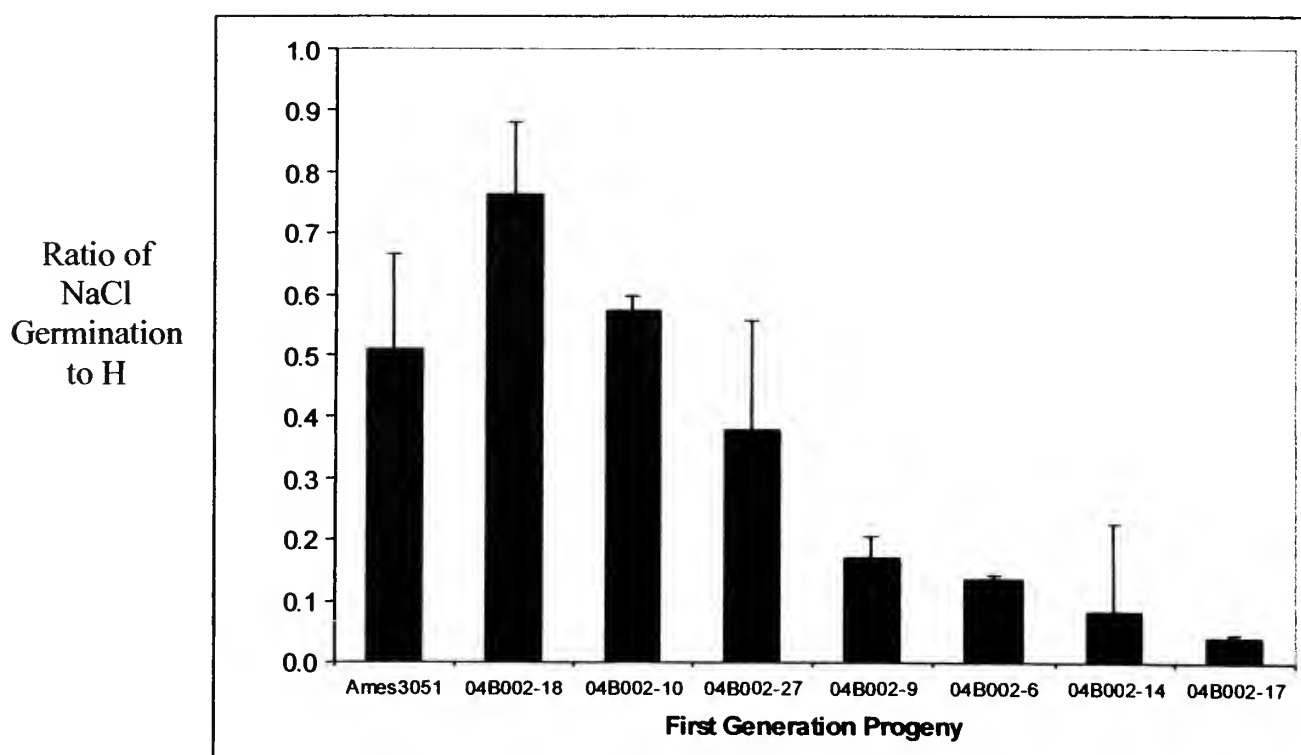
Plant material used were progeny derived from Ames 3051 selected under the stress of 150mM NaCl, with individual identification numbers of 04B002-06, 04B002-09, 04B002-10, 04B002-14, 04B002-17, 04B002-18, and 04B002-2. Seeds of Ames 3051 that germinated within 96 hours were grown in the greenhouse, vernalized, and allowed to inter-pollinate. Three replications of 15 - 25 seeds (depending on seed availability) were germinated in a 150mM NaCl solution or 0.3% H₂O₂ solution for 96 hours, with germinated seeds being counted and removed at 48 hours and a final count at 96 hours. Emergence ratios were based upon their emergence under optimal conditions (determined by the number germinated in H₂O₂), and the number germinated under stress (NaCl). Germination under the two treatments are show in Table 1. Germinated seeds were removed from the NaCl treatment at 48 hours, planted in cone-tainers, and grown under grow lights in the lab for 8 weeks. After 8 weeks the plants were transferred to the greenhouse where they are being grown for seed production.

The applied goal of this study is to determine if breeding for improved stress tolerance will result in greater field emergence. Investigations in other crops suggest that responses to stresses, such as drought, cold, salt and heat, follow a common biochemical stress response pathway. If true for sugar beet, breeding for improved salt stress tolerance during germination may yield improved germination under drought or other stress. In this study, germination percentages varied between accessions, with 04B002-18 showing the highest germination (0.76; on a scale of 0 - 1, where 1 = 100% germination) and the lowest being 04B002-17 (0.04). The overall mean of the progeny germination was lower than that of the parent, however, 04B002-18 showed a marked increase in germination over the parental line. These results indicate an apparent segregation for stress germination ability, and the genetic basis of this trait is of some importance. Overall, stress germination selection may yield an improvement in emergence and stand establishment, however only a proportion of the progeny will have an increased germination. Improved germination in two of seven progeny tested from Ames 3051 was observed, and suggests perhaps the genetic basis for improved salt tolerance may be inherited in a relatively simple manner. Progeny of the Ames 3051 progeny have again been selected under salt stress, and their progeny will be tested for salt stress germination performance, concomitantly with introgressing into sugar beet breeding materials.

TABLE 1. Mean germination of Ames 3051 progeny listed in order of progeny plant ID. Ratio is the number of seeds germinated at 48 hours divided by the total number of seeds in treatment.

Plant ID #	Ratio	Trt	Plant ID#	Ratio	Trt
04B002-6	0.07	NaCl	04B002-6	0.26	H ₂ O ₂
04B002-6	0.13	NaCl	04B002-6	0.20	H ₂ O ₂
04B002-6	0.20	NaCl	04B002-6	0.40	H ₂ O ₂
04B002-9	0.04	NaCl	04B002-9	0.56	H ₂ O ₂
04B002-9	0.08	NaCl	04B002-9	0.40	H ₂ O ₂
04B002-9	0.12	NaCl	04B002-9	0.56	H ₂ O ₂
04B002-10	0.04	NaCl	04B002-10	0.76	H ₂ O ₂
04B002-10	0.08	NaCl	04B002-10	0.68	H ₂ O ₂
04B002-10	0.12	NaCl	04B002-10	0.64	H ₂ O ₂
04B002-14	0.04	NaCl	04B002-14	0.08	H ₂ O ₂
04B002-14	0.08	NaCl	04B002-14	0.08	H ₂ O ₂
04B002-14	0.12	NaCl	04B002-14	0.28	H ₂ O ₂
04B002-17	0.04	NaCl	04B002-17	0.84	H ₂ O ₂
04B002-17	0.08	NaCl	04B002-17	0.68	H ₂ O ₂
04B002-17	0.12	NaCl	04B002-17	0.72	H ₂ O ₂
04B002-18	0.04	NaCl	04B002-18	0.88	H ₂ O ₂
04B002-18	0.08	NaCl	04B002-18	0.76	H ₂ O ₂
04B002-18	0.12	NaCl	04B002-18	0.88	H ₂ O ₂
04B002-27	0.04	NaCl	04B002-27	0.40	H ₂ O ₂
04B002-27	0.08	NaCl	04B002-27	0.60	H ₂ O ₂
04B002-27	0.12	NaCl	04B002-27	0.40	H ₂ O ₂

FIGURE 1. Comparison of the average germination expressed as the ratio of seeds germinated in NaCl divided by the total number germinated under optimal conditions.



LIST OF PREDICTED SIMPLE SEQUENCE REPEATS FROM SUGAR BEET GENBANK ACCESSIONS

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The Caryophyllales as circumscribed by Angiosperm Phylogeny Group contains 31 families, 692 genera, and 11,155 species, and no reference genome yet exists for the Caryophyllales, nor is a complete genome sequence available for a species phylogenetically near this large group of families representing >5% of eudicot diversity. Caryophyllales are thought to have diverged from other major core eudicots around 100 million years ago. Included among the Caryophyllales are the Amaranthaceae (now includes Chenopodiaceae), which contributes several ornamentals and grain species (Celosia, Amaranth), several noxious weeds (pigweed, lamb's quarter's, kochia), quinoa, and, of course, sugar beets (and other leaf and root crops). The Aizoaceae contributes ornamentals such as common ice plant and *Lithops* spp. (living stones) and the leafy vegetable New Zealand spinach, the Portulacaceae contributes purslane as both an ornamental and weedy species, and the Cactaceae contributes *Opuntia* spp. as ornamental and food (prickly pear) as well as psychoactive alkaloids (peyote). Phylogenetically less tightly associated Droseraceae (venus fly trap, sundew), Nepenthaceae (old world pitcher plants), Polygonaceae contributing weeds (smartweed), ornamentals, and minor crops (buckwheat, rhubarb), and the Viscaceae (epiphytic mistletoe, witches' broom). As of 3/12/2007, there were ~130,000 nucleotide sequence records for Caryophyllales, and the second largest EST (Expressed Sequence Tag) collection came from *Beta vulgaris* (27,083, after ice plant).

A total of 56,006 sequences from the species *Beta vulgaris* (including a small number from the subspecies *vulgaris* and *maritima*) are deposited in the NCBI nucleotide database. These are divided into three categories: Core nucleotide (genomic DNA, full length mRNA, etc.) which has 868 sequences, EST, 26,745 sequences and GSS, 28,393 sequences. A single StackPACK project was performed with all 56,006 sequences. This generated a collection of 43,559 unique sequences; 37,135 singletons and 6,424 multisequence consensi (containing 18,830 sequences). 41 sequences were rejected as too short. These 43,559 sequences were used as queries in BLAST searches against the NCBI RefSeq protein database, the *Arabidopsis thaliana* protein database and the TIGR *Beta vulgaris* Gene Index. The individual reads have been previously BLASTed against RefSeq, *A. thaliana* and the TIGR BvGI. They have also been analyzed for the presence of SSRs.

Beta vulgaris ESTs from GenBank as of January 2005 collapsed into 13,618 unique clusters (4,023 Tentative Consensus sequences, 9,595 singletons), and 35% were contributed via work partially supported through the BSDF. These sequences were parsed through SSR-Primer software for discovering potential SSR genetic markers, and there 2,175 potential SSR markers within this set are designated in Table 1 as derived from the EST library. 23,067 paired BAC end sequences were determined as of 8/30/2006 with assistance from Syngenta (Hilleshog), and these sequences were parsed for SSR motifs in a similar manner as the ESTs, yielding 457 potential genetic markers (listed as BES in Table 1). An additional set of 2,523 sequences were obtained via a pilot project with Orion Genomics, and of these 44 returned a potential SSR marker (listed as GSS in Table 1).

Library	Accession	Repeat Type	Start	End	Length	Score	Repeat Unit	Left Primer (5'-3')	5' end Length	Tm	Right Primer (5'-3')	5' end Length	Tm	Product Length		
EST	AW063027	trinucleotide	428	442	15	12	AGC	TCTGGACATACCTGCTTGATTG	159	21	56.2	GGAAGAGACTGAAGAGGAGAA	484	21	55.3	326
EST	AW063027	trinucleotide	510	521	12	9	TCA	TTCTCCTCTTCAGTCTCTTCC	464	21	55.3	GGTTTGGATAGTTAGATGCC	787	21	55.4	324
EST	AW063028	pentanucleotide	186	205	20	8	TTACA	AAGCCTCAAAATGCTCTGTT	149	19	54.7	TTACAAGGTGTTGGATGTG	506	19	52.5	358
EST	AW119338	dinucleotide	449	458	10	8	CA	CTCAATCTCCAAATAATCACCC	366	21	56.1	GCTCCTTGTTCTCATCAAAAT	630	21	56.1	265
EST	AW119345	trinucleotide	880	891	12	9	CTC	ATCTGCCGTAGGACTGTTT	825	19	54.8	ACTTCTGGTATGGAACATGA	947	20	55.5	123
EST	AW697730	trinucleotide	143	160	18	15	TCT	ACCCAATCTCTGCTCTCTTC	108	21	55.0	ATTATCACTCTCATCCACCAA	288	21	54.5	181
EST	AW697732	trinucleotide	216	230	15	12	AGA	TATTACGCACATCAACACC	76	21	57.0	GTCAGAAAGCAAGAGAGAAA	430	21	54.1	355
EST	AW697734	dinucleotide	38	60	24	15	AG	CTGTGGCGGAGGAGAGAG	10	18	59.6	CAGGAAGAAGAAAGACGCG	205	20	56.7	196
EST	AW697737	trinucleotide	190	201	12	9	TCT	AGAGAAAGAAAGAGCGAGA	56	21	55.4	ATCTAATGSGTGGCTTGT	410	19	54.5	355
EST	AW697740	trinucleotide	166	192	27	10	GAT	CTTCTCGCGCTCATCTC	99	18	59.8	CTTCTCTCACTTCTGCTCTG	272	21	54.6	174
EST	AW697743	dinucleotide	52	65	14	12	CT	ATTCACTCTTTGCTCTTT	15	19	51.5	GCACCCCTGATTGCTCCA	298	18	60.8	284
EST	AW697743	dinucleotide	65	76	12	10	CT	ACAACATTCGGGTTCTTT	32	18	52.8	CATTACTCGCAGACCTTATTG	230	21	55.2	199
EST	AW697744	trinucleotide	238	249	12	9	ATC	TATCGGGTAGCAATAAGGTC	200	20	54.5	AATCCCATCGTCAATGT	487	18	56.0	288
EST	AW697744	tetranucleotide	165	176	12	8	ATTG	GGCTGTTCTCTTACTTCTT	60	21	54.7	TGTTCTCACTCTCTTTGTT	309	20	54.8	250
EST	AW697758	dinucleotide	143	162	20	18	TC	AGACTGAAGATAGCAAGGG	97	21	55.4	AGAAGTAGAAGGCAACTCCAC	274	21	55.3	178
EST	AW697758	trinucleotide	284	295	12	9	TTC	GGTGGAGTTGCCCTCTACTT	253	20	56.0	CCCTCTGAACATTTACCAAT	626	20	54.1	374
EST	AW697761	trinucleotide	327	338	12	9	TTG	ACTCTCTCTCTCGTCTATT	184	21	54.0	TGGTGTCAACAGATAACAACAT	532	22	54.8	349
EST	AW697761	dinucleotide	186	195	10	8	CT	AACCAACATACCCTCTACTT	46	21	55.1	CAGAGAAGACCAACCAACAAC	278	20	55.6	233
EST	AW697768	trinucleotide	286	297	12	9	CCA	CAGAGAGGTGATGTTGAAG	173	20	56.1	AGCAGAGTGAACCACTTGA	509	19	54.1	337
EST	AW697771	tetranucleotide	48	59	12	8	CATT	CTCTCCTCTGCCCTTCTCTT	0	20	55.5	CGACTTCTTCTCCAAACATC	391	20	54.9	392
EST	AW697777	trinucleotide	526	540	15	12	ATG	CTGTGAGACTTGTCTTCTCTG	421	21	55.1	ACATCCACCCTTAACCTTAAC	572	20	55.4	152
EST	AW697777	trinucleotide	205	216	12	9	AAG	ATTTCACACTTCTCTCTCTCC	30	21	55.0	AGTAATCGTCGGCTCTCTTATT	401	21	55.0	372
EST	AW777151	trinucleotide	208	225	18	16	TC	CTAATCCAAACCCATAAACC	24	20	53.7	GAGAATGAGGAGGAGGAGGAGT	365	21	55.6	342
EST	AW777151	trinucleotide	347	358	12	9	CTC	CTATTACCATTCGACCCTCT	253	21	54.9	CATACTACGCTTGGCCATC	515	19	56.8	263
EST	AW777159	trinucleotide	58	81	24	14	CCA	TCTCTACTCTCGGCCACC	6	18	56.3	GTCGGGATGATTGACTCT	271	18	53.0	266
EST	AW777160	trinucleotide	341	355	15	12	GAT	ATCTTCACACAGAACTGGTC	65	21	54.2	TCTCTCTCGGCTCTCATC	388	19	55.2	324
EST	AW777184	trinucleotide	414	431	18	15	ACA	ATCTGCTGCTTACTCAAACT	177	21	55.0	TTCACTCCCTTCAATCCAA	465	20	55.6	289
EST	AW777184	trinucleotide	91	105	15	12	TAG	TTGGTTCACTTCTGATTCTC	19	20	55.1	CAGTTTGTAGTAAGCAGCAGA	197	20	54.4	179
EST	AW777193	trinucleotide	180	194	15	12	CAT	CTCCCTCTCTCTTATTCTCA	131	20	56.0	TAATGGCTCTTCTCTGTAGT	396	20	51.7	266
EST	AW777193	dinucleotide	228	239	12	10	TA	TTCACTCACTTATTAACATCA	163	21	54.4	GAGGAGGAGCAGCAGTAG	523	18	53.4	361
EST	AW777193	tetranucleotide	125	136	12	8	TCCC	GACCAACTCTTCTCTTCTTT	5	21	52.2	TAATGGCTCTTCTCTGTAG	396	19	50.5	392
EST	AW777209	trinucleotide	318	329	12	9	AAG	TGCTAAGAAAGCGTAAGAAAG	265	21	55.0	AATCTCAACAAACGATAAACC	640	21	55.7	376
EST	BE590263	dinucleotide	70	79	10	8	CT	ATTCTCTCTCTCTCTCTCTCA	41	19	53.8	ACGAACAACCTTCAACATTCAC	197	21	55.2	157
EST	BE590276	trinucleotide	465	476	12	9	TAG	AAAGAAAGGTTGGGTTGTG	435	19	55.1	AAGCAAGCAATGACTCTAATCT	578	21	53.6	144
EST	BE590292	trinucleotide	149	160	12	10	TC	ACAACAACAACATCACTCTCT	9	21	55.0	ATTGCTTCCACAACCC	337	18	55.9	329
EST	BE590302	trinucleotide	473	487	15	12	GAT	AGTCAAAAGTCAACCGACAG	263	20	55.4	AATCACTCTTTCATCTTCA	568	20	55.0	306
EST	BE590312	trinucleotide	372	383	12	9	TGC	TGAACCTTACTGCTCTTGG	302	21	54.9	GTCACCAACCGTCATCAAC	515	18	55.4	214
EST	BE590314	trinucleotide	57	77	21	18	CAT	CAGGTTCAAGAGTTTGTTCCT	6	21	56.4	GCAATGAGGCTTTAGTGA	126	19	56.4	121
EST	BE590349	trinucleotide	68	79	12	10	GA	GAGAGAGAAAGGAGTGAGG	34	21	54.9	ATGACTGAGGGAAGTTGAAAG	166	21	56.0	133
EST	BE590363	trinucleotide	63	74	12	9	CAC	CGAATCCTCTCTGTCTCCC	33	19	57.3	CAAACTGAGGCTTCCCAATGA	255	20	55.2	223
EST	BE590366	trinucleotide	55	66	12	9	AGA	GCACCTCTCCATCTCTCTC	23	20	54.0	CAGCACATCAAAACCATACTTG	183	21	56.7	161
EST	BE590367	trinucleotide	50	61	12	9	CTG	TAGCCCTTCTTGTCTTCTCT	19	20	55.8	ATTTCTTCCACCACTGTCT	203	20	56.1	185
EST	BE590368	trinucleotide	38	49	12	9	GGT	TATGGTGGTGGTGGAAAC	1	18	54.8	ACAACACTCAAGCAATACCCCA	321	22	54.0	321
EST	BE590374	pentanucleotide	155	164	10	5	AATCA	ATCCCTCAACAATCAACA	33	19	53.7	GTGGAATGGAACGAGCAA	233	18	58.1	201
EST	BE590375	trinucleotide	89	103	15	12	CAA	TTTCACAACCTCCGCAAG	1	18	55.8	ATGGGCTCTAATCTTCAATT	169	21	55.7	169
EST	BE590376	trinucleotide	325	339	15	12	GAT	GCTTCATCATCACTATTCT	119	20	55.1	TGGAGTGTCTTCTTGTACTG	410	21	55.5	292
EST	BE590391	trinucleotide	78	89	12	10	CT	CCATTTCTTCTCACTTTCTC	23	21	55.6	CGTCCCATTCACCAAACT	217	18	56.8	195
EST	BE590403	trinucleotide	541	552	12	9	TCA	TTCTGTTCTTCTCTTCAAC	437	21	54.9	CTCCATTCTCCCTCCTG	600	18	55.5	164
EST	BE590424	trinucleotide	573	590	18	15	TGA	TTTGTGGGTGATAGATCTTG	315	22	54.5	AAATGCTCTGTACGCTTTCT	695	21	55.7	381
EST	BE590452	pentanucleotide	298	307	10	5	TTTTG	TCTGTCAACCAACAAAGAAATACA	215	22	55.1	CCCAGTAAGGCATAGAGGT	609	19	54.3	395
EST	BF011006	trinucleotide	286	297	12	9	CAA	CAAATCTCAAGAACCCCAATA	116	21	54.5	GAATGTAAAGGAACCAACCAAA	476	21	55.1	361
EST	BF011006	trinucleotide	349	360	12	9	CTT	TCGTCAACAACAACAACATACA	281	21	55.2	GTAAGAACCAACCAACACTGA	472	21	55.2	192
EST	BF011024	trinucleotide	80	91	12	9	GAA	GGAGGAGAGAGAAAGTGAGAA	44	21	55.3	CGGTAAAGTAAAGATGGATGG	218	22	54.9	175

EST	BF011027	dinucleotide	110	119	10	8	CT	GGCAGGAGGGTTTCATTAG	28	18	56.6	AGTGAAGTGGTGAGGAAG	283	19	55.1
EST	BF011033	trinucleotide	179	205	27	17	CAA	TTTCTCTCTCTCTCTCTAC	38	22	54.6	ATCTTTCTTTTTCAGTGGGTGTT	305	21	55.4
EST	BF011033	trinucleotide	249	260	12	9	AAC	TTTCTCTCTCTCTCTCTAC	38	22	54.6	ATCTTTCTTTTTCAGTGGGTGTT	305	21	55.4
EST	BF011046	trinucleotide	57	74	18	8	CTT	AACCTTCATCAGCTTCC	1	18	54.7	ATCATGCTTCCCTACCTTT	364	21	56.0
EST	BF011050	trinucleotide	430	447	18	15	GAT	TATTACCGCTCTTACTCTC	249	21	55.0	ATCAAGAGTACCTTCTCTGT	617	20	55.5
EST	BF011050	trinucleotide	350	364	15	12	ATG	CTATTACCGCTCTTACTCTC	248	21	55.0	TCITTTATCAACCATCAACAACA	421	21	54.1
EST	BF011069	trinucleotide	229	240	12	9	TCT	TGCGAATAAATAAGCAGG	68	19	54.2	CCACAGACCCCAAGATGATT	324	19	55.8
EST	BF011076	trinucleotide	499	510	12	9	AAG	GGCTCTATTGTCTACGAGTT	207	21	55.3	ATTGCCGAGTCTGAGTTACA	576	20	55.9
EST	BF011086	trinucleotide	234	245	12	9	CTA	ATTGCTTCATCTAAACCTCC	178	21	55.2	TTCTTGCTTCCCAACTTCA	302	21	55.2
EST	BF011100	trinucleotide	163	174	12	9	TGC	ACTCTTACTGCTCTTGGTGT	97	21	56.0	CAATCTCTCTTCACTCTGTG	477	21	54.9
EST	BF011105	dinucleotide	337	346	10	8	AG	TAGTGGGTATCTGTTGTGAG	278	21	55.4	AGCCTTTTCATTTCTATCTGT	493	21	54.8
EST	BF011123	trinucleotide	238	261	24	21	ACA	CTGTGTGATGTTGTTGTATG	76	21	55.0	ACCTGAAGATTGGAAGAAAGG	338	21	55.2
EST	BF011123	trinucleotide	93	110	18	15	TGA	GCAGCAACAACAACAAGA	20	18	57.1	AGAAGATCAACCAACAACAAGA	233	21	54.8
EST	BF011128	trinucleotide	195	206	12	9	CAG	AGAACCAAGAAATGAAGCAA	141	20	55.1	GAATGAACCATAGGACGACT	428	21	55.7
EST	BF011134	trinucleotide	174	185	12	9	TCC	ATCACCTCAACAACCAACA	77	18	52.6	CCTGAAGAACAAGTAAATCCCT	303	21	55.1
EST	BF011138	trinucleotide	78	89	12	9	CCA	AGTCGGTTTCTGCTCCCTTT	27	18	57.1	CGTGTGAGATTGTGTGTT	250	19	54.5
EST	BF011138	trinucleotide	376	387	12	9	CCA	AACAACAACCCATAACCGTC	211	19	55.0	CTTGAGGAAGAAGAAATGGG	609	21	55.8
EST	BF011145	tetranucleotide	265	276	12	8	TTGC	ACAAATAAGCGAAGATGAGGA	193	21	54.6	AGGAATAAGATTGAGAGGCC	319	21	54.4
EST	BF011150	tetranucleotide	183	194	12	8	CTTT	CCTCTTTCTCTCTCCCTTATC	133	21	56.2	CAACATTACAAACCGAACCT	349	20	55.2
EST	BF011150	pentanucleotide	400	409	10	5	ATGGA	TCATCTCTCTCTCTCTGCGT	195	21	56.0	AAGGTCATTTCCATTCTCC	534	19	53.9
EST	BF011151	dinucleotide	44	55	12	10	TA	ACCTTTCAGTTTCACTACTTT	2	22	54.7	TAGCGCGAGTTTGAGTTTATC	141	21	57.2
EST	BF011156	trinucleotide	251	262	12	9	GAA	AATGCGGGAAGTCGTAAA	208	18	56.9	TAAGCAGAGATTGAGGACAG	402	20	54.5
EST	BF011163	dinucleotide	123	140	18	16	CT	GGGAGGAAGATACACTATTAC	25	23	53.8	ATTGGGTTTGAAGAAGAGAA	196	21	55.6
EST	BF011166	dinucleotide	30	43	14	12	TC	CTTCTCTCCGAGTCGCAC	0	19	64.4	AACCTGATCTCTTGACCTTC	360	21	55.1
EST	BF011171	trinucleotide	318	329	12	9	TGC	TGAACTCTTACTGCTCTTGG	248	21	54.9	GCCTTCTCAAACTCTCATC	515	21	55.7
EST	BF011174	trinucleotide	269	291	33	16	GTG	ATCAACAGCCTTAGCAGGA	205	20	55.0	AAACCTAAGACAGAAACAACCT	398	21	54.6
EST	BF011182	trinucleotide	319	344	12	9	TGC	TGAACTCTTACTGCTCTTGG	263	21	54.9	GCCTTCTCAAACTCTCTCT	530	20	55.3
EST	BF011184	trinucleotide	332	343	12	9	TGC	TGAACTCTTACTGCTCTTGG	262	21	54.9	GCCTTCTCAAACTCTCTCT	529	20	55.3
EST	BF011185	trinucleotide	332	343	12	9	TGC	TGAACTCTTACTGCTCTTGG	262	21	54.9	GCCTTCTCAAACTCTCTCT	529	20	55.3
EST	BF011192	trinucleotide	113	127	15	12	CAG	GAAAGAGATAGGCGGCGACT	76	20	55.3	CAGAGATACAGAGATTTGAC	364	21	56.0
EST	BF011205	tetranucleotide	371	386	16	12	TTTG	TGTTTATGTTGATGTAAGGAA	224	22	54.2	AAGTTGAGGAAGAGAAATGAC	513	21	55.0
EST	BF011206	trinucleotide	540	554	15	12	CAC	CTTTCGCTCTTACTCTGCTGC	423	21	56.0	ATGATGCTCTGGAAGAGG	634	21	54.9
EST	BF011208	dinucleotide	328	337	10	8	CA	TTGGTCAGGAGATAGGAC	229	20	55.0	CGTATGTTGTTGTTGTTGTT	483	20	55.7
EST	BF011212	trinucleotide	316	327	12	9	GCA	GGTGTGAGTCTTATGTTGG	270	20	56.6	TGGTTGTCATCAAGAGATTAG	541	22	54.6
EST	BF011237	trinucleotide	530	544	15	12	ATG	AGAAGAAGAAGACGAGAA	209	22	54.4	TTTCATAACATCTCCACAAA	601	21	55.7
EST	BF011237	trinucleotide	209	220	12	9	AAG	ATTTCCACACATTTCTCTCTCC	35	21	55.0	AGTAATCGTGGCTTCTTATT	405	21	55.0
EST	BF011253	trinucleotide	583	600	18	15	ACA	ATCTGCTGCTTACTCAAACTG	346	21	55.0	TTATACCCCTTCAAAATCCAA	634	20	55.6
EST	BF011253	trinucleotide	280	274	15	12	TAG	TTGGTTTCTTCTTGTATTTCC	188	20	55.1	CAGTTTGAGTAAGCAGCAGA	366	20	54.4
EST	BF011254	trinucleotide	258	272	15	12	ATA	TGGTAGTGGTGTGGAATAA	165	21	55.6	TTCAATGGCTTCTCAGTCTC	512	20	55.5
EST	BG577444	trinucleotide	313	324	12	9	CTC	TTATGATTTCTTGGCATTTTC	238	21	54.6	GGTGTGGATGACATTTCTTT	493	22	54.9
EST	BG577454	trinucleotide	97	108	12	9	CCG	CCCACGGTTGTCAGTAAA	40	18	55.3	AAATCTTCTCGGGCATC	318	18	57.6
EST	BG577459	trinucleotide	362	373	12	9	TGC	GTGTGGGAAGAAGAGAAATGT	259	21	55.8	ATGAGGTGAGAAAGCCGAG	620	18	56.3
EST	BG577465	trinucleotide	294	305	12	9	AGC	CAGAGGCAAGAACAAGAAA	55	20	55.8	GGAGATGCTGGAGAGGAC	434	18	55.5
EST	BG577466	pentanucleotide	496	510	15	10	TGATT	GTCTTTCATAGTCTCTGTTGT	426	22	55.0	CTCTAAACCTTTTCCATC	539	19	53.7
EST	BI073124	dinucleotide	434	445	12	10	GA	CCTCATACGACGGTGTGA	314	19	55.4	TTGTATACGAATCTCTCTCT	504	22	54.9
EST	BI073125	trinucleotide	225	234	10	8	TA	CCCTTATCTCTCTCAACAAA	92	21	50.8	AGTGTCTTCTTCCCAAC	435	19	54.9
EST	BI073132	trinucleotide	145	162	18	15	TAC	TACAGAGCACCTCAACATTTC	56	21	55.5	CCAACCATTAGAGAACCC	451	19	54.6
EST	BI073138	trinucleotide	166	177	12	9	CAA	CTGTGTTGTTGTAATCTGGTG	72	21	55.7	AGGTAGGTGACGAGACAG	465	19	55.1
EST	BI073149	trinucleotide	370	381	12	9	TAC	CTGCTCTAAATCAACAGAC	194	21	54.8	GCTCAATCTACTCGCTCTCA	523	21	55.0
EST	BI073153	trinucleotide	349	360	12	9	TAC	TACACCTTTTCTTCTCTTCA	41	21	55.0	GGATTCTCTGGCATTTTC	408	18	55.4
EST	BI073161	trinucleotide	334	345	12	9	CAC	ATCACAATCTACCCCAACCC	100	20	54.7	GAGGAGGAAGAAGAACCACT	437	20	55.0
EST	BI073190	trinucleotide	174	191	18	15	CTT	TTCTCTTCTCTCTCTCCAAC	109	21	55.3	GTATCTGATGCTTGGCACT	446	20	55.4
EST	BI073192	trinucleotide	174	191	18	15	CTT	TTCTCTTCTCTCTCTCCAAC	109	21	55.3	GTATCTGATGCTTGGCACT	446	20	55.4
EST	BI073199	trinucleotide	42	68	27	24	TCA	CGAGGCAACTTCTCTTTCAC	3	19	56.1	ATTGGTGTTCGTCCAGTC	250	19	55.8

EST	BI073215	trinucleotide	384	395	12	9	TGC	TGAAACTCTTACTGCTCTGG	314	21	54.9	GCTCTTCTCAAACTCTCTCT	581	20	55.3	268
EST	BI073216	trinucleotide	384	395	12	9	TGC	TGAAACTCTTACTGCTCTGG	314	21	54.9	GCTCTTCTCAAACTCTCTCT	581	20	55.3	268
EST	BI073228	trinucleotide	57	68	12	9	GAA	TTTCAATCCAGAGAGAGA	14	20	55.0	CCTCAAGGTAGCGCTGT	380	18	55.2	367
EST	BI073244	dinucleotide	122	152	32	16	TC	GAGGTCTCTTTCAATCTCC	30	21	54.7	TAATGCTGTGTGTGTGTGT	227	21	54.3	198
EST	BI073244	trinucleotide	207	221	15	12	AAC	AACCTCCATCCATCTATCTC	66	21	55.5	GAGAGCGGAAGCGTATCT	413	18	55.6	348
EST	BI073250	trinucleotide	59	68	10	8	TC	TCGTCTCATCTCTATCTGTG	9	21	55.4	ATACAGGAACACCTCCATT	207	20	56.2	199
EST	BI095871	dinucleotide	91	100	10	8	TC	TCATTTCTTCAACACACA	20	21	54.3	ACCTTTTCGGAGCATTAG	258	18	55.3	239
EST	BI095873	dinucleotide	81	105	26	10	TC	AGATAAOCCTAAATCCCTAAA	23	22	54.0	CACTGAACAAAGCCCTAAC	394	20	55.0	372
EST	BI095878	dinucleotide	115	124	10	8	CT	AGATAAOCCTAAATCCCTAAA	23	22	54.0	CACTGAACAAAGCCCTAAC	394	20	55.0	372
EST	BI095888	dinucleotide	34	45	12	10	CT	AGGTCTCATCTCCCTCTT	5	18	50.7	AAACATCTGGTCAGTTCC	301	19	54.8	297
EST	BI095890	trinucleotide	254	271	18	15	CTT	AGGTCTCATCTCCCTCTT	5	18	50.7	AAACATCTGGTCAGTTCC	301	19	54.8	297
EST	BI095893	trinucleotide	42	59	12	10	CT	TTTCTCTCTCTCTCTCTCT	27	23	53.6	CTGCTCATCTGGCTCATCT	343	20	55.6	317
EST	BI095893	trinucleotide	101	112	12	9	TC	GCTCTCTCTCTCTCTCTCT	7	19	55.1	CAATCTCTTGATAACCTTCTG	250	22	55.6	244
EST	BI095896	trinucleotide	147	158	12	9	TGC	ATTCGTTCTCTCTCTCTCTG	117	20	53.7	GAACCTCAACCAACATAACAAC	301	21	52.2	185
EST	BI095928	trinucleotide	38	49	12	9	AAT	AGGGACCAAGAGAAGAGAA	5	20	55.6	AATAGAGCAAGAGGAAGGTG	330	21	55.4	326
EST	BI095932	trinucleotide	248	259	12	9	AGA	ATCCAAAGATGAATGACACC	100	20	54.8	AAGCAACTCTGAACAACAAG	476	21	54.8	377
EST	BI095936	trinucleotide	351	362	12	9	TGG	TTTCTCTGTGTGTGTGTGTG	167	20	55.0	ATTAGGTGAGCCAGGACCT	437	20	55.5	271
EST	BI095945	tetranucleotide	324	335	12	8	TTAA	CATTAGTTATGGGCTCTGTG	257	22	54.1	TCATCTTCAACATTTCTCTT	549	21	54.0	293
EST	BI095956	trinucleotide	173	187	15	12	TCT	CATCCTTCTCTCTCCATCTCT	25	21	55.1	CAACAATCAACCCATCAA	322	19	55.2	298
EST	BI095975	trinucleotide	316	330	15	12	AGA	GATGAGAGTGACGACGATG	259	19	54.9	ATGGATTGAGTGATTGCTGT	544	21	55.3	286
EST	BI095975	trinucleotide	84	95	12	9	GAA	ACGAGGAGAGATGAGAGAG	2	19	54.4	CGAAGAAAGAGAGAGAGAG	191	20	55.9	190
EST	BI095983	trinucleotide	409	426	18	15	ATA	CTACATCACCACATCTCAAC	297	21	55.4	ACCATTCTATCTCTTCTCTC	651	20	55.7	355
EST	BI095983	dinucleotide	158	169	12	10	AT	CTATTCTCTCTCTCTCTCTG	8	21	54.9	AAGTGGTATTGGTAATGG	227	21	55.6	220
EST	BI095987	pentanucleotide	583	597	15	10	TTTTA	TCTCTTCTCTCTCTCCACAT	514	22	54.9	TATCATCAACCCAGCAATC	629	19	56.6	116
EST	BI095987	trinucleotide	453	464	12	9	CTG	ATCACCTCTCTCTCCACCTAC	279	21	57.2	ACGCAATCAAACTATAAA	569	21	52.2	291
EST	BI095997	dinucleotide	90	101	12	10	TC	CCTTCTCACTTCTCTAATGG	33	21	55.6	AGACTCAATGGGGTTC	352	18	56.1	320
EST	BI095997	dinucleotide	146	157	12	10	TC	CTCTCTCTTCCCAACCTAC	115	21	54.8	TAGAACCAACCACTATCTT	477	22	54.8	363
EST	BI096000	trinucleotide	149	168	10	18	TC	AGACTGAAGTATGAGCAAGGG	103	21	55.4	AGAAGTAGAAGCACTCCAC	280	21	55.3	178
EST	BI096000	trinucleotide	290	301	12	9	TTC	GGTGAGATTGCGCTTCTACTT	259	20	56.0	CCCTCTGAACATTTACCAT	632	20	54.1	374
EST	BI096002	dinucleotide	94	119	26	24	CT	ATTCCTCGTTTCTCTATCAAC	57	21	55.0	GCTTCTCTCAGTTTCTCTC	394	21	55.0	338
EST	BI096002	trinucleotide	262	288	27	24	GAA	ATTCCTCGTTTCTCTATCAAC	57	21	55.0	GCTTCTCTCAGTTTCTCTC	394	21	55.0	338
EST	BI096002	trinucleotide	176	196	21	18	ATG	ATTCCTCGTTTCTCTATCAAC	57	21	55.0	GCTTCTCTCAGTTTCTCTC	394	21	55.0	338
EST	BI096003	trinucleotide	135	146	12	9	TCT	GGAGCAACACACACTCAAC	6	20	55.8	CATCAGCAAGAAGAAGAGAGA	383	21	55.0	378
EST	BI096007	dinucleotide	53	66	14	12	CT	AGGGTTCGTTGTATTCAAGT	5	21	55.4	CAGATGATTGTGTGGGTAA	348	20	54.3	344
EST	BI096013	trinucleotide	351	362	12	9	TGG	TTTCTCTGTGTGTGTGTGTG	167	20	55.0	ATTTAGGTGAGCCAGGACTT	437	20	55.5	271
EST	BI096016	tetranucleotide	67	78	12	8	AATC	GAAACACCCCAACATCTCAA	8	19	54.2	AGCACCAATCAAACTACTCC	296	20	54.3	289
EST	BI096019	trinucleotide	83	94	12	10	AG	ACTCCACACACACACCTAC	50	20	55.6	TTCAATCATCTCAACAGATT	423	21	54.7	374
EST	BI096027	tetranucleotide	45	56	12	8	TTTC	AGGCACCTCTCTCTCTCTCT	5	21	54.2	TTCAATCTCTCAATCTTTCTT	290	22	54.9	286
EST	BI096036	dinucleotide	55	73	18	10	CT	CCTCTCAACCTCTCTCTCTC	15	21	54.9	ATTTCTCACCATCTCTCTCT	265	21	54.5	251
EST	BI096042	trinucleotide	194	205	12	8	TGTT	GCGGTGTGTGTGTGTGTGTG	95	21	54.9	TCATTTGGTCTGTTCAAGT	378	19	56.5	284
EST	BI096063	trinucleotide	66	77	12	10	GA	GAGAGAAACAGACAGACAGA	32	21	54.0	GGTCATCCATAAATCCCAA	331	19	55.6	300
EST	BI096068	trinucleotide	41	52	12	10	TC	TCCACCTCTATTATCAAC	9	18	54.8	TTCAACACCAACAACTTATCC	375	21	55.1	367
EST	BI096068	trinucleotide	53	64	12	10	AC	CATCACTTTCCACTCTCAATC	21	21	54.7	GTGCTATGGTGCTGTATGG	317	19	54.8	297
EST	BI096100	pentanucleotide	431	445	15	10	ATATG	ATCGGAGATGGGCTTTCTCT	212	19	64.2	AAGACAAACAACATTAGACCA	488	22	54.8	277
EST	BI096108	trinucleotide	243	257	15	12	ATG	GAACAACCTTCTCTCTCTT	24	18	54.0	CTCACACAAGTTTCTCTCCAC	380	20	55.6	337
EST	BI096110	trinucleotide	360	371	12	9	TTC	CCTTCTCTCTCTCTCTCTCT	329	20	55.3	GTGACTCGGTTCTGGCT	473	18	56.2	145
EST	BI096110	tetranucleotide	302	313	12	8	CCGC	GCACGAGGAACAATGAA	0	18	55.5	AGATTGAACGAGAGAGGAGAG	354	21	55.3	355
EST	BI096113	trinucleotide	481	492	12	9	ACT	AAACAGAGGAAGACCCAGT	270	19	53.6	ATTCACCAACCAACCCAGT	626	18	56.0	357
EST	BI096123	trinucleotide	517	528	12	9	CAA	AAACAGAGGAAGACCCAGT	270	19	53.6	ATTCACCAACCAACCCAGT	626	18	56.0	357
EST	BI096141	trinucleotide	54	65	12	9	CTC	AAACTCTCTCTCAACCAAA	11	20	51.6	GCTCAACTCTTCACTATTCT	356	21	53.7	346
EST	BI096141	trinucleotide	39	50	12	9	CTG	QACGAGGGTTATGTTCTCTG	1	20	55.8	CCTGCTATTTCACCTGCTGT	186	20	55.7	186
EST	BI096141	trinucleotide	74	85	12	9	TCT	CTACCTACTGCTACTGCTGCT	25	21	54.4	GAGGAGATGAAGAATCAACC	255	21	55.3	231
EST	BI096148	trinucleotide	303	317	15	12	AAC	GGAGTAACCCCTACAGCCC	102	18	54.5	ACATAAACACCTTGAGCCCTT	456	21	55.6	355
EST	BI096150	trinucleotide	212	223	12	9	GGC	CCTTTCTACTCCAAACAACCT	42	21	55.2	ATATCAACTCTGCTCTCTCT	371	21	54.7	330

BI096160	EST	trinucleotide	483	494	12	9	CTT	AGAAATGACTGCTTTGAGGT	294	21	55.7	CTTGATAAGTGGGAGGTTT	565	20	55.7	272
BI096165	EST	trinucleotide	121	141	21	11	AAC	CATTGTCATCTTCTCTCAA	62	20	55.4	GCCTCTTATTTCATCTCT	428	21	54.4	367
BI096166	EST	pentanucleotide	93	112	20	15	CTTTT	CTGAGAGGTTAGGTGTGCT	20	20	51.7	GCGAAAGAAAGGAAATCA	175	19	55.3	156
BI096175	EST	trinucleotide	114	138	25	13	TAAAC	CCACCTTCACTCTCACT	62	19	55.1	GCCTTACTGACAAACCGTG	293	19	56.7	232
BI096175	EST	trinucleotide	330	341	12	9	CCG	GCAGTCCCATCTTCACT	190	18	57.2	GTCATTTACAAATCTTCT	562	21	55.7	373
BI096189	EST	trinucleotide	296	305	10	8	CT	TAAACGAGAAACCCAAATAA	95	21	54.2	CGACCTCTTACAAATCAAGA	389	21	54.7	295
BI096200	EST	trinucleotide	257	268	12	9	TGA	GCGTCACTAACTCTTGTG	142	20	55.0	GTTTCATCTTCTTCCAG	299	20	54.6	158
BI096211	EST	trinucleotide	120	134	15	12	AGA	CTCAGTCCATCTCTCTATT	18	21	55.0	GCCTTCAAGTATCTCACTCA	339	21	55.9	322
BI096214	EST	trinucleotide	114	138	25	13	TAAAC	AAATCATACCACCTCACT	15	21	55.9	GCCTTACTGACAAACCGTG	293	19	56.7	279
BI096214	EST	trinucleotide	330	341	12	9	CCG	GCAGTCCCATCTTCACT	190	18	57.2	GTCATTTACAAATCTTCT	562	21	55.7	373
BI096218	EST	trinucleotide	375	389	15	12	CAC	TAAACGGAACGATAACATAGA	255	21	55.0	GAATGAACGGAACAACTT	619	20	55.1	365
BI096218	EST	trinucleotide	337	348	12	9	TCC	TAAACGGAACGATAACATAGA	255	21	55.0	GAATGAACGGAACAACTT	619	20	55.1	365
BI096235	EST	trinucleotide	454	465	12	9	CAT	ATGTCAGTTTGTGCTTCTC	354	21	54.6	CGATTGGAGTCTGTGATTCT	548	20	55.2	195
BI096241	EST	trinucleotide	34	67	34	12	TC	GCACGAGGAAGTTGTGTG	0	18	56.0	CAGTTGTCAGCATCAAGACC	398	20	56.8	399
BI096245	EST	trinucleotide	98	109	12	9	CAC	ATACAACAACAGTGGCGTG	58	19	55.4	TGATGCTGAGATTACCGAAG	343	21	54.9	286
BI096256	EST	trinucleotide	372	383	12	9	GAT	CGTGAACCTACCTTTTGTCT	185	20	54.8	GCACATTAACCTTCTCTT	573	19	55.0	389
BI096261	EST	trinucleotide	481	495	15	12	TGA	CCAGAAATAACCTTCTCTCT	269	19	55.1	GTCCTCATCTCTCGTCTCTCT	642	21	55.1	374
BI096265	EST	tetranucleotide	45	56	12	8	ATCT	CTCTGGCTCTTACTCTCTCT	13	21	54.8	TCTGAAACAATCAAGTGG	220	21	55.2	208
BI096268	EST	trinucleotide	128	139	12	9	GAA	ATTGACCTCCAAAGGAA	91	18	55.4	AACAACATCATCCACAAGAA	453	21	55.6	363
BI096270	EST	trinucleotide	83	97	15	12	CAA	TTCTCTCTCTCTTCTCTCTC	49	21	54.5	TTCTCTTATTCACCTTGACTT	231	21	55.5	183
BI096274	EST	trinucleotide	136	147	12	9	AAG	AACATCCGAACAACATCACT	32	20	55.4	ACAACGCCAGTAACGAAA	205	18	55.2	174
BI096276	EST	tetranucleotide	107	118	12	8	TGCT	CATTCTATCTGAGCGGG	38	18	56.7	TGTTATGGCAGCAAAAGAG	325	19	55.0	288
BI096282	EST	trinucleotide	336	347	12	9	AAG	CGAGAGAGAGGTCAGAAA	34	20	54.8	AATCTAGCAGAAATCAGAAACC	397	22	54.5	364
BI096306	EST	trinucleotide	230	246	16	8	TA	ACTTCGATTAACAGTTT	115	18	50.5	TGAATCTTTACCAAGAACAGA	332	21	54.9	218
BI096312	EST	trinucleotide	31	48	18	15	TGG	TACGAGGTTTGGGAGTG	1	18	57.0	TTATACGCCATTTCTCTT	131	18	50.9	131
BI096334	EST	trinucleotide	457	477	21	18	CAC	GCCTTCTCTTGGTCTCTGT	380	18	55.1	GGTGTGAGGTTGGTTGCT	596	19	56.0	217
BI096343	EST	trinucleotide	324	347	24	14	AGT	AACACCCAGAAACTATTCAAG	270	21	54.3	TCTATCAAAATCAACCATCAGG	559	21	55.2	290
BI096343	EST	trinucleotide	348	359	12	9	TGT	AACACCCAGAAACTATTCAAG	270	21	54.3	TCTATCAAAATCAACCATCAGG	559	21	55.2	290
BI543232	EST	trinucleotide	382	393	12	9	GCT	GGCGAGATTCACCAAGTAAG	292	20	57.3	CCATAGCGTCAGTTATTAGA	505	21	54.7	214
BI543245	EST	pentanucleotide	46	55	10	5	CTCTT	ATGTTGACTTCTCTCTCTCC	16	19	54.0	TTTCAGTGTGTTGGTGGT	294	18	54.8	279
BI543248	EST	trinucleotide	83	94	12	9	CTT	GACTCTTCTCTCTCTCTCTCT	36	23	54.4	GCCTCTAAACCTCGCAAAAC	210	19	57.6	175
BI543257	EST	trinucleotide	91	102	12	9	AGA	TATTCGTTCCCAATCTTCT	45	19	55.0	ATTTCTTCCCTTGTAAATCAG	437	21	52.8	393
BI543260	EST	trinucleotide	347	364	18	15	CCA	TACACCAACCACTCTCTTAT	277	21	54.6	AGCATCTAACCCCTACAAAGACC	531	21	55.1	255
BI543264	EST	trinucleotide	326	337	12	9	ACC	TCTCCAATACAAATCGAAA	240	19	55.2	TAAAGCATCAACAAGCCATAC	609	21	55.6	370
BI543269	EST	tetranucleotide	108	119	12	8	TCAT	ATAAATCTTCTTCCCTCAA	14	20	50.8	ATTCCTTACCTCTCTCTTCT	204	21	55.2	191
BI543280	EST	trinucleotide	260	271	12	9	CTA	ATTGCTTCATCTAAACCTTCC	204	21	55.2	TCTTTGCTTCCAACTTTCA	328	21	55.2	125
BI543287	EST	tetranucleotide	45	56	12	8	ATCT	GCAACTCTCTCTCTCTTCT	7	21	54.6	TCCATCTGCAACAATAATCAA	224	21	55.6	218
BI543288	EST	trinucleotide	384	398	15	12	TCA	CGTTAGTATTTTCATCATCGG	190	21	55.0	ATTTCTTACGCTTGGAGGA	480	19	55.0	291
BI543312	EST	trinucleotide	476	502	27	24	CAA	TACTTTGCTATTCTCTCTGGT	347	21	55.7	TGATCTCTGCTTGAGTTTGA	567	21	54.8	221
BI543317	EST	trinucleotide	38	61	24	15	TC	GCACGAGGAAATGACAAA	0	18	55.5	ATCGCCTGAAACAACAAG	280	18	54.6	281
BI543348	EST	trinucleotide	65	78	14	12	AG	AGAGAGAGAAAGAAAGGAAA	34	21	51.8	CCAGAAGACAGAGTAAGTCCA	197	21	54.6	164
BI543349	EST	tetranucleotide	62	77	16	12	AACA	ACGAGGCATTTACAACTTTAC	2	21	53.8	CTCCACTTCTTCCATCACC	267	19	55.4	266
BI543352	EST	trinucleotide	341	352	12	9	TGC	TGAAACTCTTACTGCTCTTGG	271	21	54.9	ACCTTCCAGGCAAAACAC	391	18	58.5	121
BI543353	EST	trinucleotide	213	224	12	9	TTC	TGGAGGTGAGTTTATGTTGTT	113	21	54.7	TAAACGAGCAAGATAGTAGGA	256	21	55.4	144
BI543354	EST	trinucleotide	181	192	12	9	ATG	GATGAAACCGGAGGTTTATG	95	21	56.3	CTTGTGTCAGGGTCACTC	307	19	53.7	213
BI543362	EST	trinucleotide	48	59	12	9	TCT	GTCCTCAACCGCTCTTCAATT	7	19	54.0	ATTCATTTAGCAACAACACT	306	21	55.2	300
BI543362	EST	trinucleotide	260	271	12	9	GAA	TTCTACCCGCAATAATAACAA	210	21	55.1	GCAACCTAAGATAACCAACA	386	21	55.3	177
BI543376	EST	pentanucleotide	200	214	15	10	TTTCA	CTCAATCCGAAAGAAACCC	162	18	55.5	TACGAACTTCTTCCATCC	377	19	54.9	338
BI543377	EST	trinucleotide	123	136	14	12	CT	CCTCACTCTTATCAACCTTCC	40	21	55.3	ATCAAACTTCTTCCATCC	498	21	54.7	376
BI543378	EST	trinucleotide	344	355	12	9	GAT	AACCTCTGTAATCGCAAACT	123	21	55.9	ATAGTCTCTGGCTCATCTT	313	20	55.9	202
BI543381	EST	trinucleotide	260	274	15	12	TAG	ATCCCAATACCTTACTTCCAC	112	21	54.7	CGTCTTCAATGCTGTAGTCC	299	22	54.5	282
BI543382	EST	trinucleotide	69	80	12	10	TC	GTTTCAAGTTTCTCTCTCTTC	18	21	54.7	CATCATCAAGGACATTTCTTAA	282	20	54.8	398
BI543385	EST	trinucleotide	224	241	18	15	AAC	ACTTCTCCAAATAACACTCC	47	21	54.9	CATCAGCCCAATCACTCTCT	444	20	54.8	398
BI543393	EST	trinucleotide	357	368	12	9	TGC	ACTTACTGCTCTTGGTGCT	291	21	56.0	CAATCTCTCTTCACTCTGTG	671	21	54.9	381
BI543402	EST	trinucleotide	257	271	15	12	TAG	TTGGTTTACTTCTTGATTTC	185	20	55.1	CAGTTTGTAGTAAGCAGAGA	363	20	54.4	179

EST	B1543422	trinucleotide	293	304	12	9	TTC	CCCATTATCTCTATTCAAT	256	21	50.4	ATCAAAACAAACAGAACTCAC	607	21	54.2	352
EST	B1543427	trinucleotide	578	601	24	21	AAT	GTGGTGTAGTGGTAGTGGT	524	20	54.7	GCTGACTGATTCTCTCTCA	675	19	53.7	152
EST	B1543434	dinucleotide	106	115	10	8	CT	GCACGAGTTCTCTCTCTCA	0	19	56.5	TTCAATGATCTCATCTTCAAC	322	21	55.1	323
EST	B1543435	trinucleotide	68	79	12	9	ACT	CCAAGCATCTCAGACTG	26	18	55.2	ATAGTAGGGAACGAGAAAGG	293	21	55.1	268
EST	B1543435	dinucleotide	110	119	10	8	AG	TCCTCAGCATCTCAGACTG	47	20	55.2	CATCTCTCAACCTCTCTTCC	422	21	55.6	376
EST	B1543444	dinucleotide	106	115	10	8	CT	GCACGAGTTCTCTCTCTCA	0	19	56.5	TTCAATGATCTCAGCTTCTCAC	322	21	55.1	323
EST	B1543450	trinucleotide	429	447	12	9	AAC	TCCTCTGCTGCTGTTCACTT	281	21	54.0	GCTGCTAGGTGGTGGTATT	676	19	55.4	396
EST	B1543457	trinucleotide	453	467	15	12	GCT	AAGGTAATGCTCCTGCTTC	309	19	54.6	GACATAGTTACAGATGCTCC	614	20	54.7	306
EST	B1543457	trinucleotide	374	385	12	9	TGA	AAGTAATGCTCCTGCTTC	309	20	55.8	TTCTCCTCTCAGTCTCTTCC	429	21	55.3	121
EST	B1543459	pentanucleotide	178	192	15	10	ATTTT	TCCTCTCTCTCTCATCACTT	14	21	53.2	ATTAGGTTGGATTACGAAGA	285	21	55.4	272
EST	B1543464	trinucleotide	263	274	12	9	GAA	TTTGGCTCTCTTCTATGTT	155	20	55.1	GATGGTAGTTGCTCCTTCA	348	19	53.6	194
EST	B1543472	trinucleotide	336	347	12	9	TGC	AATCTGACTGCTCTCGGT	269	19	55.0	GCTCTCTCAACCTCTCTCA	533	19	55.3	265
EST	B1543474	trinucleotide	243	254	12	9	GAA	TTCTACCCGCAATAAACA	193	21	55.1	GCAACGATAAGATACCAACA	369	21	55.3	177
EST	B1543480	trinucleotide	336	347	12	9	TGC	ACTCTACTGCTCTTGGTGCT	270	21	56.0	CAATCTCTCTTCACTCTTG	650	21	54.9	381
EST	B1543488	trinucleotide	256	267	12	9	TCC	GGAGAGAAACCCAGAGAG	61	21	54.9	TTGAAGAACAGTAAATCCCTT	384	21	53.3	324
EST	B1543491	trinucleotide	559	573	15	12	GAT	TCACCTCTTGGGATACAATAC	326	21	54.2	GTCTGAACCACTGTCACTCTT	629	21	54.2	304
EST	B1543491	trinucleotide	359	370	12	9	ATG	TCACCTCTTGGGATACAATAC	326	21	54.2	GTCTGAACCACTGTCACTCTT	629	21	54.2	304
EST	B1543498	trinucleotide	172	183	12	9	ACC	AATACTCCAAACCCCTCACTT	72	21	54.9	AATCCTCTTGACCTCTTCTTG	387	21	55.2	316
EST	B1543499	trinucleotide	172	183	12	9	ACC	AATACTCCAAACCCCTCACTT	72	21	54.9	AATCCTCTTGACCTCTTCTTG	387	21	55.2	316
EST	B1543507	trinucleotide	485	499	15	12	TCT	CTCTCTCTCTCTCATCTTAC	304	21	54.7	TTCAATCCCAATCAAACTCTT	690	21	54.8	387
EST	B1543513	trinucleotide	588	605	18	15	ACA	ATCTGCTGCTTACTCAAACTG	351	21	55.0	TTCAATCCCTTCAAACTCA	639	20	55.6	289
EST	B1543513	trinucleotide	265	279	15	12	TAG	TGGTTAGAGAAGCGCTTATT	173	21	55.8	AAAGAGGGAAGCAGAAAG	506	20	55.5	334
EST	B1543514	trinucleotide	588	605	18	15	ACA	ATCTGCTGCTTACTCAAACTG	351	21	55.0	TTCAATCCCTTCAAACTCA	639	20	55.6	289
EST	B1543514	trinucleotide	265	279	15	12	TAG	TGGTTAGAGAAGCGCTTATT	173	21	55.8	AAAGAGGGAAGCAGAAAG	506	20	55.5	334
EST	B1543539	trinucleotide	80	91	12	9	ATA	CACCGTTACTCAACCATATC	36	21	54.7	GGAAGAGACACAGGAGG	356	18	55.8	321
EST	B1543554	trinucleotide	329	340	12	9	ATG	CTCTCTCTCTCTCTTATCCC	250	21	54.0	ACTCTTCAAACTCAAGATT	536	21	54.1	287
EST	B1543555	trinucleotide	56	67	12	9	GAA	CTACCCGCAATAATAACAACA	8	21	55.5	GCAACATAAAGATACCAACA	182	21	55.3	175
EST	B1543566	trinucleotide	368	382	15	12	CAG	TGAAGAAAGTGAAGAGATGA	212	21	55.1	ACATGAGAAAGATTGACCT	604	21	52.9	393
EST	B1543561	trinucleotide	311	325	15	12	AGA	AGAGTGACGAGGATGATGATG	258	21	54.3	ATGGATTGAGTGTATTGCTG	539	21	55.3	282
EST	B1543619	dinucleotide	112	128	18	9	CT	GCTGGACTCAAAACAACA	46	19	54.7	ACAAGTGAAGAACCAATTAGCA	389	21	55.1	344
EST	B1543626	trinucleotide	158	175	18	8	TCT	CCATTGAAGAAGAAGAGAGAGA	22	22	55.5	TGAGAGAAAGAGGAGAGAGAA	229	22	55.2	208
EST	B1543628	dinucleotide	554	567	14	12	AG	CCCTTGACAGCATCTTGAGT	227	20	55.4	TATCATCTCTTGAGACTTCC	597	20	51.7	371
EST	B1543628	trinucleotide	517	534	18	9	AG	GAATCTCTTGACAGCATCTT	222	21	56.1	CTTCAGCATCTCTCTCTCTC	576	21	55.9	355
EST	B1543642	tetranucleotide	157	168	12	8	TATT	CGCCCTATTCCCGCAAA	62	18	66.3	CGTAAGTTGAAGCGATG	433	18	50.1	372
EST	B1543649	trinucleotide	57	68	12	9	TAA	CACGAGGCACTAACTAAATAA	5	21	52.6	TAATAAGACTCCCGCTGT	214	18	50.6	210
EST	B1543670	pentanucleotide	423	437	15	10	TCTAT	GAAAGAAAGCAGGAGATGAAC	125	21	55.7	TTCCAAAGATAATAGGTAAAGA	505	22	52.7	381
EST	B1543677	trinucleotide	226	237	12	9	TCT	GCTACCCCTTGTGCTTATTG	101	21	54.2	ACGACTTTGATGGAGATGAG	276	20	55.2	176
EST	B1543677	pentanucleotide	472	481	10	5	ATTTA	TTCTCTCTCTCTCTCTCTCTC	227	21	54.5	GCTACACCTTAAACGCAAGT	597	21	56.4	371
EST	B1543688	dinucleotide	277	286	10	8	CT	CGCTTAGTGAACCATCAACT	207	21	56.2	GCTTGATTTCTCTCTCATTT	413	20	55.9	207
EST	B1543690	trinucleotide	156	176	21	18	CTT	GTCCAAATGTCCAAACCA	43	18	55.0	ATGGCTAACCAACTTCCAG	293	19	52.8	251
EST	B1543690	trinucleotide	443	463	21	18	TCT	CTTCTCAGTACCCCACTTCT	170	21	55.1	AGTATTTCTCCCACTCAACT	522	22	54.5	353
EST	B1543690	trinucleotide	173	184	12	9	GCT	AACAATGAGTTGGTAGAGAG	52	20	54.9	ATCTAAAGTGGGATCTGCT	285	20	54.4	234
EST	B1543694	trinucleotide	160	177	18	8	TCT	CCATTGAAGAAGAAGAGAGAGA	23	22	55.5	TGAGAGAAAGAGGAGAGAGAA	231	22	55.2	209
EST	B1543700	trinucleotide	108	119	12	10	GT	TGCTCTATTGTTGGGAGT	68	21	55.0	ACACTTGATTTGAGGGAA	439	18	51.0	372
EST	B1543709	dinucleotide	253	264	12	9	GCT	TCCTTTCATCAGTGGGTATG	76	21	55.2	TCTCTCAACCTCTCTCTCT	295	21	54.9	220
EST	B1543710	trinucleotide	438	453	16	14	GT	TCCAATCTTCAACAAATACAA	280	22	55.0	GATCCACACAAACCTCAA	512	19	54.3	233
EST	B1543712	dinucleotide	109	120	12	10	GT	TGCTCTATTGTTGGGAGT	69	21	55.0	ACACTTGATTTGAGGGAA	440	18	51.0	372
EST	B1543713	trinucleotide	128	139	12	9	AGA	TTGTTCTCTCTCTCTCCGT	83	19	54.9	CCTCACTCATCATCTCAAAGT	359	21	54.3	277
EST	B1543717	trinucleotide	128	139	12	9	AGA	TTGTTCTCTCTCTCTCCGT	83	19	54.9	CCTCACTCATCATCTCAAAGT	359	21	54.3	277
EST	B1543722	dinucleotide	555	568	14	12	AG	CCTTTGACGATCTTGAGT	228	20	55.4	TATCATCTCTGAGACTTCC	598	20	51.7	371
EST	B1543722	dinucleotide	519	536	18	9	GA	ATGCTTTCTCTCTCTCTCTCA	394	21	55.9	CCTCTTCACTCATCTCTCTCT	580	21	55.1	187
EST	B1543724	dinucleotide	555	568	14	12	AG	CCTTTGACGATCTTGAGT	228	20	55.4	TATCATCTCTGAGACTTCC	598	20	51.7	371
EST	B1543724	dinucleotide	519	536	18	9	GA	CGCTTCTCTCTCTCTCTCTCT	448	21	56.0	CCTCTTCACTCATCTCTCTCT	580	21	55.1	133
EST	B1543734	trinucleotide	93	107	15	12	AAC	GAAGCACACAACATGGG	40	18	55.8	AGTGCGGTAGAGAGAGAA	179	19	55.1	140
EST	B1543742	trinucleotide	109	120	12	9	ACG	CTCTCTCTCTCTCTCTCTCA	67	18	55.2	TGGTAAGAAGCATACATCA	378	21	54.3	312

EST	B1543750	trinucleotide	120	140	21	18	CCA	AATGTTTCTCTCTCTCTCA	63	20	56.3	AATGTTTCTGATTCCACAA	415	21	55.6	353
EST	B1543762	trinucleotide	165	182	18	15	ACA	TCTCTCTAAAGCAACAA	39	18	55.2	AAATGACGCCGCAACAG	414	18	58.4	376
EST	B1543770	trinucleotide	298	315	18	8	TTC	GGCATAAGGAATGGTCT	245	18	54.9	AAACAACAGCCCAAGGAAA	560	19	55.9	316
EST	B1543775	trinucleotide	66	93	28	26	GA	TTCCCAAGAAAGACGATG	27	19	53.2	CTTCAGCATCACAAGAATAGA	250	22	54.9	224
EST	B1543778	trinucleotide	196	207	12	9	CAT	ATACCAAGCATCAGCATT	120	21	55.4	AGCAAGAGACATAGATACA	462	21	54.2	343
EST	B1543783	trinucleotide	109	120	12	9	ACG	TTCTCTCTCTCTCTCTCT	47	19	55.5	AGTGAATGGTAATCTTGTGG	419	21	54.2	373
EST	B1543784	trinucleotide	161	178	18	8	TCT	CCATTGAAGAAGAAGAGAGA	23	22	55.5	TGAGAGAAAGAGAGAGAGAAA	232	22	55.2	210
EST	B1543799	trinucleotide	226	237	12	9	TCT	GCTACCTTTGTGCTCTATTG	101	21	54.2	AGACTTTGATGGAGATGAG	276	20	55.2	176
EST	B1543799	pentanucleotide	472	481	10	5	ATTTA	CTTCTCTCTCTCTCTCTCT	229	21	56.0	AGACTGGTTGTTCTCTCTTT	627	21	54.6	399
EST	B1543800	trinucleotide	226	237	12	9	TCT	GCTACCTTTGTGCTCTATTG	101	21	54.2	AGACTTTGATGGAGATGAG	276	20	55.2	176
EST	B1543800	pentanucleotide	472	481	10	5	ATTTA	CTTCTCTCTCTCTCTCTCT	229	21	56.0	AGATGGGTTTGTCTCTCTTT	627	21	54.6	399
EST	B1543861	trinucleotide	547	558	12	9	CAT	TATCACTTCTCTCGCTGTTCT	248	21	54.4	TCTGTCTCTCCACATACCA	603	20	54.0	356
EST	B1543863	trinucleotide	282	293	12	9	GAA	ACACTTTCTCAAAACCTTAACC	82	21	55.0	CAAAACAAGATAGCATACCC	350	21	55.0	269
EST	B1543864	trinucleotide	109	120	12	9	ACG	TTCTCTCTCTCTCTCTCTCT	47	19	55.5	GTGAATGGTAATCTTGTGGT	417	21	54.1	371
EST	B1543871	trinucleotide	109	120	12	9	ACG	TTCTCTCTCTCTCTCTCTCT	47	19	55.5	AGTGAATGGTAATCTTGTGG	418	21	54.2	372
EST	B1543881	tetranucleotide	317	332	16	12	TTAT	CCACTCAATCGGACCOAG	171	18	60.0	GCTGCCACTCTCTTACTT	554	18	50.2	384
EST	B1543884	trinucleotide	96	110	15	12	AAC	GAAGCACACAACATGAGG	43	18	55.8	AGTGCGGGTAGAAGAAGAA	182	19	55.1	140
EST	B1543900	trinucleotide	612	626	15	12	TAT	ACCGCATAGAAAGATGAGAA	367	21	55.8	ATCCATAACCAAAACCCAAA	661	19	55.3	295
EST	B1543903	trinucleotide	485	499	15	12	TAT	AAGTGAAGCCAACTGAAGAA	341	20	55.2	ATCCATAACCAAAATCCAAGT	651	21	55.1	311
EST	B1543933	trinucleotide	307	318	12	9	AAG	AAGAGAGAGAAACAAGAAACA	203	23	54.4	TCGTCACTTAAATCAAGCA	586	19	55.3	384
EST	B1543933	trinucleotide	451	462	12	9	GAT	ATAAGAGCAAGTAGCAGCA	325	20	54.8	TCGTCACTTAAATCAAGCA	586	19	55.3	384
EST	B1543942	trinucleotide	155	169	15	12	TAT	AAGTGAAGCCAACTGAAGAA	12	20	55.2	ATCCATAACCAAAATCCAAGT	322	21	55.1	311
EST	B1543948	dinucleotide	58	67	10	8	AG	ACAGAGGAGATACAGACACA	7	21	54.7	AATAAGGACAACATCAGGGAG	173	21	55.8	167
EST	B1543984	trinucleotide	129	140	12	9	TGA	GGAAGAGAGAGCAGATGGTAG	7	21	55.8	ATCCATAACCAAAATCCAAGT	322	21	55.1	311
EST	B1543998	trinucleotide	457	468	12	10	TC	CCTCATACAGCGTGCTAC	240	18	55.0	ATGGCTAACAACTTCCAG	293	19	52.8	251
EST	B1544016	trinucleotide	156	176	21	18	CTT	GTCCAAATGTCCAAACCA	43	18	55.1	AGTATTCTCTCCCAATCAACT	522	22	54.5	353
EST	B1544016	trinucleotide	443	463	21	18	TCT	CTTCTTCACTACCCACTTCT	170	21	55.1	AGTATTCTCTCCCAATCAACT	522	22	54.5	353
EST	B1544042	trinucleotide	179	205	27	24	CAA	GTCTCTCTCCAAACTCATCAA	76	21	54.4	TCATCAACCAACAACACATTC	382	20	55.1	307
EST	B1544042	trinucleotide	167	178	12	9	CAG	GTCTCTCTCCAAACTCATCAA	76	21	54.4	TCATCAACCAACAACACATTC	382	20	55.1	307
EST	B1544042	trinucleotide	149	166	18	8	CAA	TTGTCTCTCTCCAAACTCATC	74	21	54.4	TGTTGTTGTTGTTGTTGTTG	200	21	54.9	127
EST	B1544047	dinucleotide	463	472	10	8	AG	CTCGATCTCTCTTATCTCT	321	21	54.8	TTCTACGCTCTCTATTATTT	504	22	54.3	184
EST	B1544050	dinucleotide	171	184	14	12	TC	TTCTCAACTCTCACTACCAA	17	21	55.0	TTTCTCTCTCTCTCTCTCTCT	245	21	54.5	259
EST	B1643126	trinucleotide	309	336	28	26	AT	GTGATGCCCTTCTCTATTATC	80	20	53.7	TGTAACCTTAAACCAATCGTG	433	22	54.7	334
EST	B1643133	tetranucleotide	213	224	12	8	GAAA	GAGCCCTCTGTGCCCTGT	155	18	58.9	ACACTACCTTTCTCTCACTCAA	411	22	53.3	257
EST	B1643133	tetranucleotide	426	437	12	8	TTCT	TTCTACCATCTCCCATTT	320	19	55.2	CATTACTCTTCACTTCCCGT	564	21	55.9	245
EST	B1643181	trinucleotide	246	290	45	42	TAT	TTCTCCATTCTCTCTCTAAA	34	21	53.4	TAGTCCCTTCTTTGTACGCT	412	21	55.9	379
EST	B1643207	pentanucleotide	177	191	15	10	CAGTC	TTGGACTGGACTGGACTTATT	72	21	56.2	CATTGTTGGGCTTAGGTG	389	18	54.9	318
EST	B1643207	pentanucleotide	201	210	10	5	TGGAC	TTGGACTGGACTGGACTTATT	72	21	56.2	CATTGTTGGGCTTAGGTG	389	18	54.9	318
EST	B1643249	trinucleotide	462	471	10	8	AT	GAGGTAGTGGTGGTCACAA	162	18	54.2	AAACATCTTCTTGTGTTGGTCT	534	21	55.7	373
EST	B1643257	trinucleotide	320	333	14	12	GT	TACAAGGGAGATTCGGGT	178	18	55.4	ATACAATAGGGCGTAAAGA	541	19	50.1	364
EST	B1643275	trinucleotide	247	261	15	12	TAT	AAGTGAAGCCCAACTGAAGAA	104	20	55.2	ATTCCATAACCAAAATCCAAGT	414	21	55.1	311
EST	B1643304	trinucleotide	540	551	12	9	GAA	CAGCACAGAGAGGAGGTATT	357	21	56.2	TCATCGTAGTCAACCATTTATCTT	588	22	54.0	232
EST	B1643310	trinucleotide	79	90	12	8	AGAA	GTAGAGAGAGAGAGAGGCGTT	30	21	54.7	ATACTAACTGGCGTTCTCTCA	130	21	56.6	101
EST	B1643310	trinucleotide	106	117	12	10	AG	GACAGAGCGATACATAGACAGA	60	22	54.7	CCCAAACTAAGGAGAGAGAGAG	333	21	55.0	274
EST	B1643322	trinucleotide	472	483	12	10	AT	AGAGAGCGCTGAAGAAAGAAAG	398	21	54.8	AAAGTTGTAGAGAAATGGAAA	581	21	51.0	184
EST	B1643364	trinucleotide	145	156	12	9	GAA	ATTCAACACACATTTCCCAA	20	19	54.6	TAAAGTTGCCCTCTTCTCTCA	285	21	54.6	266
EST	B1643378	trinucleotide	536	549	14	12	GT	TTACTATCCACGAAACATCA	435	21	54.1	ATCCACAGAAACCTCAAA	606	18	53.6	172
EST	B1643381	tetranucleotide	144	155	12	8	TCAG	CGAAGTCAGGAAGAGGAA	25	18	54.7	AACAACCATACATCCACAATC	299	21	54.8	275
EST	B1643406	trinucleotide	350	361	12	9	CTT	TTTATTCTCTCATCCCTTTC	202	21	55.1	TCAACCGAACTTACTTTGTCTTT	471	23	54.4	270
EST	B1692556	trinucleotide	608	621	14	12	TA	CATCTCACTACATCAATACATCA	556	23	52.8	CGGTCTTACTACTCAAAATCA	668	21	54.6	113
EST	B169272	trinucleotide	363	374	12	10	AC	CGAATCTCACTTCTTACTTGT	174	21	51.4	CAATCTTTATGCCCTATTTC	559	21	54.6	386
EST	B169295	trinucleotide	364	375	12	10	AC	TCACAACACTCTAATCTCACTTC	165	23	53.8	TTACTATCCACAGACGGCA	476	19	55.1	312
EST	B1698310	trinucleotide	569	582	14	12	TA	CATCTCACTACATCAATACATCA	517	23	52.8	CGGTCTTACTACTCAAAATCA	629	21	54.6	113
EST	B1698324	trinucleotide	614	625	12	9	TCT	AATACCACACACATTGCTAC	394	20	50.8	TACTGAAGTCCCAACAAAG	692	19	54.7	299
EST	B1698382	pentanucleotide	235	244	10	5	CAAGA	TTTACTTCCATTTTACCATCTTC	145	23	52.3	GCTTCTCTTTTGTGTTGG	436	18	55.0	292

EST	BQ487753	trinucleotide	162	173	12	9	CTT	ATGAACAGAGCTCAATCCAAC	131	21	56.5	AGCAGCTAAACACAATCCATAA	304	21	52.6	174
EST	BQ487768	dinucleotide	191	202	12	10	AG	GCAATAGAGGAGACTGAGAA	121	21	53.9	AGTGGAGAAGGTGTAGATGG	393	20	54.1	273
EST	BQ487768	dinucleotide	95	104	8	AG		CATCACTCAACTCCCAA	36	18	55.1	CTCTCCTTCTTCCAAATCTTC	228	21	54.8	193
EST	BQ487771	trinucleotide	196	213	18	15	TGA	CCAAACAACCTTCTCTCTCT	35	21	55.3	TTACCAACAACAACAACAACA	286	21	55.1	252
EST	BQ487771	trinucleotide	267	281	15	12	TGT	TTTATTTCTGGGTTGTGTG	66	20	55.2	AGTGCTCATGCTTCAGT	431	18	51.0	366
EST	BQ487771	trinucleotide	297	311	15	12	TGA	TGTTGTTGTTGTTGTTGTTA	266	21	55.1	AGTGCTCATGCTTCAGT	431	18	51.0	166
EST	BQ487778	pentanucleotide	250	259	10	5	CAGTT	CAGGTTTGTCTTACCTTGTCT	66	20	55.0	TCTTAAGGAGCTGGAATCTCTGA	349	23	55.1	284
EST	BQ487779	trinucleotide	400	420	21	18	CAC	CATTGTTATGCTTATTTGCT	116	22	54.2	CCAAACCCACTTATGGTGA	462	18	55.0	347
EST	BQ487783	trinucleotide	162	173	12	9	CTT	ATGAACAGAGCTCAATCCAAC	131	21	56.5	AAGCACTAAACACAATCCATAA	304	21	52.6	174
EST	BQ487799	trinucleotide	353	373	21	18	CCA	TCTTTCTCTTCTCTCTCTCT	182	21	54.1	ACACCTACACCGACTGGAC	478	19	55.8	297
EST	BQ487801	trinucleotide	148	159	12	9	CAA	ATTTGAGGGTAGTGAGGACAG	107	21	55.8	TCCAAGTCAGAAGGCAAG	223	18	54.7	117
EST	BQ487801	trinucleotide	193	204	12	9	GAT	AGCAACAACAACAAGAAGAAC	145	21	54.7	ATCCACAACAAGACAGTAG	269	20	55.5	125
EST	BQ487805	trinucleotide	290	304	15	12	CAA	ATGGAGAACAACAACAATCT	92	20	54.8	ATTACACCAACAACAACCCTT	439	21	56.0	348
EST	BQ487833	trinucleotide	82	96	15	12	AAC	ACACAACAATGGCGGCTC	35	18	60.7	AGTGGGGTAGAAGAAGAA	168	19	55.1	134
EST	BQ487834	trinucleotide	225	236	12	9	TGC	TGAAACTCTTACTGCTCTTGG	155	21	54.9	GCTCTCTCAAACTCCTCCT	422	20	55.3	268
EST	BQ487851	tetranucleotide	290	304	15	12	CAA	ATGGAGAACAACAACAATCT	92	20	54.8	ATTACACCAACAACAACCCTT	439	21	56.0	348
EST	BQ487859	trinucleotide	147	158	12	8	ACCA	TTTCAGACACTGGCATTCAC	41	19	56.0	GGATTAGTAGGACGGTGAGAC	283	21	55.3	243
EST	BQ487872	trinucleotide	83	94	12	9	CTT	CTCTCTTTGCTCTCTCCATCT	6	21	55.3	TTCTCTCTGCTATTAACCTAAA	256	22	53.1	251
EST	BQ487872	trinucleotide	83	94	12	9	CTT	TTTCTCTCTTCCGGGTCTC	3	19	54.5	GCAGGATTTCTCTCTCTATGT	147	22	52.3	145
EST	BQ487875	trinucleotide	83	94	12	9	CTT	CTCTCTTTGCTCTCTCCATCT	6	21	55.3	TTCTTATCATTTCAACCCAA	355	20	55.6	350
EST	BQ487888	tetranucleotide	95	122	28	17	AATC	TACTCCAACATCACACAACA	5	21	55.0	GAGACTGTAACGCCCTGTAA	243	20	55.5	239
EST	BQ487909	pentanucleotide	555	569	15	10	TGATA	ATGCCACTACACAATTTCA	429	19	52.2	TATGACTTGGGTATTTCTCC	613	20	51.7	185
EST	BQ487910	dinucleotide	67	76	10	8	AC	ACTCTCAGTCCCACTCTTT	6	20	55.3	GTTGATGTTGTTCTTGGTGT	219	21	55.0	214
EST	BQ487912	tetranucleotide	103	118	16	12	ACAT	AAGCACCAACCCACACACT	40	18	57.4	CTACATTGAGAACCACACATAA	367	21	52.8	328
EST	BQ487914	trinucleotide	299	316	18	15	ATC	TATTTCACTCTCTGCTCCCTT	157	21	55.6	ATAAAGTGCCATCCAAAGTAG	535	21	53.8	379
EST	BQ487914	trinucleotide	469	480	12	9	TTC	CTCTCTCTCTCTCTCTCTCT	427	20	55.1	AGATAAAGTGCCATCCAAAGT	537	21	55.5	111
EST	BQ487916	trinucleotide	256	267	12	9	AGA	AGACAGGATGAATGATGGAG	109	20	54.9	TGTAGTTGTAGGGTCTCTTG	501	21	55.8	393
EST	BQ487921	trinucleotide	104	121	18	16	CT	CGTTCAATCATTCATATCTCC	57	21	54.7	GACGAAGAGACATCCGTTT	240	19	55.2	184
EST	BQ487950	trinucleotide	402	422	21	11	GAA	ATTACAGGAACACGACGCA	343	18	52.5	CCGTCATCATCGTATCTTT	468	20	55.2	126
EST	BQ487955	trinucleotide	157	183	27	10	CAT	GTTGTATCTCTCTCTTCCACAC	113	23	54.7	TACTGGGATTTGGCTGGG	243	19	60.8	131
EST	BQ488027	trinucleotide	51	62	12	9	CTT	GACTCTTTCTCTCTCTCTACCT	4	23	54.4	GCCTCTAAACCTCGCAAC	178	19	57.6	175
EST	BQ488037	dinucleotide	95	118	24	22	TC	CACCTAACTCTCTCTCTCTCC	47	21	54.8	TTCTCTGACTCCAACTATCA	255	21	56.7	209
EST	BQ488040	trinucleotide	205	216	12	9	AAT	AATAGAGCAACATAACATCTC	83	22	50.8	GGCTCTCTCTCTCTCTCTTT	291	21	54.0	209
EST	BQ488072	trinucleotide	53	72	20	18	TC	GCTCTCTCTCTCTCTCTCTCT	0	23	54.8	TACTTGTCTGAAATGGTGCT	110	20	56.1	111
EST	BQ488072	pentanucleotide	33	42	10	5	CTACA	GCTCTCTCTCTCTCTCTCTCT	0	23	54.8	TACTTGTCTGAAATGGTGCT	110	20	56.1	111
EST	BQ488076	dinucleotide	64	75	12	10	TC	ACTCTCACCTACCATTTCTCCTC	20	21	54.9	CTGTTTCTCCCTATCCCTAA	206	21	55.2	187
EST	BQ488077	trinucleotide	196	216	21	18	CCA	CATCTTCACTCTCTCTCTCTAC	135	22	53.2	GAAGTAGGTGGCTTGGCT	272	18	55.4	138
EST	BQ488092	trinucleotide	232	243	12	9	CAG	AAAGAATGAAGCAACAACAAC	184	21	54.6	CTATCTGAGGAGCAGCAAGA	285	20	55.9	102
EST	BQ488110	dinucleotide	110	119	10	8	AG	CAAGTTCTCAAACTCCCTAC	26	21	55.5	GGTCCAAGATAAAGCCAAA	280	19	55.3	255
EST	BQ488143	trinucleotide	176	202	27	10	GAT	CTTCTCGCGGCTCATCTCTC	109	18	59.8	CTTCTCTCACTTCTGCTCTG	282	21	54.6	174
EST	BQ488151	trinucleotide	217	228	12	10	CT	TCCCCTGTGAAGAAGAAGT	101	19	55.7	AAGTGAGGAGAGAGAATGGAG	267	21	55.2	167
EST	BQ488158	pentanucleotide	172	192	20	9	AAAAG	AGAGAGTGGAGGAGAGAGATT	72	21	53.8	CAAAACAGTAAACCTTGAACCA	282	21	55.4	211
EST	BQ488173	trinucleotide	274	285	12	9	GAA	TAAGAAAGCAACACCTCTCA	17	20	56.0	TTGCACTGATTAACCA	316	18	55.4	300
EST	BQ488179	trinucleotide	333	347	15	12	ATG	TAAATCCCTTCCCACTTTTC	288	19	54.2	ACGCAACCTCATCCGCGC	554	18	62.1	267
EST	BQ488191	trinucleotide	230	241	12	9	AAT	AAATCAACAACAGATCAAAA	84	20	54.2	AACCTCATCATCACTAATCC	342	21	55.5	259
EST	BQ488197	trinucleotide	197	208	12	9	CAG	AAAGAATGAAGCAACAACAAC	149	21	54.6	GAATGAACCACTAGACGACT	430	21	55.7	282
EST	BQ488205	trinucleotide	92	103	12	9	AAC	TAGTAACAATGGCAGCAAG	8	19	52.4	CGAATGGAAGAAGGTGTGT	275	19	56.0	268
EST	BQ488210	trinucleotide	256	267	12	9	AAT	TTCTAGTCTGCGTTTCTTCA	53	21	55.5	ATTGGTTCTCTTCAAGTTTC	308	21	55.0	256
EST	BQ488237	pentanucleotide	36	45	10	5	TTCTC	CTTCTCTCTCTCTCTCTCTCT	0	21	54.8	ATTGGTTCTCTCTCTCTCT	360	19	55.2	361
EST	BQ488254	trinucleotide	407	421	15	12	AAC	CACCTCATCTCACTCATCTCT	289	21	54.7	GGTTTGTCACTTTCTTCACTTT	490	22	55.1	202
EST	BQ488270	dinucleotide	66	81	16	14	AG	ACGCTTGTAGAGAGAGAAAG	9	22	55.0	AGCATCAAGGTAGCACATAG	338	21	55.5	330
EST	BQ488276	trinucleotide	110	127	18	15	CAA	TCAACCTTCCGACATGA	30	18	55.9	AGTCTCTTTCGATCAACT	351	19	54.9	322
EST	BQ488278	trinucleotide	196	210	15	12	TGC	CACGAGAAACCAAGAAAGAC	62	20	54.8	ACTTATCCAGGACAGCATCA	340	21	54.9	279
EST	BQ488281	trinucleotide	108	122	15	12	AGA	CTCAGTCCACTCTCTCTCTATT	6	21	55.0	AGCATCAAGTATCTCACTCA	327	21	55.9	322
EST	BQ488306	trinucleotide	263	286	24	14	GAT	TGCCAAACCTATCACTAAGAC	33	21	54.6	ACATCATCTCATCATCTCTC	368	20	54.6	336

EST	BQ488306	trinucleotide	103	117	15	12	TGA	TGCCAAACCTATCACTAAGAC	33	21	54.6	CTCCAGTAAACCAAGACACAG	229	21	55.0	197
EST	BQ488306	trinucleotide	299	310	12	9	GAT	TGCCAAACCTATCACTAAGAC	33	21	54.6	ACATCATCTCATCATCCTC	368	20	54.6	336
EST	BQ488306	trinucleotide	326	337	12	9	GAT	TGCCAAACCTATCACTAAGAC	33	21	54.6	ACATCATCTCATCATCCTC	368	20	54.6	336
EST	BQ488308	trinucleotide	386	403	18	15	TAA	TTCTATCTCTTTGTTGCTG	258	21	54.3	ATAAACCCAGACACCAAA	575	18	55.1	318
EST	BQ488310	trinucleotide	175	190	16	14	TC	GCAACTCAAAATACAACTTCAAC	53	22	54.2	ATTCTCTCCCGTCCATT	340	18	56.8	288
EST	BQ488310	tetranucleotide	278	289	12	8	TTTG	GCAACTCAAAATACAACTTCAAC	53	22	54.2	ATTCTCTCCCGTCCATT	340	18	56.8	288
EST	BQ488313	dinucleotide	284	295	12	10	AG	CCCTCTCTATCGATTCTTC	41	21	54.7	CTCTGATGTTGTTGTAG	412	21	54.9	372
EST	BQ488323	dinucleotide	36	49	14	12	TC	GATTTCCTCTCTACACAAA	0	20	52.7	ATACGCCACACACACAC	377	18	54.9	378
EST	BQ488324	trinucleotide	364	375	12	9	TGC	TGAATCTCTACTGCTCTGG	194	21	54.9	GCTCTCTCAAACTCTCCT	561	20	55.3	268
EST	BQ488326	trinucleotide	216	227	12	10	TC	TCTTCTCTTTCTCTCTCAAA	132	22	55.2	ACCACAGGCTCATCAAA	484	18	55.8	353
EST	BQ488334	trinucleotide	201	212	12	9	AAG	ATTTCACACTTCTCTCTCTC	25	21	55.0	AGTAATCGTGGCTCTTATT	397	21	55.0	373
EST	BQ488365	dinucleotide	170	181	12	10	TC	TTCACTCAATATCTTCGGTT	78	21	54.2	CTGTAAGGGCGTGTGG	300	18	57.7	223
EST	BQ488387	trinucleotide	362	382	21	18	CCA	TCTTCTCTTCTCTCTCTCT	191	21	54.1	ACACTACACGACTGGAC	488	19	55.8	298
EST	BQ488398	tetranucleotide	232	247	16	12	ATTG	TATCTCTTACCACACACGAA	58	21	54.8	ACCCTCAGAAACTCATACAC	322	21	55.7	265
EST	BQ488420	dinucleotide	288	297	10	8	CT	TCCATCTCTCTCAAACTCAAA	11	21	55.1	CATACGCTTTGTAATCTTTCT	387	21	53.9	377
EST	BQ488422	trinucleotide	206	217	12	9	GAT	AATCAATCAATCCACCTTCT	44	21	55.2	CATACCACCTAAGACCCCTGA	394	20	55.1	351
EST	BQ488427	trinucleotide	256	267	12	9	TGC	ACTCTTACTGCTCTTGGTCT	190	21	56.0	GTCACCTTCAAACTCTCCTT	537	21	55.1	348
EST	BQ488489	trinucleotide	138	149	12	9	TCT	GGCTTCACTCTCTGTTCTT	67	21	55.3	CATCCACATCGCTAATCTTT	266	20	55.3	200
EST	BQ488502	dinucleotide	155	166	12	10	TC	TCAAACAGAGGAGAGAGAGAA	3	21	54.3	TAAGACAGAAATAGTCCGCC	238	21	56.2	236
EST	BQ488502	pentanucleotide	86	100	15	10	ACAAA	TCAAACAGAGGAGAGAGAGAA	3	21	54.3	ACGAGAGAGAGAGAGAGAA	172	21	55.0	170
EST	BQ488555	dinucleotide	155	166	12	10	CT	TCCTTCACTCTCATCTTCATC	78	21	54.3	ATTACAGGAGTTGTTGG	402	19	55.0	325
EST	BQ488567	trinucleotide	113	122	10	8	CT	CTCTTCCACCATCTTCTCT	38	21	55.2	AAATGCTCTCTCCATCTGT	370	20	53.9	333
EST	BQ488570	trinucleotide	80	91	12	9	TCT	GGCATCTACTTTGAGACATC	39	21	56.3	GTTATCCTCTTGACCCACTC	285	21	55.3	247
EST	BQ488577	trinucleotide	48	59	12	10	TC	ACTCTCACCTACATTTGCTC	4	21	54.9	CTGTTCTTCCCTATCCCTAA	190	21	55.2	187
EST	BQ488581	trinucleotide	127	138	12	9	TCT	GTCACACTCTTCTCTCAAC	91	21	53.9	CAATAGATGCCAACCTCTTTC	306	21	56.5	216
EST	BQ488588	tetranucleotide	99	126	28	17	AATC	TACTCCAACTACACACACAAA	9	21	55.0	GAGACTGTAACGCCCTGTAA	247	20	55.5	239
EST	BQ488598	dinucleotide	51	66	16	14	TC	AATCAATCATCTCTATCTCTC	18	23	53.4	CCTATGACCTCGGAACATAATG	340	21	56.3	323
EST	BQ488605	trinucleotide	369	380	12	9	GCT	ATAGTCGCTACTCTCTCTTACC	68	21	54.9	TTCTGTGCTCTTTCTTTTCTC	453	21	54.8	386
EST	BQ488620	pentanucleotide	59	68	10	5	AAAAC	CTCTTACACACAAAGAGAAA	14	20	55.1	TTACTCAACTCAATATGCCCCCTC	385	21	53.8	372
EST	BQ488659	trinucleotide	203	214	12	9	TTG	GGAAGAGTAGAAGGATGATA	112	21	50.4	GGGAGTGAAGAAAGGTTCTC	279	20	55.4	168
EST	BQ488680	trinucleotide	85	96	12	9	TAG	CAATGAAGTGTGGTAAGATA	33	21	54.8	TTCCAGTATCAGAAATAGCC	337	21	53.7	219
EST	BQ488687	trinucleotide	291	302	12	9	TGG	AGGTTGAGGAGAGAGAAAGAA	160	21	54.9	TGATGAATGTGATGGAGAA	209	20	54.3	178
EST	BQ488698	trinucleotide	63	74	12	9	AAC	CAACAAAGAGAGAAACAAAGAA	32	21	54.8	TGATGAATGTGATGGAGAA	209	20	54.3	178
EST	BQ488704	trinucleotide	63	74	12	9	AAC	CAACAAAGAGAGAAACAAAGAA	32	21	54.8	TGATGAATGTGATGGAGAA	209	20	54.3	178
EST	BQ488706	trinucleotide	169	183	15	12	CTT	TCTCCACTCTCTCTCTCTCAA	104	21	55.0	GAAGATAATACCGAAACGAAAGA	370	22	55.3	267
EST	BQ488736	trinucleotide	228	239	12	9	CAC	TCTCTATGTTTGTACTTCTTC	37	23	54.8	ATTGTTGTGACCCCTTGTG	334	20	55.9	298
EST	BQ488779	dinucleotide	238	247	10	8	TC	GGCAAGCAGTGAAGTATGAG	122	21	55.3	CTAAGAGAGGAAAGGAGGAATG	289	21	54.9	168
EST	BQ488793	tetranucleotide	75	86	12	8	TTCT	ATCATCTTTCATTTCTTCTCC	16	21	54.9	ATGTTCTCAGCACCTTCC	247	19	55.2	232
EST	BQ488798	trinucleotide	377	388	12	9	TGC	TGAACCTTACTTCTCTCTGG	307	21	54.9	ACCCTTCCAGGCCAAACAC	427	18	58.5	121
EST	BQ488801	trinucleotide	93	104	12	9	TTC	ACCCACTCTCTTCTTCTCTC	59	20	55.0	GGTAAGTCCCAAGGTTTCAG	410	19	54.6	352
EST	BQ488804	tetranucleotide	35	46	12	8	ATCT	CTCTCTCTCTTCTCTCTCTCT	1	23	54.7	TCCATCTCTGAACAATAATCAA	214	21	55.6	214
EST	BQ488820	trinucleotide	104	115	12	9	AAC	TAGTAACAATGGCAGCAAG	20	19	52.4	CGAATGGAAGAAGGTGTGT	287	19	56.0	268
EST	BQ488823	trinucleotide	368	379	12	9	TGC	TGAACCTTACTGCTCTTGG	298	21	54.9	ACCCTTCCAGGCCAAACAC	418	18	58.5	121
EST	BQ488825	trinucleotide	335	358	24	21	CAA	TCTTTGCTACTCTCTCTCTCT	215	21	55.1	GATTTCTGGCTCATCCT	499	18	55.0	285
EST	BQ488827	trinucleotide	159	170	12	10	AG	CTTGGAGAGATGGTGTCT	0	19	55.0	GAGAAGAGAAATGATGGGTTT	204	21	55.0	205
EST	BQ488828	trinucleotide	62	73	12	9	TCT	AGTGAAGATAGCAATAAGTGA	10	23	55.0	GTGAGCAACCCACATAGA	183	18	52.5	174
EST	BQ488858	trinucleotide	278	292	15	12	CGG	AGCCAGTATCTCCACATC	230	18	56.8	ATCTCTGTTTCATCTCTCTCAC	509	21	55.7	280
EST	BQ488867	trinucleotide	287	298	12	9	TCT	CCCTTCTCTCTCTCTCTCT	184	20	55.1	TGATCTCTCTGTTCTTCA	363	19	51.4	180
EST	BQ488892	trinucleotide	253	264	12	9	GAA	ACACTTTCTCAAAACCTTAACC	53	21	55.0	CAACAAACGAATACGATAACC	321	21	55.0	269
EST	BQ488893	trinucleotide	162	173	12	9	CAC	GCAAGGAGGATAGAGAAAG	42	21	55.0	AATGGAGTAAAGCAGAAAGGA	310	21	55.8	269
EST	BQ488904	trinucleotide	165	179	15	12	AGA	CTGCTCTGAACTTTCTTCT	32	22	54.9	ATGCCAACACACTTCTCTG	412	18	55.3	381
EST	BQ488904	trinucleotide	200	211	12	9	TCT	CACGATGAAGAGAAAGAAAG	154	21	54.4	AACGTGGCAAAATGAGAGTAA	481	21	55.1	328
EST	BQ488904	trinucleotide	264	275	12	9	CTG	CACGATGAAGAGAAAGAAAG	154	21	54.4	AACGTGGCAAAATGAGAGTAA	481	21	55.1	328
EST	BQ488907	tetranucleotide	63	82	20	16	TTCT	TCTACTTCTCTCTCTCTCTCC	30	22	54.4	CATCAAACTTCAACCACTTC	222	20	55.5	193
EST	BQ488911	trinucleotide	300	311	12	9	GCT	TTCTTTCATCAGTGGGTATTG	123	21	55.2	TTCTCTTCAACCTTCTCTCT	342	21	54.9	220

EST	BQ488912	trinucleotide	43	57	15	12	TCT	1	21	54.4	AGCACATTAGCAACAACACT	304	21	55.2	304
EST	BQ488912	trinucleotide	258	269	12	9	GAA	1	21	54.4	AGCACATTAGCAACAACACT	304	21	55.2	304
EST	BQ488919	dinucleotide	176	185	10	8	TC	137	21	54.8	ACCCGAAGCAACAACAA	456	18	55.0	320
EST	BQ488935	trinucleotide	271	285	15	12	AAT	243	18	55.3	AACGGTAAAGAAATCAACCATC	397	21	55.7	155
EST	BQ488935	trinucleotide	358	369	12	9	ACA	235	19	54.9	GGTGAACGAAAGGAAAC	454	19	57.1	220
EST	BQ488936	trinucleotide	83	97	15	12	ACC	51	21	55.9	TCTCCATCAATAGCACATCTT	401	21	54.9	351
EST	BQ488948	trinucleotide	74	85	12	9	CAC	31	18	57.3	TACGTCACGACGACCA	273	18	62.5	243
EST	BQ488957	trinucleotide	58	69	12	10	TC	10	19	53.1	TGGAGGAAGAAGATGTAG	281	21	53.7	272
EST	BQ488958	trinucleotide	239	268	30	27	GCA	161	20	55.2	CTGGAAAGTTGGTGATTGT	421	19	53.3	261
EST	BQ488958	trinucleotide	309	320	12	9	CCA	161	20	55.2	CTGGAAAGTTGGTGATTGT	421	19	53.3	261
EST	BQ488973	trinucleotide	243	254	12	9	CAG	178	21	54.7	ATTATGAAGAGTGTGGTGGTG	539	21	55.0	362
EST	BQ488984	trinucleotide	156	167	12	9	TCT	120	21	55.1	ATAACCTCAACCATCAACA	426	21	54.7	307
EST	BQ489008	trinucleotide	111	120	10	8	TC	75	21	55.0	GTAACATTTGGCTTTCTACC	247	21	55.5	173
EST	BQ489033	trinucleotide	90	110	21	11	CCA	57	19	55.1	CGATGTACGGATAATAGTTTG	388	22	54.3	332
EST	BQ489064	trinucleotide	215	226	12	9	CAG	150	21	54.7	ATTATGAAGAGTGTGGTGGTG	511	21	55.0	362
EST	BQ489104	trinucleotide	248	262	15	12	CGT	217	21	55.8	CGTTCACTGCTCTATCTC	455	20	55.0	239
EST	BQ489104	trinucleotide	177	188	12	9	GCA	100	19	55.3	TCTATCTTTCTTGCGCTG	443	21	54.9	344
EST	BQ489122	trinucleotide	65	82	18	8	TCA	16	21	56.1	CACTTTCTCTCTCTCTCGG	376	21	56.0	361
EST	BQ489125	trinucleotide	305	325	21	11	AGT	251	21	54.3	TCTATCAAAATCACCATCAGG	534	21	55.2	284
EST	BQ489147	tetranucleotide	364	375	12	8	CTTC	132	21	54.8	GAAATACGCTCCCTTGTTG	421	19	54.5	290
EST	BQ489163	trinucleotide	139	165	27	10	CAT	98	21	51.8	CAATAGTTGGGATTTCAAGG	290	20	54.7	193
EST	BQ489164	trinucleotide	212	223	12	9	CAA	51	21	54.8	AACCCACATATTCTCGACT	332	21	55.2	282
EST	BQ489176	trinucleotide	89	100	12	9	ATG	31	21	55.3	AAACCTTACTACCTTTCTGTG	246	22	54.4	216
EST	BQ489184	trinucleotide	158	169	12	9	CTT	31	21	54.8	ATCATAAGGTTTGTAGGCAC	257	21	55.9	227
EST	BQ489184	dinucleotide	37	46	10	8	CT	0	19	54.2	ATCATAAGGTTTGTAGGCAC	257	21	55.9	227
EST	BQ489186	trinucleotide	382	393	12	9	TGC	312	21	54.9	ACCCTTCCAGGCAACAC	432	18	58.5	121
EST	BQ489195	trinucleotide	118	129	12	9	ACC	52	21	55.2	ATGAAGTACCAATACACACTC	365	21	54.9	314
EST	BQ489210	trinucleotide	379	390	12	9	GAA	321	21	54.5	CTTATCAAAATCAACCTCTC	421	21	56.1	101
EST	BQ489211	trinucleotide	318	329	12	9	ACA	269	19	56.7	ATTCAGGGTTCCCTTGCTC	453	19	56.4	185
EST	BQ489221	dinucleotide	80	89	10	8	TC	18	21	54.8	GTGATGATTGGTTTACTGGTT	144	21	54.1	127
EST	BQ489228	dinucleotide	81	94	14	12	AG	5	18	55.4	AATACTCCACCTCCATAAAC	327	21	54.7	323
EST	BQ489239	trinucleotide	108	119	12	9	CTA	70	22	54.9	TAAACGACAAATCAACACAG	311	21	55.5	242
EST	BQ489247	trinucleotide	188	205	15	12	ATC	140	21	55.5	GCATCTCCATCTCCATTTGT	419	20	57.5	280
EST	BQ489249	trinucleotide	168	182	15	12	CAA	33	21	55.2	ATTCGTCGTCATCCAAATC	349	19	52.2	317
EST	BQ489253	trinucleotide	234	254	21	11	AGT	180	21	54.3	TCTATCAAAATCAACATCAGG	463	21	55.2	284
EST	BQ489256	trinucleotide	123	134	12	9	TAA	55	23	50.0	AGGGTATTGCTGTGACTCT	182	21	55.6	128
EST	BQ489281	trinucleotide	213	224	12	9	CAA	52	21	54.8	AACCCACATATTCTCTGACT	333	21	55.2	282
EST	BQ489294	trinucleotide	284	295	12	9	AGA	140	21	54.6	GCCACCTTGTCCACCTTTG	379	18	60.1	240
EST	BQ489303	trinucleotide	131	142	12	9	ATC	35	23	54.9	AAGAAGCAACACCAATCTAC	283	21	55.8	249
EST	BQ489309	dinucleotide	182	191	10	8	TC	81	21	55.2	TACAAACATCTCTTCAATGCT	397	21	54.8	317
EST	BQ489314	trinucleotide	263	274	12	9	AGA	53	21	55.1	GTCCAAACCCAGCAAGTAG	368	19	55.7	316
EST	BQ489316	trinucleotide	138	153	16	14	AT	11	18	54.3	AGAAGATGAAGATGGTTATTG	219	22	55.0	209
EST	BQ489323	trinucleotide	108	119	12	9	ACC	8	21	53.3	GTTTGTGACGGAGTTTGA	323	21	55.2	316
EST	BQ489324	dinucleotide	40	49	10	8	GT	0	18	53.3	GTTTGTGACGGAGTTTGA	116	19	54.5	117
EST	BQ489326	dinucleotide	58	79	22	13	GA	22	21	54.7	AACCTGACTACTTGACCGAAAC	239	22	55.2	218
EST	BQ489337	trinucleotide	281	295	15	12	CCT	71	21	54.3	CGAATTTCTGAGCATTTGA	352	18	55.6	282
EST	BQ489360	trinucleotide	235	246	12	9	GAA	185	21	54.8	GCAACCATAAAGATACCAACA	361	21	55.3	177
EST	BQ489367	dinucleotide	122	131	10	8	CT	36	21	55.3	CTTACGATGCTCTTAAATGCT	226	21	54.6	191
EST	BQ489380	trinucleotide	380	391	12	9	GAG	52	18	55.3	GACATCTAGCCACCTTATC	432	21	53.9	381
EST	BQ489382	trinucleotide	73	84	12	9	AGA	3	18	57.5	TCTTGTGTTGATGATAGCA	220	20	55.1	218
EST	BQ489405	trinucleotide	59	70	12	9	TCC	8	20	55.0	GTGAAAGATCGCATAAGT	139	19	50.2	132
EST	BQ489410	trinucleotide	128	139	12	9	TTC	55	20	55.5	CTCAGGACATACCATACCCA	284	20	55.8	230
EST	BQ489411	trinucleotide	288	299	12	9	AAG	61	20	50.0	TCACTAACCAACCAACAAC	411	21	53.2	351
EST	BQ489418	trinucleotide	168	179	12	9	CAG	103	21	54.7	GTGAGAACCAATCAAGAG	285	20	54.7	183
EST	BQ489434	pentanucleotide	172	186	15	10	TTCAA	8	21	55.6	AGTTTGTGTTTCTCTCTCCAA	227	21	54.1	220

EST	BQ489908	trinucleotide	187	201	15	12	AAT	GCATTCTCACCTTCTCTCTT	19	21	55.3	TAGCAGTCTCCCTCTCTCTCT	408	21	55.1	390
EST	BQ489908	trinucleotide	314	325	12	9	ATC	GCATTCTCACCTTCTCTCTT	19	21	55.3	TAGCAGTCTCCCTCTCTCTCT	408	21	55.1	390
EST	BQ489908	trinucleotide	457	468	12	9	GAA	TCAGTAAAGAGAGAGAGGAGA	381	22	55.1	TTGCTCGGTTGAGAGT	578	18	56.8	198
EST	BQ489911	trinucleotide	98	109	12	9	AGA	TTGTTCTCTCTCTCTCCGT	53	19	54.9	OCTCACTCATCTCAAAAGT	329	21	54.3	277
EST	BQ489915	trinucleotide	474	485	12	9	TGT	TAGCAAGCGCGAATAAAC	407	18	55.0	CCACCCACATCTCCATAA	548	18	55.0	142
EST	BQ489916	dinucleotide	60	71	12	10	TC	TATCATCTTACCACTCTCA	7	19	51.1	CGCCATTGTTTGGACT	111	18	55.5	105
EST	BQ489919	trinucleotide	207	218	12	9	TTG	GGAAGAGTAGGAAGGATGAGA	116	21	55.1	ACCAGGAGAAACAAGAGT	283	20	55.4	168
EST	BQ489923	trinucleotide	281	292	12	9	CGG	TCTCTCTCTCTCATCTCTC	185	21	55.2	AAACCATCTCAAGAACGAA	527	20	54.9	343
EST	BQ489923	trinucleotide	236	253	18	8	CCT	TCTCTCTCTCTCATCTCTC	185	21	55.2	AAACCATCTCAAGAACGAA	527	20	54.9	343
EST	BQ489925	trinucleotide	197	211	15	12	CAT	CTCATCTCTCTCTCTCTTCC	137	21	54.8	CTCACATTGCGTCCCTTT	306	18	57.1	170
EST	BQ489947	tetranucleotide	204	215	12	8	CAAA	ACTCGTCACTCCAAAGAC	124	19	55.1	CAGCCAGATTCAGAGACAA	318	19	54.7	195
EST	BQ489949	pentanucleotide	71	85	15	10	TTTCA	CAGGGTTATTCCACTCTCTT	10	21	55.1	GCTCTTTGGTTTCTTTGT	397	20	54.6	388
EST	BQ489951	tetranucleotide	145	184	40	36	AAAG	CACCCACAGACACACAAA	117	18	54.3	GTGAAGAGATGAAGAATAAGA	239	22	50.6	123
EST	BQ489957	trinucleotide	307	318	12	9	CTC	TTATGATCTCTCGCATTC	232	21	56.5	AATAACTGAACCCAGCAGA	487	22	54.9	256
EST	BQ489965	dinucleotide	30	46	18	9	CT	GTCCACCTCTCCCTCTT	0	18	55.0	CTGGATTCTTTGATTCTTG	356	21	54.2	285
EST	BQ489966	trinucleotide	182	193	12	9	GAT	ATCTGGTTGGACAGGCTAC	72	19	54.7	ATGACCAAGAGCCAAAGTATC	515	21	55.9	243
EST	BQ489975	trinucleotide	308	337	30	13	GCA	AACAACAACAGCAACAACAG	273	20	56.7	ATGACCAAGAGCCAAAGTATC	515	21	55.9	243
EST	BQ489975	trinucleotide	273	290	18	8	CAA	CACAATCTGCCACACAC	221	18	55.1	ATGACCAAGAGCCAAAGTATC	515	21	55.9	243
EST	BQ489982	trinucleotide	65	76	12	9	TCC	AAGCGGAAGAGATGAAGA	31	21	55.1	ATGACCAAGAGCCAAAGTATC	515	21	55.9	243
EST	BQ489986	trinucleotide	279	290	12	9	AGT	CTTCTCTCTCTCTCTCTCT	87	21	55.0	CCCAATCAACCTCAACA	348	18	55.2	262
EST	BQ489993	trinucleotide	285	347	63	18	ATC	CTGTGCTTTTTCAGACCAATC	239	20	55.9	GGAGAGAGAGATGAGTAAGG	546	21	52.3	308
EST	BQ490046	trinucleotide	165	176	12	9	CAG	GGAGGAAAGAGTTGAGAGAC	100	21	54.7	ATTATGAAGAGTGTGGTGTG	461	21	55.0	362
EST	BQ490055	dinucleotide	191	200	10	8	GA	AAATGTGCGGTACACAGAG	126	19	56.0	TCCTGAAGCAGATCAAGGT	297	20	54.9	172
EST	BQ490066	tetranucleotide	42	53	12	8	ATCT	GCTCAACTCTCTCTCTCTT	0	21	54.6	TCTCATCTCTGAACAATAATC	223	21	54.2	224
EST	BQ490072	tetranucleotide	133	172	40	36	AAAG	CACCCACAGACACACAAA	105	18	54.3	GTGAAGAGATGAAGAATAAGA	227	22	50.6	123
EST	BQ490089	pentanucleotide	50	64	15	10	TCTTC	ATCTTAGCTCTCTCTCTCTC	19	21	51.8	TATCTCTCTTATGGAGCTTCT	314	21	55.7	296
EST	BQ490099	trinucleotide	103	114	12	9	AAC	TAGTAACTTTGCGAGCAAG	19	19	52.4	CGAATGGAAGAGGTGTGT	286	19	56.0	268
EST	BQ490104	trinucleotide	92	103	12	9	TCT	CACGATGAAGAGAAGAAGAG	46	21	54.4	AACGTGGCAATGAGAGTAA	373	21	55.1	328
EST	BQ490104	trinucleotide	156	167	12	9	CTG	CACGATGAAGAGAAGAAGAG	46	21	54.4	AACGTGGCAATGAGAGTAA	373	21	55.1	328
EST	BQ490115	trinucleotide	165	191	27	10	GAT	CACCTCGTCACTTATCTCT	9	21	55.1	ACTCTCTCTCACTCTCTGCT	256	21	55.0	248
EST	BQ490117	trinucleotide	361	381	21	18	CCA	TCTTCTCTCTCTCTCTCTCT	190	21	54.1	ATGATCGGACACCTACACC	495	20	54.8	306
EST	BQ490131	trinucleotide	311	322	12	9	TCT	CTCGCACATCTCTCTCTCT	131	20	56.1	TTGCTCTTATGGAGCTTCT	361	23	54.2	231
EST	BQ490137	trinucleotide	173	184	12	9	CAG	CTCGCACATCTCTCTCTCT	131	20	56.1	TTGCTCTTATGGAGCTTCT	361	23	54.2	231
EST	BQ490139	trinucleotide	196	216	21	18	CCA	CATCTTCACTCTCTCTCTCT	135	22	53.2	GAAGTAGGTGGCTGGCT	372	18	55.4	138
EST	BQ490151	trinucleotide	46	60	15	12	CCA	CTCCCTCAAACTCTCTCTCT	1	20	55.2	AGTAGAACATCGTCGCCTT	372	19	54.9	372
EST	BQ490153	trinucleotide	442	453	12	9	TGC	GTGACTTCTGGGTATGGAC	359	20	54.4	TCGTTCTCAACCCATCCC	508	18	56.9	150
EST	BQ490172	dinucleotide	74	85	12	10	TC	CTTACCAACCACTCAAGG	25	19	53.1	TGGAGGAAGAAGAAGATGTAG	297	21	53.7	273
EST	BQ490186	trinucleotide	75	101	27	24	ACA	GCTTACTCTCTGACTTCCCTT	0	21	54.5	GCGGTTGTCTAATCTCTCTT	293	20	56.0	294
EST	BQ490190	dinucleotide	144	155	12	10	AC	CTTCAAACTCCAACAGTCC	51	19	55.5	GTGATTTCTGTCAGTGTGT	240	20	55.1	190
EST	BQ490195	trinucleotide	178	201	24	21	AAC	AGGCATGATTCATCTCTCT	22	21	55.5	ATAAGGGTTTGTGGGA	308	18	52.8	287
EST	BQ490197	pentanucleotide	244	253	10	5	CAGTT	CAGGTTTGTCTTACTTGTCT	60	20	55.0	TCTTAAGGACTGGAACACTGA	343	23	55.1	284
EST	BQ490208	dinucleotide	54	63	10	8	TC	CTCCAAACAACACCCAAA	23	19	55.4	TGAGCAACGGATGAGACTAC	143	20	56.4	121
EST	BQ490217	trinucleotide	174	194	21	18	CCA	CATCTTTCACCTCATCTCTAC	113	22	53.2	GAAGTAGGTGGCTTGGCT	250	18	55.4	138
EST	BQ490218	dinucleotide	122	143	22	13	TC	TTTCTACATTCATCATCTCC	40	21	55.2	GCTTCAATCAACGATACAAA	330	21	55.6	291
EST	BQ490221	trinucleotide	182	193	12	9	TTG	GTGTTTGGTGTGCGTAGT	97	21	55.2	CGGTAGTATTGGAAGATGAG	275	21	54.1	179
EST	BQ490221	trinucleotide	211	222	12	9	CTG	GTGTTTGGTGTGCGTAGT	97	21	55.2	CGGTAGTATTGGAAGATGAG	275	21	54.1	179
EST	BQ490230	pentanucleotide	153	182	30	11	TTTTG	CTCTCTCTCTCTCTCTCTTG	1	21	55.1	ACTATCACTCTCTTTGGTGG	257	21	53.5	257
EST	BQ490233	dinucleotide	64	75	12	10	TC	GACCATCACTCCCACTTCT	11	19	54.8	GCTTCTCTCAATGAACATAA	257	21	56.2	247
EST	BQ490237	trinucleotide	377	388	12	9	TGC	TGAAACTCTTACTGCTCTTGG	307	21	54.9	ACCTTCCAGGCAACAC	427	18	58.5	121
EST	BQ490238	trinucleotide	256	300	45	21	TCA	CACCTATCGTCTCTTGT	56	18	51.5	TTGAGAGGTGAATCGGAG	352	20	55.4	297
EST	BQ490247	trinucleotide	352	378	27	17	TGA	ACTTCAACCTCAACTTTCACA	95	21	54.9	TTCCGATAACACCAATAAACAC	426	21	55.1	332
EST	BQ490247	dinucleotide	127	136	10	8	CT	ACTTCAACCTCAACTTTCACA	95	21	54.9	TTCCGATAACACCAATAAACAC	426	21	55.1	332
EST	BQ490266	trinucleotide	92	103	12	9	AAC	TAGTAACTATGGCAGCAAG	8	19	52.4	CGAATGGAAGAGGTGTGT	275	19	56.0	288
EST	BQ490267	trinucleotide	177	191	15	12	TGG	TCCTCTGCTTGGGATACA	79	18	55.0	GGATAGATGTTGTTGAGATGG	238	21	54.5	160
EST	BQ490293	pentanucleotide	130	144	15	10	TGCAG	GCTACTCTTACCCCTACTGGC	54	21	55.0	GGTGTGTTGGTTGGACATAA	184	19	54.1	131

EST	BQ490309	trinucleotide	330	353	24	21	TTG	ATCTCCCGATTCTCTAAAC	146	21	56.4	TCATCATCTGTGCGCTACTC	430	20	56.3	285
EST	BQ490309	trinucleotide	172	183	12	9	TTC	ATCATCTCCCGATTCTCC	143	19	56.4	ACAACAACAACAACAACA	350	21	54.9	208
EST	BQ490309	trinucleotide	354	365	12	9	ATG	ATCTCCCGATTCTCTAAAC	146	21	56.4	TCATCATCTGTGCGCTACTC	430	20	56.3	285
EST	BQ490313	trinucleotide	202	219	18	8	AAC	CITCATCTACCTTCTCTCAT	56	21	55.0	TCATCAACAACAACAACA	367	22	55.2	312
EST	BQ490322	trinucleotide	211	222	12	9	AAT	GCACCTTCTCTCTCTCTCTCT	0	21	54.9	CTGCTTCTCTCTCTCTCTTT	297	21	54.0	298
EST	BQ490334	trinucleotide	265	285	21	18	CAA	CTGAATCCGAACAACAATCTC	116	20	54.7	GTTGACTCGCTGCTAAGG	358	18	54.5	243
EST	BQ490337	trinucleotide	103	114	12	9	GAA	CTCACACCTCAGTTCTCAAA	22	20	53.7	GTTACCTTACGACGGCT	218	19	57.9	197
EST	BQ490355	trinucleotide	231	251	21	18	CAC	ACGCTTAGTTATGTTTCATT	108	21	53.4	CCACCTTATGGTGATGCC	289	18	57.2	182
EST	BQ490361	trinucleotide	175	186	12	9	CAG	GGAGAAAGATTGGAGAGAC	110	21	54.7	GTCAGAACCAAAATCCAAGAG	292	20	54.7	183
EST	BQ490370	trinucleotide	197	208	12	9	CAT	ACCGATGAAGACGACAA	122	18	57.5	GGAGGTTTGAGCGGTAGA	264	18	56.3	143
EST	BQ490384	dinucleotide	148	157	10	8	TA	CTCTCTTCTCTCTCTCTCTC	27	21	54.1	GGCTTTGATTCTCTATTCTCT	343	21	55.3	317
EST	BQ490385	trinucleotide	235	246	12	9	TAC	GGAGAAGATTGGGTGAGA	93	19	55.1	AGCAGTAGGGAAGGTATTGT	458	21	54.7	366
EST	BQ490401	trinucleotide	46	66	22	13	TC	TAAGAGTTTACACTTTCACCC	10	21	54.4	CGTTTATTGAGCAGGACACA	275	20	56.7	266
EST	BQ490454	trinucleotide	192	203	12	9	TCC	ATTTCTCTCTCATCCGACC	111	19	54.1	GACCTCAACCAAGCACATAC	413	20	55.6	303
EST	BQ490455	pentanucleotide	141	155	15	10	CAATT	TGATAGAGAGAGTGGGAGA	60	21	54.1	GGGTATTATGGGTTTGTGTT	247	21	54.7	188
EST	BQ490461	trinucleotide	384	398	15	12	CCT	CTCTTTCTCTCTCTCAACAA	173	21	54.3	CGGATTTCTGAGCATTTGA	455	18	55.6	283
EST	BQ490473	trinucleotide	175	186	12	9	CTT	TCTTTCTCTCTCTCTCTCTCT	26	21	54.9	CTTGACCTCGGCACATTC	323	18	56.8	298
EST	BQ490478	trinucleotide	263	277	15	12	ATG	GGAAGAGCGAACAACGAAA	215	18	57.4	TCAAGAGGTGGAAGCAAA	367	18	55.2	153
EST	BQ490481	trinucleotide	383	394	12	9	AGA	TCCAGATGAGTTGTCCAGT	94	19	53.7	GAGTCAGAGTTATTAGCCTCCT	444	22	53.7	351
EST	BQ490493	trinucleotide	121	132	12	9	ATC	TCATCATCAACTCATACCAT	3	21	52.8	TCAACTTCACCAACTACAACC	333	21	55.2	331
EST	BQ490494	trinucleotide	121	132	12	9	GAA	TCTTTCTCTCTCTCTCAACAA	2	21	54.4	GGAATCAAACTCTCAACAG	313	19	55.5	312
EST	BQ490500	dinucleotide	316	329	14	12	AG	TATCTTTGCTGCTTCTTCCCT	29	21	55.8	CAGTCTGAGGCTTTGG	382	18	57.7	354
EST	BQ490504	trinucleotide	381	392	12	9	GAT	AACGGAATCAAGAAAGAG	71	21	55.2	GACACCTCAACAGGACAAAC	424	21	55.5	354
EST	BQ490507	trinucleotide	61	81	21	11	AGT	AACACCCCAACAATTTCAAG	7	21	54.3	TCTATCAATCAACCATCAGG	290	21	55.2	284
EST	BQ490508	trinucleotide	395	406	12	9	TGC	TGAACCTCTACTGCTCTTTGG	325	21	54.9	GTCACCAACGCTCATCAAC	538	18	55.4	214
EST	BQ490512	trinucleotide	232	243	12	9	CAC	TCTCTATGTTGCTACTTCTC	41	23	54.8	ATTGTTGATGACCCCTGTG	338	20	55.9	298
EST	BQ490513	trinucleotide	115	126	12	9	GAA	CTCACACCTCAGTTCTCTCAA	34	20	53.7	GTTACCTTACGACCGGCT	230	19	57.9	197
EST	BQ490514	trinucleotide	55	84	30	27	AAC	GAGTAGTCAAGGTTTCTCTG	14	22	54.9	TGTTGTTGTTGTTGTTG	188	21	55.6	175
EST	BQ490514	trinucleotide	169	189	21	18	CAA	TGGAGCAAGTAACAGAAAG	98	19	53.9	AGCAGCCATCAACTCGTC	492	18	57.4	395
EST	BQ490518	trinucleotide	262	276	15	12	ACA	AAACCCCAACCAACAACCT	50	18	55.2	GGAGAGAAATCAGAGAGAGA	371	21	55.2	322
EST	BQ490546	dinucleotide	64	73	10	8	AGA	ATCAAGAAAGAGAGAGCCATT	19	21	54.9	AAGAACAAGTAGAACACAGAGA	165	22	51.0	147
EST	BQ490560	trinucleotide	334	360	27	17	CAA	GCATCTCATCTCTCATCTCA	34	21	55.4	TCTCAACTACACCTTCGTTT	396	21	54.2	363
EST	BQ490560	dinucleotide	57	68	12	10	TC	TGCTCTCTTCACTTACTACTTC	1	23	52.8	TCTCAACTACACCTTCGTTT	396	21	54.2	396
EST	BQ490565	dinucleotide	55	68	14	12	TC	CTCTCTTCACTTCTCTCTCTC	11	21	54.8	GTAAGGTTGTCGGGAGTTT	250	19	54.2	240
EST	BQ490565	dinucleotide	40	51	12	10	AC	GCCTCTCTTCACTTCTCTCTC	10	20	55.7	GTAAGGTTGTCGGGAGTTT	250	19	54.2	241
EST	BQ490575	trinucleotide	314	325	12	9	AAG	GTGAATGATGGTGTCTGATT	156	21	54.9	ATGAAGCGGAGTAACAGGA	483	19	55.8	328
EST	BQ490581	trinucleotide	179	190	12	9	CTT	CTCCACTCTCTCTCTCTCTCTC	52	21	54.8	ATCATAAGGTTTCGTAGGCAC	278	21	55.9	227
EST	BQ490581	dinucleotide	58	67	10	8	CT	TCTAACAATGGGTTCTCTCTG	20	20	56.5	ATCATAAGGTTTCGTAGGCAC	278	21	55.9	259
EST	BQ490591	trinucleotide	66	77	12	9	AGA	TGTTTCTCTCTCTCTCTCTCT	21	19	54.9	CCTCACTCATCATCTCAAACT	297	21	54.3	277
EST	BQ490600	trinucleotide	307	324	18	15	CAG	CACTGAACACCTTACCTCAAA	109	21	55.4	AGAAACACGACGACACCT	438	18	59.4	330
EST	BQ490603	trinucleotide	147	158	12	9	TTC	TCTCTCACTAACCTTAACCT	93	21	54.7	CTTCTGCTTATTACAACCTGG	323	21	54.5	231
EST	BQ490609	trinucleotide	101	112	12	9	TAG	CAATGAAGTGGTGAATGATAA	49	21	50.4	TTTGTGCTTAATGGTGGA	420	19	54.7	372
EST	BQ490628	trinucleotide	421	441	21	18	TGA	TCACAAAGACATGATTGAGG	115	21	55.2	GCTCTCCCAACAACAAGAA	470	18	54.5	356
EST	BQ490628	trinucleotide	168	179	12	9	TCT	CTTCAACTCTTCACTACCT	132	21	55.1	ATAACTCAACCTATTTCACCA	438	21	54.7	307
EST	BQ490639	trinucleotide	92	103	12	9	AAC	TAGTAACAATGGCAGCAAG	8	19	52.4	CGAATGGAAGAAAGGTGTGT	275	19	56.0	288
EST	BQ490642	dinucleotide	138	153	16	14	TC	ACTGAAGATGAGGAGGGAG	94	21	55.4	CAAGGAGGAGAGAAAGAAAG	408	18	54.1	230
EST	BQ490646	trinucleotide	287	298	12	9	TTC	TTAGAGTTGGTGGTGTGTC	179	21	55.2	TTGACAGAGGCTTGT	533	20	55.7	245
EST	BQ490642	trinucleotide	491	502	12	9	GAG	CTTGAACAGATTGGTGTGT	289	20	55.9	AAGTGGTCTTCTCTCTCTT	308	21	55.1	215
EST	BQ490658	trinucleotide	300	311	12	9	ATC	ATTGCGTTGTATGCGAGT	177	18	55.1	GAGCACGAAGAGTGTTC	370	19	54.8	194
EST	BQ490658	trinucleotide	416	427	12	9	ATC	ATCATCAACCTCTCAACGG	305	19	55.9	CGAAGACGACGCTATTAC	567	18	54.4	263
EST	BQ490659	tetranucleotide	477	488	12	8	CTTC	TTATGGATTGGTTGTAGCATT	245	21	54.8	GAATACCCCTCCCTTTGG	534	19	54.5	290
EST	BQ582300	dinucleotide	242	257	16	14	TC	AGTCTTTACATCTTCTCTCTC	210	22	53.5	TCTTCAATATCTCTCTTGG	515	21	53.7	306
EST	BQ582308	trinucleotide	254	265	12	9	TGA	CAGAACCGCAGCAACTAA	43	18	56.0	GCACCATAGTGGAACCTG	326	18	52.1	284
EST	BQ582316	trinucleotide	254	265	12	9	TGA	CAGAACCGCAGCAACTAA	43	18	56.0	GCACCATAGTGGAACCTG	326	18	52.1	284
EST	BQ582322	tetranucleotide	296	307	12	8	TTGC	GCTACCTCCTCTGACATCC	208	18	55.4	GTGTGGTGGAAAGAGCAG	465	18	54.9	258

EST	BQ582333	trinucleotide	254	265	12	9	TGA	CAGAACCGGAGCAACTAA	43	18	56.0	GCACATAAAGTGGAACTG	326	18	52.1	284
EST	BQ582340	trinucleotide	179	190	12	9	ATG	CGTCTGAGGCACTAAATCA	37	19	54.8	GGAGGTTTGTATTCCTTTCA	230	20	54.3	194
EST	BQ582364	trinucleotide	254	265	12	9	GCA	AGGCATCAGTGGAGACA	145	18	58.8	AATGCCCTTTATCAGTTT	436	19	54.0	292
EST	BQ582377	trinucleotide	275	288	14	12	TA	TGGCTTTTCTCTCTCTGTTG	213	21	54.9	CTTTAGCCCATACCTCATCTT	603	21	55.2	391
EST	BQ582410	trinucleotide	215	226	12	9	AGA	GTTACGGTTTAACTATCTCA	106	21	54.7	ACAATTCATTAGCATCCCAAG	276	21	54.6	171
EST	BQ582436	trinucleotide	95	106	12	9	CAA	GATGGAGGTAAGATGATGAAC	60	21	54.5	CCACAGTAGTAACAGCACCTT	244	21	54.6	185
EST	BQ582447	trinucleotide	124	135	12	9	CTG	TCAGACCTTCACTTCTCC	52	19	55.1	ATCTGGGCTAATGTTGTG	382	19	53.5	331
EST	BQ582457	trinucleotide	476	487	12	9	GCT	TAACCTGATTGAGTTGGATGT	375	21	54.6	TACTGATGCTGCTATTCTCC	647	21	54.8	273
EST	BQ582458	tetranucleotide	120	131	12	8	CTTG	CTCTTTCTCTCTCTCTTCC	45	21	54.1	TCCTTCATCAAAATCAACAC	230	21	55.2	186
EST	BQ582486	trinucleotide	259	270	12	9	CGT	TTCTTCTCTCTCTCTCTTCC	35	21	54.3	ACCTCTTACCTTCTCTTCCA	429	21	54.8	395
EST	BQ582492	tetranucleotide	299	310	12	8	TGTT	ATGTAAACTCTCTCGCTAC	269	20	51.2	GTCAACACCCCAATATAACA	517	21	53.4	249
EST	BQ582500	trinucleotide	184	195	12	9	TCG	TACACCTCTCATACACATCC	90	21	54.9	ACTCTCCCTTGATACTTACA	236	21	53.9	147
EST	BQ582560	trinucleotide	399	410	12	9	CAT	AGACCACCAATTTCTGTC	88	18	55.7	AAACGACGACGAGGATAA	473	19	53.6	386
EST	BQ582562	trinucleotide	473	484	12	9	TTC	TAGCATCAACCGGAACGG	292	18	58.2	TTGTAGAGAGTGGAGAAA	591	20	52.5	300
EST	BQ582568	trinucleotide	219	233	15	12	GAA	TATCATCTCCACTCCACTC	41	20	54.9	TGGTAAACGAGATATCAGGG	294	21	56.8	254
EST	BQ582578	trinucleotide	174	183	10	5	GCCCC	TGACACTTGGGATTCGTT	124	18	54.7	TTTGTAGTGGAAATGGAAG	223	21	54.5	100
EST	BQ582596	trinucleotide	138	147	10	8	AG	CGTGGGACACAAATCCTT	6	18	56.8	GGAGAAGTGACAGAGAAGAAC	282	21	55.5	277
EST	BQ582597	trinucleotide	329	340	12	9	TGC	GTTCTTCTCATCTCCTCT	17	20	54.9	AATTCGTGCAACCATC	406	18	57.3	390
EST	BQ582597	tetranucleotide	554	565	12	8	AACA	CAACAATACCCACATCTTC	498	21	55.4	CCACCTCCACCACTCCA	673	18	63.1	176
EST	BQ582623	trinucleotide	214	225	12	9	TGG	ATGAAGCAATCAGAACAGAA	78	21	55.1	ACAAACAGAACTCCAAATGTC	448	21	54.2	371
EST	BQ582626	trinucleotide	155	166	12	9	TGG	ATGAAGCAATCAGAACAGAA	19	21	55.1	ACAAACAGAACTCCAAATGTC	389	21	54.2	371
EST	BQ582628	trinucleotide	210	221	12	9	TCA	ATTCTCCCAACCAACACTAC	92	21	55.7	TATTCCTCCAGCAACAAAG	290	20	55.6	199
EST	BQ582650	trinucleotide	153	167	15	12	ATC	TCCCTCTTCTCTCTCTCTCT	11	21	54.5	TGACGGTGGTGATTAGG	258	18	55.2	248
EST	BQ582656	trinucleotide	99	113	15	12	ACC	ACCACCAACACTTCTCTCTC	67	21	55.9	TCTCATCAATAGCACATCTT	417	21	54.9	351
EST	BQ582664	trinucleotide	341	352	12	9	GCC	GACAAAGGTGAGGAGTGA	130	19	56.0	AAAGCAGTGTGAAAGTGAA	516	20	55.0	387
EST	BQ582664	trinucleotide	431	442	12	9	GCC	CTAACACACCAACCAACACAC	392	21	54.0	ATTCTCAGATTGCCAGTAA	535	21	56.5	144
EST	BQ582680	trinucleotide	82	93	12	9	CAA	GATGGAGAACATGATGAAC	47	21	54.5	CCACAGTAGTAACAGCACCTT	231	21	54.6	185
EST	BQ582688	trinucleotide	245	256	12	9	CGG	TATCTGACCAAGGAAGG	203	19	56.3	AGACAAAGCAGGACCACTAC	302	21	55.7	100
EST	BQ582699	trinucleotide	275	301	27	24	CTC	CAGCAGCAAAAGTATGATT	130	20	55.8	GGAGAAAGAGAGAGGAGTGT	374	21	54.3	245
EST	BQ582703	tetranucleotide	66	93	28	26	TC	TACACCTTCTCTCTCTCTCC	19	21	55.2	CATTCAACAACTCCGTCAG	410	20	55.0	304
EST	BQ582704	trinucleotide	184	199	16	12	AAAT	CTCTCTCTCTCTCTCTCTCC	78	21	54.8	GACATACCAGAAACCCCTCAA	422	19	55.0	333
EST	BQ582704	trinucleotide	73	87	15	12	CAA	CACAATCTCCAAACAGAAA	27	19	51.8	GAAATGAAAGGTGGGTGG	394	18	56.2	368
EST	BQ582704	trinucleotide	359	368	10	8	CT	AACAACCAACCAACACAGCAA	73	20	55.2	GGAAATGAAAGGTGGGT	396	18	57.2	324
EST	BQ582706	tetranucleotide	313	328	16	12	GAAA	TACTCTTGTAACCATCATCAG	134	21	54.6	GTCTTCTCTCTCTCTCTCTC	401	21	54.5	268
EST	BQ582718	tetranucleotide	84	103	20	16	AATT	AATAGTGGGATGAGGTTCTC	2	22	54.7	AGGGAAGATTGAAAGAGGATT	333	21	56.0	332
EST	BQ582723	trinucleotide	45	59	15	12	AAG	AAGCAAAAGTTAGAGAGAGAA	4	22	54.5	AAGTGAACACGAGAGGA	165	19	53.2	162
EST	BQ582737	trinucleotide	149	160	12	9	GAT	CGACATCTCAATCAGACGA	78	18	56.4	CTTCATCATCTCTTATCCTT	387	21	54.9	310
EST	BQ582737	trinucleotide	326	337	12	9	GAG	ATTCTTCTATGCCACCTGAA	242	20	54.9	TCAACTTCTCTCTCTCTCTCC	424	21	55.3	183
EST	BQ582753	pentanucleotide	86	95	10	5	AAAGA	GGAAACAATAAGAGACGAAA	51	21	53.8	ATTAGGCAGAAAGAGATGGAA	180	21	54.1	339
EST	BQ582840	trinucleotide	138	149	12	9	GAT	ATTGATGGAGGATTATGCGG	79	20	59.7	TATGTGACTCTGACACCA	417	21	54.1	339
EST	BQ582846	trinucleotide	228	239	12	9	CGC	CACTCATACCACTACCAACA	22	21	56.0	ACAGCGGAGGATTATTT	295	18	54.6	274
EST	BQ582851	trinucleotide	67	76	10	8	TC	TCCAATCTCTCTCTCTCTTT	19	21	54.8	CAGTTCCTCATCGTTTCTCAC	396	21	55.0	378
EST	BQ582853	trinucleotide	485	496	12	9	TGA	TTGAGCTCACCCTCTCTCC	135	20	55.2	ACAATCCAGAAACCCATAAAC	529	21	55.6	395
EST	BQ582871	trinucleotide	256	267	12	9	AAT	GATAGAAAGGCTGAATGATG	171	21	56.4	AATAGTCAAGAAATGAGGAGATT	416	23	53.2	246
EST	BQ582879	trinucleotide	103	114	12	9	GAA	CTTTCATCAGAAACCAATGT	51	20	55.0	AACCGACGATAGAGAAATGTG	336	20	55.2	286
EST	BQ582880	trinucleotide	311	322	12	9	TGA	AGTGAAGGATTGAGGAGGAC	134	21	55.0	GAAAGGGGACATAGGGAAG	453	20	55.4	320
EST	BQ582887	pentanucleotide	89	108	20	15	CCCTT	CATCCATTCGATCTCTCTT	32	18	55.6	CGGATGTGAAGAGTGAGTT	261	20	55.4	230
EST	BQ582896	trinucleotide	95	106	12	9	TCT	GAAGAAGCAAGGATAAACA	1	21	53.9	GAGAGATAGAGATGTTTGG	160	21	55.4	160
EST	BQ582918	trinucleotide	175	186	12	9	TTC	GTTCCTCTCTCTCTCTTCAAC	139	21	54.7	ATGAGTATGCTGACCTTTC	268	20	54.3	130
EST	BQ582923	trinucleotide	179	196	18	15	ACA	CTCTCTCTCTCTCTCTTGT	0	22	52.4	TTTCTGCTGTGAGTTT	225	19	53.6	226
EST	BQ582923	trinucleotide	73	90	18	9	CT	AAGTCCATTCATTTGGCTC	23	19	55.1	CGACCACTCACAAGATTTCAG	308	20	56.8	286
EST	BQ582938	trinucleotide	131	142	12	9	TTC	CAACCAATCATCCCAAA	14	18	57.6	TTGAAGAAAGAAACCCCTG	191	20	54.6	178
EST	BQ582948	trinucleotide	176	187	12	9	GTG	CCATTGTCTCGTGGTAGTAG	135	20	53.2	AGCAAACTTCTTAGCCTCATC	272	21	55.5	138
EST	BQ582955	trinucleotide	41	52	12	9	AAG	CCAACTTTTGGAGGAGAG	12	19	52.3	TAAACGACGACGACAAA	207	18	50.9	196
EST	BQ582967	trinucleotide	175	186	12	9	TTC	GTTTCTCTCTCTCTCTTCAAC	139	21	54.7	ATGAGTATGCTGACCTTTTC	268	20	54.3	130

EST	BQ582969	tetranucleotide	60	79	20	16	TTTC	GCCTACCCCACTTATCTCTTC	5	21	54.8	AATGGTGTTATTTGATGTTGG	339	21	55.0	335
EST	BQ582969	trinucleotide	366	380	15	12	ATC	TCCTTTCTTCTCTTCTCGT	69	21	55.1	TGGACTTCATCTTGGTTATG	415	21	55.2	347
EST	BQ582992	trinucleotide	309	338	30	13	GCA	AACAACAACAGCAACAACAG	274	20	54.7	ATGACCAAGAGCCAAAGTATC	516	21	55.9	243
EST	BQ582992	trinucleotide	274	291	18	8	CAA	CACATCTGCCACACCAC	222	18	56.7	ATGACCAAGAGCCAAAGTATC	516	21	55.9	295
EST	BQ582998	dinucleotide	73	90	18	9	CT	ATTGAGAGAGCAAGATCCA	11	19	53.1	AGAAGAGAGCCCAAGAGAAA	214	21	54.9	204
EST	BQ583002	trinucleotide	229	243	15	12	TAC	AGACCAAGAGAGTACAATGA	95	21	54.7	CACAGATGAACCAACACAC	468	19	55.5	374
EST	BQ583023	trinucleotide	182	196	15	12	GCA	CGCTTACCATACATTCCTT	136	19	55.2	ATTGAGTGGCTTTACCAATC	496	21	54.4	361
EST	BQ583023	trinucleotide	64	75	12	9	TTC	GGCTCCGAATAGAGAGAAA	5	19	55.6	TTGGTGAGGAGAGAGAAAG	133	20	54.0	129
EST	BQ583044	dinucleotide	80	89	10	8	AG	CAAGAAGGAGAGAGAGTGAA	36	21	54.0	ACATCAACACCCCTAACTGTG	306	21	55.1	271
EST	BQ583049	trinucleotide	466	477	12	9	AAG	CGTATCTAAACCCCTAACCCCTC	163	21	54.7	CACCACTAACTTCTCCTCTTC	537	22	54.9	375
EST	BQ583059	trinucleotide	190	204	15	12	GAT	CTTCTCCTCTCAATATCCG	64	19	51.3	TAATCAATCAAGTAATCGGACA	250	21	53.3	187
EST	BQ583078	trinucleotide	223	237	15	12	ATG	ACGGAAGAAGAGAGTAACAG	150	19	55.6	CCAATGAGAGCTTAGAGAA	356	19	55.5	207
EST	BQ583078	trinucleotide	137	148	12	9	TGG	GAATCAGAGGGTGTCTCTTC	3	20	53.7	CGAGCGTTAGTGGTCCATC	333	20	57.3	331
EST	BQ583081	trinucleotide	157	171	15	12	CCG	GGGAGCAATAGAGAGAGAGA	9	21	55.4	GTCCAAACTCAACGAAAG	361	19	53.3	353
EST	BQ583098	trinucleotide	236	265	30	13	GAT	ATTGGGAGGAGAGAGAAAC	192	20	54.9	CCAGTCAATGACGAGTAGAAG	309	21	54.3	118
EST	BQ583110	trinucleotide	423	437	15	12	AGC	GTCTCCTTTGCTTCTCAGG	326	19	55.0	GCCTCTCTGTCCTCCACTC	562	18	55.6	237
EST	BQ583112	trinucleotide	246	257	12	9	ACC	CGTCTCTCTCTCTCAATC	48	21	54.8	TCTCTCTCAACTTCTCTTC	296	21	55.3	249
EST	BQ583112	trinucleotide	261	272	12	9	ACA	ACATCAACCCCTAACCCCTAAC	108	21	54.8	CGAGGAAGAGAGAGAGAGAGA	323	21	55.6	216
EST	BQ583112	trinucleotide	273	284	12	9	AGA	ACATCAACCCCTAACCCCTAAC	108	21	54.8	CGAGGAAGAGAGAGAGAGAGA	323	21	55.6	216
EST	BQ583134	trinucleotide	433	444	12	9	ACA	GGGACTGGATGTGTGGAG	321	18	57.2	CCAAGACAGACTCAGGTT	567	19	55.4	247
EST	BQ583142	pentanucleotide	259	268	10	5	AGAGA	ATTAGCCCTTTCTGATGAT	83	21	54.7	ACTCGTCGCTTCTGTCAG	433	20	55.5	351
EST	BQ583151	trinucleotide	205	219	15	12	TCT	AGAGAAGCAGCAATGGAA	161	19	56.1	CAACAACAGGGTATGTATCAAG	468	22	54.8	308
EST	BQ583160	trinucleotide	284	295	12	9	CCA	CCGAAGGAGAGAAATGAAG	227	21	55.7	ATTTAGGCACAGGAGGA	380	18	56.6	154
EST	BQ583169	pentanucleotide	101	110	10	5	TTTTA	TCGAATGCTGTTGTGAT	42	21	55.9	CGTACTGTTCTGCTTAGCC	347	22	54.3	306
EST	BQ583173	trinucleotide	251	265	15	12	GAT	CAGAAGATTAGGGTTGTGACT	138	21	53.5	AGAAACATCAAGGAAGTGATT	461	20	54.5	324
EST	BQ583192	dinucleotide	167	178	12	10	AT	AATACCTGTGAACCCCTCA	108	19	55.3	CATTGTGTGCTTGTGTG	256	18	50.7	149
EST	BQ583206	trinucleotide	218	232	15	12	CAA	AAACAACCCCTCCGCCCTC	8	18	60.1	TCTTACCCACTTCACTAAATC	294	22	55.1	287
EST	BQ583206	trinucleotide	233	244	12	9	CAT	CAAGATTAGCCGTTTACCAA	125	20	55.6	AAAGAGGAAGTGAGGATGAT	242	21	54.6	118
EST	BQ583208	trinucleotide	157	171	15	12	TCA	CAAGATTAGCCGTTTACCAA	125	20	55.6	AAAGAGGAAGTGAGGATGAT	242	21	54.6	118
EST	BQ583208	dinucleotide	173	184	12	10	TC	TCAGCAAGATTAGCCGTTT	121	19	56.1	CGAGTAAACCGAGTGAAG	439	18	54.2	319
EST	BQ583208	trinucleotide	252	263	12	9	CCA	TCGAATGCTGTTGTGAT	42	21	55.9	CGTACTGTTCTGCTTAGCC	347	20	54.3	306
EST	BQ583226	pentanucleotide	101	110	10	5	TTTTA	TTTCTCTCTAAATCCTCCC	1	21	54.9	AGTAATCGCTGGCTTCTTAT	395	21	55.0	395
EST	BQ583232	trinucleotide	199	210	12	9	AAG	CTTCTGCTTACTCATCCTT	99	21	55.4	ATTTCTTACCCCTGCTTTCT	315	21	54.6	217
EST	BQ583235	trinucleotide	252	266	15	12	GAA	ATTGAAGGAACATCTCTCA	249	19	50.3	ATCCAACTCTCACCCATAGT	561	21	55.2	313
EST	BQ583238	trinucleotide	492	503	12	9	ATG	CCATTCTCAATCTCCTCTCT	95	21	55.1	CTCAACCTCCGAAACTACAC	413	20	54.9	319
EST	BQ583245	trinucleotide	269	280	12	9	GTG	ATGCTCTCTCAACTCAACGA	43	21	55.0	CAGCAACAATCCAAACAG	422	19	55.2	380
EST	BQ583252	dinucleotide	123	132	10	8	TC	CGTCTCTCTCAACTCAACGA	43	21	59.7	AAAGTATTATCCCATTCCTCC	349	21	54.0	273
EST	BQ583263	trinucleotide	132	143	12	9	CTC	CGTCTCTCTCAACTCAACGA	77	18	55.5	GAATCCGAGCCCTCAGAG	426	18	55.9	261
EST	BQ583275	trinucleotide	276	287	12	9	GAA	ATGCGACACCAAGTCAAG	166	18	54.1	GCTTGACTGTTTACTCTTCT	409	21	50.7	158
EST	BQ583275	trinucleotide	291	302	12	9	GAA	CTTTATTGGAGGATGGTGT	252	20	54.0	ACTGCTACCCCTGCTCCCT	374	18	54.6	351
EST	BQ583280	trinucleotide	72	86	15	12	AGA	CATTAATGCTGTGATCTGG	24	22	53.2	AGCAAACTCTTAGCCCTCATC	272	21	55.5	138
EST	BQ583292	trinucleotide	176	187	12	9	GTG	CCATTGCTCTGGTAGTAG	135	20	55.1	AATAAAGCAACAATAAGCAA	310	22	54.6	135
EST	BQ583324	trinucleotide	229	240	12	9	CAC	TTCAAGCAATCTCCTCCA	176	18	56.0	TCTGAGTCTATGTTCTCGCT	320	21	54.4	263
EST	BQ583380	pentanucleotide	524	533	10	5	AAAGA	TAGGGCTCTCTCTCTTGA	58	19	56.1	TTCCGCCCTTTCCACAA	562	18	60.3	264
EST	BQ583392	tetranucleotide	511	522	12	8	ACAA	TTTCAACCCCAAGCCCTACC	299	18	54.6	TGTGAATGTATCCATCCTT	556	20	55.3	100
EST	BQ583394	trinucleotide	80	94	15	12	TGA	CTCCCTCTTAATCTTTGCTCT	457	20	54.7	CATAGTACGCAACAACAACAA	201	21	54.9	202
EST	BQ583394	trinucleotide	181	192	12	9	GTT	GTCAATCCAGAGGACAGAG	0	20	54.7	TCTTGGTGAGAGAGTGTTT	286	21	54.0	174
EST	BQ583443	dinucleotide	40	51	12	10	TC	AGAAGGATGATGGCTGAATCT	113	21	50.8	AAAGAAGATGAAGGGAGA	296	21	54.8	295
EST	BQ583448	dinucleotide	74	94	22	13	TC	TCCACAATCCACATCAA	2	18	55.5	CGTATGCTTCTCGTCAA	416	18	54.9	377
EST	BQ583455	trinucleotide	174	185	12	9	ACA	TATTGTCTTAAGGCACCGCA	40	19	55.4	TTCATGCAACAACCTCAT	372	21	55.0	263
EST	BQ583455	trinucleotide	248	259	12	9	GAT	AAACTCAACCCACTCTCATCT	110	21	55.1	TCATGCAACAACCTCAT	348	21	56.1	134
EST	BQ583520	trinucleotide	532	543	12	9	TGA	CCATTGATCTCTCTCTCTCT	215	21	55.1	AGCACATTCACATTACATC	578	21	53.7	359
EST	BQ583523	trinucleotide	115	126	12	10	AG	GATTCTCTCTCTCTCTCTCA	220	21	52.8	TCATCATACATCCATCCCA	317	20	54.1	273
EST	BQ583546	trinucleotide	265	282	18	8	GGT	GCAATGAGGAGGACTGAGAAA	45	21	53.9	AGTGGAAGAGGTGTAGATGG	371	21	55.3	349
EST	BQ583546	trinucleotide						TTCTCTCTCTCTCTCTCTCAAA	23	21	55.9	CTCAAAAGTAACCAACATCCA				

EST	BQ583571	trinucleotide	211	222	12	9	AGA	TCTGAGTCCTGTTCTTCTGGTT	158	20	54.8	TTGCTGAATGAAGGTTAGAGA	366	21	55.3	209
EST	BQ583593	trinucleotide	74	88	15	12	CCT	TCTCTCTTATTCAGTCTCTCC	3	22	54.4	GACGAGTTTGTGTTGGT	240	18	54.1	238
EST	BQ583611	trinucleotide	197	208	12	9	GTG	TTTCCATCTCTTCTGTTCTT	49	20	51.6	TCATTATTTCTCTTCTACGATT	304	23	54.2	256
EST	BQ583613	trinucleotide	46	77	33	23	ACC	TCTCCCTTCTCTCTTTGA	14	19	54.9	GGACTGGTGTGAGTATGATTG	280	21	55.4	267
EST	BQ583616	trinucleotide	160	177	18	15	ACC	TCTCCCTTCTCTCTTTGA	14	19	54.9	GGACTGGTGTGAGTATGATTG	280	21	55.4	267
EST	BQ583625	trinucleotide	182	217	36	33	TCT	GCTCTTCTTCTCTCTCTCC	72	21	54.3	TTTACAGGAATCTTCCCGTC	380	20	55.4	309
EST	BQ583628	trinucleotide	189	200	12	9	TTC	TAACCTTCAATCTCTCCCTCA	109	20	54.9	TGTGACGATGCTGTTAGGT	343	21	54.1	235
EST	BQ583632	tetranucleotide	108	123	16	12	AAGA	CCCTTCTCTCTCTCTCTCT	18	21	56.0	ACAGTCGCTGTTCTTCTTTC	156	20	55.4	139
EST	BQ583638	trinucleotide	135	146	12	9	GAT	ACAAACACACACACACAGAGA	41	21	54.9	CTGAAGGAGAGAAGGAGTAGG	368	21	54.9	328
EST	BQ583694	trinucleotide	220	231	12	9	AAT	CCAAATCTCTCTCTTACACCT	140	22	54.4	GCAGTATCTTCTAAATCTTCATC	403	23	52.0	264
EST	BQ583708	trinucleotide	180	191	12	9	GAA	CTCCCTTCTCTCTCTCTCTC	4	21	54.9	TATGTTTGGGTTTGTCTT	227	21	54.8	224
EST	BQ583721	trinucleotide	197	208	12	9	GTG	TTTCCATCTCTCTCTCTCT	49	20	51.6	TCATTATTTCTCTCTTACGATT	304	23	54.2	256
EST	BQ583722	pentanucleotide	64	78	15	10	CATTG	CTCATCTGCGGCTTATT	18	19	55.5	AGCGACATAGTTGTTGTTGT	320	21	55.0	303
EST	BQ583722	trinucleotide	301	312	12	9	AAC	AAAGAACCCATAAACAAATCTC	131	22	54.3	TGTAGGAGGAGGAGACACTGATG	378	21	54.5	248
EST	BQ583732	trinucleotide	438	449	12	9	TGA	ATGGAGAAGAGAGACAACAAC	288	21	55.8	TAAATGCGAGAGACAACAAC	570	19	54.8	283
EST	BQ583732	trinucleotide	142	168	27	24	CAA	GTCTCTCTCAAACTCATCAA	39	21	54.4	TCATCACCAACACACATTC	345	20	55.1	307
EST	BQ583732	trinucleotide	130	141	12	9	CAG	GTCTCTCTCAAACTCATCAA	39	21	54.4	TCATCACCAACACACATTC	345	20	55.1	307
EST	BQ583732	trinucleotide	112	129	18	8	CAA	TTGTCCTCTCTCAAACTCATC	37	21	54.4	TGTTGTTGTTGTTGTTGTT	163	21	54.9	127
EST	BQ583748	dinucleotide	121	134	14	12	TC	TTTCTCTCTCTCTCTCTCTCA	70	23	54.6	ACTGTCATCATCTCTTTACCAAC	435	23	55.0	366
EST	BQ583761	trinucleotide	125	136	12	9	CAC	CGTCATAGTTCCTCTCTGCT	57	19	55.4	TTCATCAGGTCCTCTCTCT	435	19	55.8	379
EST	BQ583766	trinucleotide	234	248	15	12	GAT	CCGCTTCTGACTATCATTT	123	20	54.6	TACATCATCATCTCTCTCTC	451	21	54.1	329
EST	BQ583773	trinucleotide	49	60	12	9	CTT	CGTCGCTTGTCTCTCTTCA	6	18	63.4	TGCGATGATTGTTGTTGACC	229	19	55.0	224
EST	BQ583792	trinucleotide	307	318	12	9	AGA	AAATCAGGAATGAATGACCTT	266	21	54.7	TCTGCTCTCTCTCTGAGTTG	422	19	53.8	157
EST	BQ583802	trinucleotide	231	242	12	9	AGT	TTCTCTCTCTCTCTCTCTCTT	23	23	55.1	TTGCTGCTGTTGTTGAGTT	313	19	55.4	291
EST	BQ583842	trinucleotide	255	281	27	24	TGG	AGGTTCAATTACAAACAGCA	32	19	51.5	CGTTTACCATTTGATTTCTTC	376	21	54.1	345
EST	BQ583856	trinucleotide	146	163	18	8	AAC	CTTCATCTTACCTTCTCTCAT	0	21	55.0	TCATCAACAACAACAACCAACTC	311	22	55.2	312
EST	BQ583872	trinucleotide	213	227	15	12	TCA	CTCAACTTCTCTCTCTCTCT	63	21	54.5	GATGGTGATGGTGATGATG	273	19	55.2	211
EST	BQ583872	trinucleotide	249	263	15	12	TCA	ACACTTCTCTCTCTCTCTCT	184	21	55.0	TTTATTTGCTGCTCTCTGTC	318	19	54.0	135
EST	BQ583909	dinucleotide	227	236	10	8	TC	TTCTCATCTCATCACTTAC	40	21	54.2	CAAAAGGACAACTAAATC	369	21	55.1	330
EST	BQ583929	trinucleotide	283	297	15	12	ATC	GCATTCTCACTCTCTCTCTT	18	21	55.3	TAGCAGTCTCTCTCTCTCTCT	380	21	55.1	363
EST	BQ583929	trinucleotide	429	440	12	9	GAA	TGGCTTCTCTCTCTCTCTAATG	327	21	54.1	ACTTCTGCTGCTCTCAATTC	648	21	53.8	322
EST	BQ583936	trinucleotide	234	248	15	12	GAT	CCGCTTCTGACTTATCATTT	123	20	54.6	TACATCATCATCTCTCTCTCT	451	21	54.1	329
EST	BQ583937	trinucleotide	369	380	12	9	CAA	TTACGACCTCTCTCTCTCTCT	338	20	56.0	TATCATCACCATCATTTCCAG	576	21	55.9	239
EST	BQ583937	trinucleotide	404	415	12	9	CAG	TTACGACCTCTCTCTCTCTCT	338	20	56.0	TATCATCACCATCATTTCCAG	576	21	55.9	239
EST	BQ583938	trinucleotide	129	140	12	9	TGT	GCCACTCTGTTAGCTTTTATT	8	21	55.3	GCTCTCTCTCTCTCTCTCTT	263	21	53.9	256
EST	BQ583942	trinucleotide	131	142	12	9	TGT	GAAGGGCATCTCTGTTGACT	72	18	55.9	GTTTCTTTAGCAGCAGACATT	201	21	54.1	130
EST	BQ583945	tetranucleotide	340	351	12	8	TTCA	CTACAGAACAGACAAAGGA	222	21	55.6	ATCATCCACATTCAGAGACC	610	20	54.7	389
EST	BQ583972	dinucleotide	227	236	10	8	TC	TTCTCATCTCATCACTTACC	40	21	54.2	CAAAAGGACAACTAAATC	369	21	55.1	330
EST	BQ583995	trinucleotide	360	371	12	8	TGG	CCTGAAGATTGAGAGGG	123	19	54.8	GCACAGAACATTACGAGAGAG	491	21	55.2	369
EST	BQ584003	trinucleotide	115	132	12	8	TCT	TTACCTTCCACAACTTCTTCC	51	21	56.0	ACGAGTCATCTCTCTCTCTC	269	21	55.2	219
EST	BQ584016	trinucleotide	487	498	12	9	TGA	GGAGAAGATGGAGATGAAGT	203	21	54.9	CAGTGTAGTTGCCGAACC	529	19	56.7	327
EST	BQ584027	trinucleotide	366	377	12	9	CGA	CTTGATGGAGATGGTATGATG	303	21	54.1	TCTTGTCTTGAGATAATGGT	583	21	54.2	281
EST	BQ584037	trinucleotide	165	188	24	21	AAT	TCATCTTCTCTTCACTCCA	55	21	54.3	ACCATCAAGCCCAATCAGTAA	430	20	55.7	376
EST	BQ584037	trinucleotide	102	113	12	9	TCT	TOCTTCAATCTCTCAATTC	287	19	55.0	AGCGGGTGGTCTCGTTCT	460	18	65.3	174
EST	BQ584038	trinucleotide	341	352	12	9	CTA	ACCATCATCTCATCATCTT	58	19	54.9	ACCACCCACTACTACCAAC	418	20	54.7	361
EST	BQ584039	trinucleotide	138	149	12	9	TAG	ATGAATGAGGAGATGATGG	155	20	54.9	CAAGAGAAAGTGAATGGCTAA	465	21	54.9	311
EST	BQ584043	tetranucleotide	371	386	16	12	TTGC	CTCGTCCAAAGCAACAAC	149	18	55.1	ATCCGAAATGACCCGAC	350	18	58.4	212
EST	BQ584056	trinucleotide	187	201	15	12	TCA	CTTACACTTCAAGCAATGTC	35	21	55.0	CAAACTACCTCTTACCCCTTT	260	21	54.3	216
EST	BQ584056	trinucleotide	195	206	12	9	TTC	CTTACACTTCAAGCAATGTC	35	21	55.6	GTGAGTTTCTCGCAATCTTT	365	20	54.6	162
EST	BQ584075	trinucleotide	236	247	12	9	TCT	ACCTTCATCTTCAATTCATC	204	21	54.6	CAGTAAGATATTGGGCGG	398	19	55.9	173
EST	BQ584086	trinucleotide	319	336	18	15	CTC	ATCTATCCCTGCTTCTCTCT	226	20	54.1	GGAAGTAGATACACATAATAA	459	23	50.1	395
EST	BQ584111	trinucleotide	296	307	12	9	TGA	GATGAACCTGCTCTGTTG	65	19	54.8	TCGTACCTAAATCAAGCA	292	19	55.3	262
EST	BQ584147	trinucleotide	157	168	12	9	GAT	ATAAGAGCAAGTAGCAGCA	31	21	54.6	CCATTAGTCTCGGCTTAGGT	348	21	55.1	236
EST	BQ584188	trinucleotide	183	194	12	9	ACA	ATCATACATCAGCCATTGTT	113	21	54.5	ATTGGTCTCAGCCCTCTC	499	18	55.0	266
EST	BQ584192	pentanucleotide	459	468	10	5	GAAGA	GCATCTTTACTCAACCTTCGT	234	20						

EST	BQ584240	dinucleotide	86	103	18	9	CT	ACTCTTTCTCTCTCCACCTGA	54	21	55.7	GCCTCTGCTCTATCTCTCTCT	262	21	55.4	209
EST	BQ584256	trinucleotide	55	69	15	12	CAA	ACAACAACAACAACAACAACA	14	21	54.9	ATGTCACTTTCTGTCTTTTCCA	390	21	54.8	377
EST	BQ584256	trinucleotide	91	105	15	12	CAA	ACAACAACAACAACAACAACA	14	21	54.9	ATGTCACTTTCTGTCTTTTCCA	390	21	54.8	377
EST	BQ584273	trinucleotide	65	76	12	10	GA	TTCTCTCTCTCTCTCAATCC	18	21	55.2	GAATGCTTCCCAACAATAACT	409	21	55.9	392
EST	BQ584287	trinucleotide	185	196	12	9	AAC	TTCAACCAAGAAGAGATAGAGA	3	23	55.1	AACAGGAAAGAAGAAGAGGA	240	21	54.9	238
EST	BQ584293	dinucleotide	150	161	12	10	TC	AAACGACGAATCAACCC	25	18	55.9	TAAGAACAGAATAGTCGCGC	233	21	56.2	209
EST	BQ584293	pentanucleotide	81	95	15	10	ACAAA	AAACGACGAATCAACCC	25	18	55.9	TAAGAACAGAATAGTCGCGC	167	21	55.0	143
EST	BQ584299	trinucleotide	45	56	12	9	GAA	GTGGATTACCAAGAAGGT	11	20	56.8	AACAGTACAGAGGAGTAGAG	365	21	56.1	355
EST	BQ584324	trinucleotide	225	236	12	9	CCT	GCCTCATTTCTTGCTTCT	64	19	52.2	ATCCTTTGCTTATGCAATC	358	21	55.8	295
EST	BQ584332	dinucleotide	105	114	10	8	AG	TATCATCCATAGCAACCTG	66	20	53.7	TCCTTCTCTGTCCTTTGTT	246	21	54.2	181
EST	BQ584346	trinucleotide	151	162	12	9	AAG	ATCTGTCTTCTGTTCTCTGG	61	21	53.6	CTCTTCTCGTAACCAATGT	369	20	54.4	309
EST	BQ584362	trinucleotide	293	304	12	9	AGA	TTCTCTCTCTCTCTCGTATCA	189	22	53.7	TCAACTATGTAACCCCTATCCT	508	22	54.6	320
EST	BQ584364	trinucleotide	293	304	12	9	AGA	TTCTCTCTCTCTCTCGTATCA	189	22	53.7	TCAACTATGTAACCCCTATCCT	508	22	54.6	320
EST	BQ584389	pentanucleotide	298	307	10	5	GGAGA	ACTGATGATTCTACTATGTGGG	69	22	53.4	AAGTTTCTCTCTCTTCAAC	462	21	54.4	394
EST	BQ584394	dinucleotide	226	235	10	8	CT	CAGTGAAAGTAGTGGCTCT	188	21	54.0	AGTCTTCTCGTTCCTTAGTT	313	20	51.1	126
EST	BQ584439	dinucleotide	36	45	10	8	TC	ATCTCTCTTCTCTCTCTCTCT	5	21	50.6	AGTTTGGGACTTCAATCTC	252	21	55.0	248
EST	BQ584442	trinucleotide	70	81	12	9	AAG	AAAGGAAGTGAAGAGAGAGA	17	21	54.9	AAGCAGGAAGCAAGTAGAAGT	412	21	55.2	396
EST	BQ584454	pentanucleotide	447	461	15	10	ATATG	TACGGTGTGCTCCCAAG	184	18	58.2	TCCTGTAGAAAGTGGCTC	562	19	53.1	379
EST	BQ584456	dinucleotide	42	57	16	14	CT	AACCTCCATCTCTTAACCAAC	6	20	55.6	AATCTGCTTCAACATCTCC	296	19	52.6	291
EST	BQ584456	trinucleotide	176	193	18	8	CGA	GTAGAACACATCTCTCTTTC	140	21	55.3	ATCTGCTTTCATCAGTCCA	516	20	55.6	377
EST	BQ584465	trinucleotide	342	353	12	9	GAG	GAAGGAAAGAAAGAGAGAGA	184	21	54.5	GTC-TAAGGATTCAGGTGG	413	19	54.5	230
EST	BQ584466	trinucleotide	74	88	15	12	CCA	AAAGAAGAAAGAGGAACCA	45	19	53.9	TAAGCCACTAACTGTGAAGA	348	21	55.2	304
EST	BQ584473	trinucleotide	79	93	15	12	TCC	CTCATCACAACTCACTCTCC	45	20	55.5	GTC-TCCAAGAAGCGAACA	197	18	55.6	153
EST	BQ584490	tetranucleotide	55	74	20	9	AAAC	CTTCCCATCTCTCTCTCTCT	19	18	56.5	CTTAGTGGCTGTATTGTTC	364	21	54.6	346
EST	BQ584493	trinucleotide	113	139	27	10	GAT	ATGCGTGGTCTCTATTGTA	16	20	54.7	ACTCTTCTGCTCACTCTGCT	204	21	55.0	189
EST	BQ584497	pentanucleotide	110	119	10	5	ATGAG	CTTCTCTCAACACAAACATAA	0	21	50.5	ACATCACTCCATTCTCTTC	386	21	55.7	387
EST	BQ584512	dinucleotide	310	319	10	8	GT	ACAACATAGAAAGAGCAAGCA	158	21	55.4	GTTATCTACGACTGGACAAA	542	21	55.3	385
EST	BQ584517	trinucleotide	264	275	12	9	CAA	TTAGTTCTCTCTCTCACCTC	56	21	55.2	AGCCAGCAACATAGTAGACAG	430	21	54.8	375
EST	BQ584517	trinucleotide	327	338	12	9	CTT	TTAGTTCTCTCTCTCACCTC	56	21	55.2	AGCCAGCAACATAGTAGACAG	430	21	54.8	375
EST	BQ584530	dinucleotide	65	76	12	10	CT	CTTCATCTCATCTTCTATCCA	2	21	55.3	CAGCAACTCCAGCAATAAC	278	19	54.4	277
EST	BQ584556	trinucleotide	239	250	12	9	GAA	AGAAGAACACGAAAGATCAAG	75	21	53.8	TATCTCAACAGAGTGGCTAA	352	21	52.8	278
EST	BQ584562	trinucleotide	227	241	15	12	CTT	TTTCTCTCTCTCTCTCCAGTG	15	22	55.0	GTAATCCCAAGCCCTCTGT	324	18	54.9	310
EST	BQ584582	trinucleotide	63	80	18	15	TCT	AGTGAGGAAGAAAGAGGTGAG	25	21	55.3	TATCAGAGGGGTGGTAATCAG	241	21	54.3	217
EST	BQ584594	dinucleotide	93	104	12	10	AG	GTATGACGAGGTGTTTGATTG	37	21	55.8	CGATCGATTCTTTGTGT	223	18	55.6	187
EST	BQ584642	tetranucleotide	51	66	16	12	TTCC	GTCCGCCACCTTATCTG	19	18	56.6	AGCCCAATCTCAACTAAATC	417	21	55.2	399
EST	BQ584644	trinucleotide	188	199	12	9	GTC	AGCACCTCATCTTCTTCTATCT	18	21	55.6	CTTCCGACAAACAACTCC	229	18	54.7	212
EST	BQ584658	pentanucleotide	249	263	15	10	ATTTT	ACTTGTGGATGAGTGAGAC	56	20	54.9	CCCTTCTGGCTGTCTTG	438	18	56.8	383
EST	BQ584694	trinucleotide	72	83	12	9	ACC	TCACCTTCTCTCTCTCTCTCT	22	19	56.3	GAGTTTGAAGTTTGAAGTTGG	138	21	54.9	117
EST	BQ584705	trinucleotide	67	78	12	9	TGG	AATACTTGCTGAGATGGATAAG	30	22	53.0	GAATGGGATGGAGAAGAAA	134	19	55.0	105
EST	BQ584709	pentanucleotide	78	97	20	15	CTCTC	TCGTCTCATCTCTATCTGTG	1	21	55.4	ATACCAAGGACACCTCCATT	213	20	56.2	213
EST	BQ584719	trinucleotide	595	609	15	12	CTA	ATACAGGGTAGGAGCACACA	313	20	55.6	ATAAACAAGAGACAAGCCCC	645	21	55.2	333
EST	BQ584727	trinucleotide	304	321	18	15	CAG	GCATACCAACCAATCAAGT	180	20	55.1	CGAGCAATATACAAAGGAG	484	19	54.4	305
EST	BQ584750	trinucleotide	499	510	12	9	GAA	TTTGGTATGGTAGATGAGTT	353	21	55.0	TTTGGTATCGTTGAGTT	663	19	54.0	311
EST	BQ584785	pentanucleotide	77	96	20	15	CTCTC	ATCTATCTCTGTGGCTTCTCT	7	21	55.1	ATTGCTCCCTCCCTTCTCT	134	18	56.2	128
EST	BQ584869	trinucleotide	140	151	12	9	CTT	CTTCTCTCTCTCTCTCTCTCT	4	21	54.2	TCATCAAACTCTCATCACTC	382	21	55.2	379
EST	BQ584881	trinucleotide	157	171	15	12	TCA	TCTCTTCTCTCTCTCTCTCT	65	21	54.5	GACTTTTCTTAGGTGGTGGT	459	21	55.7	395
EST	BQ584881	dinucleotide	173	184	12	10	TC	TCTCTTCTCTCTCTCTCTCT	65	21	54.5	GACTTTTCTTAGGTGGTGGT	459	21	55.7	395
EST	BQ584881	trinucleotide	252	263	12	9	CCA	TCTCTTCTCTCTCTCTCTCT	65	21	54.5	GACTTTTCTTAGGTGGTGGT	459	21	55.7	395
EST	BQ584882	tetranucleotide	141	152	12	8	AATG	TCATACCTCTCTCTCTCTCT	74	20	55.9	AACCAACAGGAGGATCAIT	196	19	54.6	123
EST	BQ584890	dinucleotide	232	241	10	8	CT	CTATAGCCGATGCCACCT	183	18	56.9	ATTACCATCTTGAACCC	455	20	55.5	273
EST	BQ584905	pentanucleotide	227	241	15	10	TATCT	AAGATTGTGCTCTTGTGT	178	21	56.2	ATACGGAGTGGTCTTTCA	306	19	55.5	129
EST	BQ584915	dinucleotide	252	261	10	8	CT	ATTCTCTCCATTCTCTCTCT	61	18	56.3	GATTCTCGGATTTGTCTCT	302	19	54.9	242
EST	BQ584923	trinucleotide	199	210	12	9	GAA	CCAAATAAATGAATGGGAA	82	20	55.1	GGAGTATCCCTGAGAGAGG	417	20	55.0	336
EST	BQ584932	trinucleotide	445	456	12	9	CAG	TTTGTGTGAAGAAAGAGAA	190	20	51.0	ACTTGAGGATGGTGGTGGT	527	20	55.0	338
EST	BQ584932	trinucleotide	451	468	18	8	TGG	AGGCACCAAGTGAAGAAAC	321	19	55.2	ACCAGCAAGCCAGAGCTCC	522	18	58.9	202

EST	BQ584934	dinucleotide	115	126	12	10	GA	GGTACGAAATCCAACTTCT	31	19	55.0	CAAAACCAATCAAAATCAAAATC	327	21	54.7	297
EST	BQ584934	pentanucleotide	308	327	20	8	GAATTT	CGTGAGCGAGAGAGAGAG	107	18	54.6	TTGTAAGCAATAGAAATCCAAAG	469	22	54.1	363
EST	BQ584942	trinucleotide	514	525	12	9	ACT	AAGTTTGCTCTTCGGACTG	288	20	54.5	TACTAATCACTTCGTGCTC	629	21	52.0	342
EST	BQ584961	pentanucleotide	202	211	10	5	TCAAT	CTTCCACATCTTCGGTAG	149	20	55.0	AATGAGAGCCCTTCGTATTT	434	21	55.1	286
EST	BQ584980	dinucleotide	745	756	12	10	CGA	AAGGAGATAAGCAACAAC	700	21	56.0	CTCTGGATGAGCAGGAT	820	18	53.4	121
EST	BQ585012	trinucleotide	749	760	12	9	TAT	GTTGGTGGCATAGATAG	678	20	55.7	CTAATCAAACTCCCTCTCC	852	21	54.7	175
EST	BQ585037	dinucleotide	243	252	10	8	TC	GGCAAGCAGTGAAGTATG	127	21	55.3	CTAAGAGAGGAAGGAGGAATG	294	21	54.9	168
EST	BQ585052	trinucleotide	692	703	12	10	AT	CTGAATGGAGAAGAGAATCA	493	21	54.6	ACCCACAGCATTACACATAC	819	21	54.9	327
EST	BQ585059	trinucleotide	431	442	12	9	GAA	CATAGTCAACCAACCAAC	269	21	55.3	GCAGATAAGCACTTGAAC	473	19	53.4	205
EST	BQ585085	trinucleotide	293	304	12	9	TGC	CCGAGACTTTGTGACGATT	104	19	56.4	GAACCGTAAATAGCAACTACA	378	21	55.5	275
EST	BQ585099	trinucleotide	404	415	12	9	CGC	GCTACAAAGAAAGACGATGA	78	21	54.9	GAGTCTAAATCCCTGAGAAA	472	21	55.1	395
EST	BQ585117	dinucleotide	393	404	12	10	TG	TATGATTGACTTGTGTTGGT	189	21	53.1	ACGCCCTACTCGGATACA	517	18	54.1	329
EST	BQ585181	trinucleotide	184	195	12	9	GAG	TGGTAATGGTGAAGAAAGAGA	22	21	55.1	GAAGATTTAGCACAAAGG	289	19	56.0	268
EST	BQ585182	pentanucleotide	377	396	12	15	TTTTG	GGGTATGGGATGTTGTATC	108	20	54.2	TACTATTGCCCTTTGCCCT	488	19	55.1	381
EST	BQ585182	tetranucleotide	346	357	12	8	TAAT	GGGTATGGGATGTTGTATC	108	20	54.2	TACTATTGCCCTTTGCCCT	488	19	55.1	381
EST	BQ585192	trinucleotide	349	366	18	15	TCA	CGATAAAGAAACCTTAACCC	257	20	55.4	CGAGTTGTGAGAAGAGAAAC	458	21	54.3	202
EST	BQ585204	tetranucleotide	357	368	12	8	TTTTG	GTTATTCATTGCTTACACGCT	186	21	54.8	ACAAGTCTGCTCTCCATC	447	19	55.1	262
EST	BQ585225	pentanucleotide	377	396	12	15	TTTTG	GGGTATGGGATGTTGTATC	108	20	54.2	TACTATTGCCCTTTGCCCT	488	19	55.1	381
EST	BQ585225	tetranucleotide	346	357	12	8	TAAT	GGGTATGGGATGTTGTATC	108	20	54.2	TACTATTGCCCTTTGCCCT	488	19	55.1	381
EST	BQ585231	trinucleotide	179	190	12	9	ATG	CGTCTGAGGCATAAATCA	37	19	54.8	TAAGTAGGAGGTTGTATCC	237	21	53.5	201
EST	BQ585249	trinucleotide	124	135	12	9	CTG	TCAGAGCTTCACTTCTCC	52	19	55.1	ATCTGGGCTAAATGTTGTG	382	19	53.5	331
EST	BQ585318	dinucleotide	275	288	14	12	TA	CAGGTCCAGCAAGAACTC	62	19	55.9	GAGGAGAAGAAATCAATCAATA	338	22	54.7	277
EST	BQ585325	dinucleotide	879	899	22	13	AC	CAACTAAACACTCCGCAA	743	18	53.1	TGGTCTCTGTATGTGGT	1079	20	52.9	337
EST	BQ585325	dinucleotide	1020	1029	10	8	CA	TTATCAACAACACACACACC	868	21	54.3	TGCTCTGGAACCTTG	1258	18	52.0	391
EST	BQ585357	pentanucleotide	344	353	10	5	TGTG	TATGAGTTAGTGTCGTGG	561	21	55.2	TTACTATGTTGTCTGCTCGG	474	21	55.7	307
EST	BQ585365	dinucleotide	855	864	10	8	CA	AAGATGGCAAGATAAAGCC	116	20	56.1	CTATGTCGTGATGCGTGT	940	20	54.6	380
EST	BQ585383	trinucleotide	159	170	12	9	AAG	GCACCTACCTACTGCTGCT	2	20	55.0	GTAATCCAAATAATCCACCC	345	21	55.1	344
EST	BQ585423	trinucleotide	50	61	12	9	TCT	GGGTATGGGATGTTGTATC	108	20	54.2	TACTATTGCCCTTTGCCCT	487	19	55.1	380
EST	BQ585429	pentanucleotide	376	395	20	15	TTTTG	GGGTATGGGATGTTGTATC	108	20	54.2	TACTATTGCCCTTTGCCCT	487	19	55.1	380
EST	BQ585442	tetranucleotide	345	356	12	8	TAAT	GGGTATGGGATGTTGTATC	108	20	54.2	TACTATTGCCCTTTGCCCT	487	19	55.1	380
EST	BQ585477	trinucleotide	255	272	18	8	CGC	ATTGATGTGGGTGGGAC	101	18	56.4	AAGTGGCTGCTTTATTAG	438	21	55.0	338
EST	BQ585483	trinucleotide	141	158	18	8	TAC	TTTATCAACAGTCAACCC	99	20	55.1	CCGAGTTATGCTGAGAGAAG	244	20	55.3	146
EST	BQ585484	trinucleotide	218	229	12	9	CAA	TTCCAACTTCTCTCTCTCT	30	21	54.9	AAATCCCTAACATCAACGAC	409	20	54.1	380
EST	BQ585487	trinucleotide	359	370	12	9	GAT	GGCGGTCTAACTCTCTGA	89	18	56.3	AATCTCTCTTTGTTGTTGTC	425	21	53.5	337
EST	BQ585488	tetranucleotide	549	560	12	8	GATA	CAAGATGGACACGATACATAC	514	21	53.0	GCCTACTCACAACAGCAAT	876	21	57.0	363
EST	BQ585505	trinucleotide	255	272	18	8	CGC	ATTGATGTGGGTGGGAC	101	18	56.4	AAGTGGCTGCTTTATTAG	438	21	55.0	338
EST	BQ585551	pentanucleotide	157	166	10	5	TTCCT	CTTTCCTTTCTCTCCCAA	62	18	55.2	CAATGTTCTTAGTGTCCAAA	260	22	54.7	199
EST	BQ585552	trinucleotide	442	453	12	9	ATA	TTGGCTATTGAACACTTTCT	142	21	54.3	GCCTTATCTACTCCGCTT	483	20	55.5	342
EST	BQ585566	trinucleotide	196	207	12	9	TCG	CTCATCTGTCACAAACCAA	117	18	55.2	GACGAACAGGATTGACGA	259	18	56.4	143
EST	BQ585572	trinucleotide	309	332	24	14	CAA	CTTCTCTTTGTTCTTTCTCC	137	21	55.1	CTATGAGGTGATTGTGGTTGT	441	21	55.0	305
EST	BQ585582	trinucleotide	44	55	12	9	TTC	GGGAAGAAGAACAACTATCA	12	20	51.8	AACCTCCGACCAATCATC	329	18	55.7	318
EST	BQ585583	trinucleotide	163	177	15	12	CAA	CTCCTCTCACTGCTCTTATC	34	21	55.8	AATGTTGGGTTTATCGG	333	18	55.7	300
EST	BQ585594	dinucleotide	322	333	12	10	TA	GTCGGTCTCTTGTAGTCTCT	7	21	55.5	ATAAGTTCTGCTTCCAAATCC	399	21	55.2	393
EST	BQ585595	trinucleotide	38	52	15	12	ACA	ACTTCACTACGCAATTC	0	18	50.8	GCCCAACACTAATCATCTC	340	20	54.7	341
EST	BQ585610	trinucleotide	32	43	12	9	AGA	GCGAGGAGAGAGAGAGACA	3	19	55.7	TTTATGCCCTGGATGGA	290	18	54.9	288
EST	BQ585613	trinucleotide	97	111	15	12	ACC	TGGTAAGAAGCAAGAAATAA	8	21	54.5	GAGGTAGAGATGTTGGGTG	181	21	55.6	174
EST	BQ585641	trinucleotide	242	253	12	9	CGG	TATGTCACCAAGGAAGG	200	19	56.3	AGACAAGACAGGACCACTAC	299	21	55.7	100
EST	BQ585651	pentanucleotide	344	353	10	5	TTGTG	CTCTCTTTCCAGTTCTATCT	168	21	55.2	TTTACTATGTTGTGCTCGG	474	21	55.7	307
EST	BQ585656	trinucleotide	732	761	30	26	CAT	CTGATTCCTCTGCCCCACTT	612	21	55.4	ACTTACACAACCCACCTCTTT	792	21	55.3	181
EST	BQ585708	dinucleotide	137	146	10	8	AG	TTATGAATCTGACCCCAAT	90	20	52.3	CCACTTGTGCTGCTGTG	278	18	56.1	189
EST	BQ585724	trinucleotide	253	264	12	9	ATC	ATGTTAGTGAGGGAATAAGCA	50	21	54.1	GGTCTGATGATGAAGTTGTGT	310	21	54.9	261
EST	BQ585725	trinucleotide	104	115	12	9	CAA	ACTTCTTACACGCCCTCTCT	18	21	55.0	CAACGACAAACCGGATGACT	229	18	55.3	212
EST	BQ585749	pentanucleotide	151	160	10	5	TATGA	CCCACCTTCTCCTTTGAAC	74	20	55.9	GGGACCTTATACCATCTTG	428	20	55.9	355
EST	BQ585756	pentanucleotide	109	123	15	10	AATTG	AACAAGGTGAGCGGAGGA	58	18	59.3	TCTCCATCCACAAAGTTACA	360	21	55.7	293
EST	BQ585783	dinucleotide	242	257	15	14	TC	TTCCATTTGCCCTTTATTT	64	19	54.8	CTAAGAACACCTTGAGAGCC	303	20	54.2	240

EST	BQ585784	trinucleotide	262	273	12	9	ATG	CTGTATCTCTCATCTTTG	17	21	54.0	AGCAGCAGCGCTATCTTT	397	18	56.2	381
EST	BQ585799	trinucleotide	339	350	12	9	CTG	CACAATCACACCATAACA	140	21	55.3	AGCATCATCAACATTAGGAAA	495	21	54.9	356
EST	BQ585801	tetranucleotide	452	463	12	8	GGAG	CTATGGTGGTTGGTGAG	401	19	54.7	GTTCTCTTCGCGCTTC	563	18	54.9	163
EST	BQ585803	dinucleotide	475	486	12	10	TA	GATGAACCAATAATGGCAG	415	20	55.6	ATGTGATCGGTGGGACTT	569	19	55.2	155
EST	BQ585805	trinucleotide	373	384	12	9	TGC	TGAACCTCTTACTGCTCTGG	303	21	54.9	GCTCTTCTCAAACTCCTCT	570	20	55.3	268
EST	BQ585806	trinucleotide	190	210	21	18	AAC	TCTAATCAGCAACCTCTTCA	130	21	55.3	CCCTCTTCCATCAATCAC	444	19	55.4	315
EST	BQ585806	dinucleotide	70	79	10	8	TC	TTCTCTCTCTCTTAGTCC	9	21	54.4	TGTTGTTGTTGTTGTTTG	207	21	55.6	199
EST	BQ585810	pentanucleotide	445	459	15	10	TAAGC	CAAGCCTCTACACAGTC	137	19	55.7	AGATAAGCCATCCATACATCA	512	21	54.7	376
EST	BQ585812	pentanucleotide	447	461	15	10	TAAGC	CAAGCCTCTACACAGTC	139	19	55.7	AGATAAGCCATCCATACATCA	514	21	54.7	376
EST	BQ585814	tetranucleotide	155	166	12	8	CAAC	GTTATTGATTGGCTGGCTAC	30	20	54.9	TAGTTGGGATTGATACACACA	320	21	53.9	291
EST	BQ585816	trinucleotide	343	354	12	9	CTG	CACAATCACACCATAACA	144	21	55.3	AGCATCATCAACATTAGGAAA	499	21	54.9	356
EST	BQ585831	dinucleotide	73	82	10	8	CT	AACCTCTCATCTCTACGCTTC	16	21	55.4	TAACTCCACACACGGATT	196	20	55.6	181
EST	BQ585843	dinucleotide	148	164	18	9	TC	TAGGGTTTCTCACTTCCAAA	109	20	54.9	GTCGGTTTCTTCCCGATT	260	18	55.0	152
EST	BQ585859	trinucleotide	138	152	15	12	CAA	TCTTCTCTCTCTTACTCCA	50	21	53.4	AACATCTCAGCCCTAATAACA	405	21	54.1	356
EST	BQ585864	trinucleotide	119	130	12	9	TCA	CTCTTCCAACTTTACACTCCA	43	21	54.6	GTATCTTCTGATTTGCGCAT	211	21	56.0	169
EST	BQ585864	trinucleotide	131	142	12	9	TCT	CTCTTCCAACTTTACACTCCA	43	21	54.6	GTATCTTCTGATTTGCGCAT	211	21	56.0	169
EST	BQ585871	trinucleotide	299	310	12	9	GAA	AACATTTCACAACTACACTC	207	21	55.0	CAATAAATAAGTCAGGCACA	606	21	53.9	400
EST	BQ585874	trinucleotide	144	164	21	11	AAC	CACAACACAAACACAAACAC	0	21	54.9	TGCCATACATCACTTCTTCT	215	21	55.0	216
EST	BQ585874	trinucleotide	183	203	21	11	AAG	CACAACACAAACACAAACAC	0	21	54.9	AACCAACCCCTAATCAACAC	364	21	55.7	365
EST	BQ585874	trinucleotide	129	140	12	9	AAC	CACAACACAAACACAAACAC	0	21	54.9	TGCCATACATCACTTCTTCT	215	21	55.0	216
EST	BQ585877	trinucleotide	181	192	12	9	AGA	CTCTCCATCCATTCTCACA	36	20	56.1	CTTCACTTGTCTGCTGTT	261	21	54.8	226
EST	BQ585915	dinucleotide	292	301	10	8	CT	TAACTCTCTCTCTTCCATC	235	21	55.1	AAACAGATCTCCACATAAA	491	20	52.9	257
EST	BQ585919	trinucleotide	102	113	12	9	AGA	TCCACTCGTTACCCACTC	15	18	54.2	TGTGAAGTCCAAAGATAGAA	409	21	54.9	395
EST	BQ585923	trinucleotide	343	354	12	9	CTG	CACAATCACACCATAACA	144	21	55.3	AGCATCATCAACATTAGGAAA	499	21	54.9	356
EST	BQ585939	dinucleotide	127	140	14	12	TC	TGCCCTACACTATATCAAC	67	21	54.4	TAGCAAAACGAATCCAACTCA	211	21	55.9	145
EST	BQ585951	dinucleotide	93	102	10	8	CT	TCCCTAGCAACCAACACC	85	18	57.0	ATTCATCATCAGTCTCAAC	460	21	54.8	396
EST	BQ585966	trinucleotide	291	317	27	24	ACT	TTTGAAGTGTGGAAATGA	124	20	55.0	AACCCAGATGTTGTCTCT	372	21	56.1	249
EST	BQ585971	trinucleotide	191	202	12	9	GAG	ATTCTCTAACCACCTTGACC	84	21	54.9	ATTCCTCCACTACTCCACTC	305	21	54.9	242
EST	BQ585995	trinucleotide	67	87	21	18	GCG	TAACTCCCTAATCAACGAACA	8	21	55.0	GCTTCCAACTCAATCAACAG	329	20	54.9	322
EST	BQ586001	pentanucleotide	447	461	15	10	TAAGC	CAAGCCTCTACACAGTC	139	19	55.7	AGATAAGCCATCCATACATCA	514	21	54.7	376
EST	BQ586016	dinucleotide	254	265	12	10	CT	ATTGGATCTGATGGGATTG	151	20	54.7	ATCTGCTGTTATGTTGTT	436	21	54.8	286
EST	BQ586022	trinucleotide	173	184	12	9	CTT	CTCCACTCTCTCTCTCTCTG	46	21	54.8	ATCATAAGGTTTCTGTTAGGCAC	272	21	55.9	227
EST	BQ586025	trinucleotide	52	61	10	8	CT	TAACAATGGCGTCTCTCTG	16	18	53.0	ATCATAAGGTTTCTGTTAGGCAC	272	21	55.9	227
EST	BQ586025	trinucleotide	305	319	15	12	GTG	CCCTCTCTTATGCTTCTCTT	49	21	54.6	GGACCTTGTCTGCTCTCTT	395	21	55.1	347
EST	BQ586030	trinucleotide	164	178	15	12	GTG	CAGAATGAGACAGATGGCAG	57	20	56.9	AGGGAATAAACAACTCCACTAA	445	22	54.7	389
EST	BQ586034	trinucleotide	483	506	24	14	TGG	GCTTCTCTAACTTACAAACA	380	21	55.2	TACTTCTCTCTCCACCTTC	551	21	55.2	172
EST	BQ586044	trinucleotide	474	488	15	12	GTG	CCCTCAAACTCTCTCTCTCT	180	20	55.2	ATTACCCACCACCATCTTC	528	20	54.7	349
EST	BQ586047	trinucleotide	244	255	12	9	CAC	CCCTCAAACTCTCTCTCTCT	180	20	55.2	ATTACCCACCACCATCTTC	528	20	54.7	349
EST	BQ586050	trinucleotide	171	182	12	9	TCT	ACTCTCTCTCTCTCTCTCTC	112	21	55.8	GATAAGGTTTGGGTAAGGT	254	21	54.8	143
EST	BQ586051	trinucleotide	52	72	21	18	ACA	GCCAACATCAACATAACA	20	20	54.5	CTTCTCCACATACTCTTCA	320	20	55.2	301
EST	BQ586061	tetranucleotide	273	284	12	8	CAAA	ACTCGTCCACTCCAAGAC	193	19	55.1	CAGCCAGATTCAGAGACAA	387	19	54.7	195
EST	BQ586074	trinucleotide	174	185	12	9	GAT	TTGGATTGGAAGACTATGATG	41	21	55.2	GGAGGTGAAGAACCCAGTGT	237	20	56.6	197
EST	BQ586078	trinucleotide	324	335	12	9	GAA	GTACACACCTTATCATCTCA	47	21	55.0	AACCCCTTGTCTCTTCA	381	18	50.3	335
EST	BQ586095	dinucleotide	87	96	10	8	CT	TCTCAGTAAGCAGTAGAGGT	18	21	53.4	AACAATCTCAGACCATATCATCT	472	23	53.9	121
EST	BQ586110	trinucleotide	409	420	12	9	AGA	AATGTCTTGGTCTGCTACT	69	20	55.0	TGTAAATCAATAAGGGAATCA	463	22	54.1	395
EST	BQ586126	tetranucleotide	38	49	12	8	CTTG	GATCTCTCTCTCTTATTGG	1	21	52.3	GTCATCTCTCTTCTATCCCT	270	21	54.1	270
EST	BQ586132	trinucleotide	125	136	12	9	ATC	TGGCTGAAGAAGTGTATGAAA	84	21	55.4	ACCTAGTGTGAATAGGGAGG	348	21	55.0	265
EST	BQ586134	dinucleotide	115	124	10	8	TC	GCAAGCAGTGAAGTATGAGT	0	21	52.3	CTAAGAGAGGAAGGAGGAATG	166	21	54.9	167
EST	BQ586142	dinucleotide	108	117	10	8	TC	GTCACCTTAACATTTCCAA	53	20	55.0	TTCAGTCCATCAACAATCTC	218	21	55.0	166
EST	BQ586147	dinucleotide	205	214	10	8	CT	CTCATCTTCTTCTCTCTCC	109	21	54.8	CAGTGAATGGGAACAATCT	418	20	52.5	310
EST	BQ586154	trinucleotide	153	164	12	9	CAT	TGAATCTTCTCCCTCTTCTCT	11	22	54.8	GTCCTTAATGGTCCCTCC	268	20	55.2	258
EST	BQ586157	trinucleotide	89	100	12	9	CAA	GCTCTTCTCTCTCTCTCTCT	13	22	53.2	ATCGGGGATTTCTTGATT	268	19	55.1	256
EST	BQ586165	trinucleotide	46	57	12	9	TGG	CGTCCAAAGCAAAAGATGAG	6	18	55.3	ATCAGAGAGAAGGAAACGAGA	270	21	55.8	265
EST	BQ586165	trinucleotide	62	73	12	9	GGC	CGTCCAAAGCAAAAGATGAG	6	18	55.3	ATCAGAGAGAAGGAAACGAGA	270	21	55.8	265

EST	BQ586177	trinucleotide	164	175	12	9	GAA	TAATGGCAGAGAAGATGGTAA	111	21	55.1	TCAAAGCAGAAAGATGAAGAAG	223	21	55.0	113
EST	BQ586184	pentanucleotide	186	200	15	10	CTCCT	GTTCTTACTTCGGTCTCTCC	108	21	54.8	CTATCCTCCATCATTAAC	401	21	55.5	294
EST	BQ586186	trinucleotide	522	536	15	12	TGA	TTCATTATCTGTGTTGCTGCA	197	21	54.2	CTATCCTCTCATCTATTCACT	570	22	55.0	374
EST	BQ586187	trinucleotide	95	118	24	21	ATC	GAGGACTGACTGTGATGCTG	26	22	54.8	TGTTGGTATTGTTGTTG	157	21	54.6	132
EST	BQ586187	trinucleotide	119	165	48	17	AAC	GGGAGGACTGACTGTGATGT	24	21	56.5	CCTGGTTGGAGAAAGTATCA	394	21	56.8	371
EST	BQ586190	trinucleotide	495	509	15	12	TGA	TTGAAACTCCCAACGA	333	18	54.8	TAACATCTCTCATCTATT	546	21	50.7	214
EST	BQ586199	trinucleotide	70	87	18	15	CAA	AAAGAAAGAAACGGAACGA	0	19	55.1	CAAGAAGAAACCAAGCAATAA	329	21	54.9	330
EST	BQ586205	trinucleotide	310	321	12	9	GCA	GTAGTGGAGTTTGTCTGGG	92	20	55.7	CGGTGTTATGCGTTATTCTC	434	20	55.9	343
EST	BQ586217	trinucleotide	346	366	21	18	AAG	GGAACTTGAGAAGAATGTAGAA	251	22	55.2	ATAGATAACCCACAGCAAC	562	20	55.3	312
EST	BQ586230	trinucleotide	182	199	18	15	TCA	ATTCACTCTCGCTCTCTCT	93	21	55.0	TCTATCAGCATCATTTCTGG	489	21	55.6	397
EST	BQ586230	trinucleotide	327	338	12	9	CTT	ATTCATCTCTCGCTCTCTCT	93	21	55.0	TCTATCAGCATCATTTCTGG	489	21	55.6	397
EST	BQ586231	trinucleotide	556	567	12	9	CAG	AAGTCCATCTCGCTCTCTCT	454	20	55.9	ATTGAGTGGTGGTATCTGTTG	617	21	55.1	164
EST	BQ586237	trinucleotide	344	370	27	24	ACA	TAAAGCAATCTCCAGTCCA	233	20	56.0	ATACTCAAAACCAACCAAC	407	20	54.8	175
EST	BQ586245	trinucleotide	332	343	12	9	GCA	CCTCTTTTCTACTTAACCTCC	4	22	55.5	GTTGATGTTGTTGTTGTT	374	21	53.4	371
EST	BQ586247	dinucleotide	234	245	12	9	AAG	CAAAGATGGAGGCTTGATG	106	19	56.7	CTAATCGCTGCTGCTGCT	313	18	57.8	208
EST	BQ586249	trinucleotide	41	50	10	8	CT	CTCTCTCTCTCTCTCTTT	0	20	54.4	TACTGAACCTGTCAAACTCG	321	21	55.4	322
EST	BQ586249	trinucleotide	292	309	18	15	GAT	TAAACCAACACTCACCATCA	92	20	54.8	CCCAAGAAAGATAAAGGACAC	491	21	55.5	400
EST	BQ586260	trinucleotide	533	547	15	12	CAT	ATTGAGTGGTGTGATGTGAG	359	21	56.1	ATGAAGATGGAGCAGTAGGTT	594	21	55.5	236
EST	BQ586274	trinucleotide	213	227	15	12	CTT	AACAACCACTCGTCTCTCT	116	21	55.6	GTTCCACATAGCCCTCAAC	448	19	55.5	333
EST	BQ586277	dinucleotide	455	464	10	8	AG	AGGAGGAGGATTATGATGTG	327	22	54.3	TAAAGGTCATGGCTCACGAA	646	21	60.6	320
EST	BQ586283	dinucleotide	49	60	12	10	TC	AACTTTCACATCTCTCCCTC	17	21	55.0	ACAGTCTCTAAGCAAAATCTC	237	21	52.9	221
EST	BQ586314	trinucleotide	179	190	12	9	CAA	TCAATCTCATCAGACTCCAC	70	21	55.2	AATGTTCTTCTGCTTTATCCTC	322	21	55.2	253
EST	BQ586344	trinucleotide	189	203	15	12	CTT	AACAACCACTCGTCTCTCT	92	21	55.6	ATGACCATAGCCCTCAAC	424	19	55.5	333
EST	BQ586371	trinucleotide	435	446	12	9	TCG	TACGAGGTAAATACGCCAAC	240	20	55.4	ATAGAAATACAGCCGACGATAA	631	20	55.3	392
EST	BQ586389	trinucleotide	240	251	12	9	CAC	ACATTTCTTAGCCCAATCCT	78	21	55.5	ATGATCGGTATCAATCTCTTT	374	21	55.3	297
EST	BQ586400	trinucleotide	474	485	12	9	AGC	GCTTGTGGGCAACTCC	366	18	61.6	AAACAGAGGCTTTCAATAATC	618	21	53.0	253
EST	BQ586423	tetranucleotide	1109	1120	12	8	TCTA	TATTACGGCTACGATAAGTG	1004	21	54.8	TATGGATGATGAACGATAAG	1188	21	55.1	185
EST	BQ586426	trinucleotide	357	368	12	9	ATA	CAAAGGCTCAAGAAAGG	224	21	55.8	TGATAGGTGGGATGGTAA	434	20	55.4	211
EST	BQ586432	trinucleotide	214	228	15	12	CTT	TCATCCTCTCTCTCTCTCT	11	19	52.2	TCAATGGTAGTAGAAGGACAA	366	21	54.8	367
EST	BQ586444	trinucleotide	67	78	12	9	TTC	CGCAGAGAGAGAGAGAGAA	0	19	55.2	ATACAAATACGCAAGCAACAC	282	21	55.5	272
EST	BQ586454	trinucleotide	93	104	12	9	GAT	AATGATGCTGTTGCTGATG	38	19	53.8	AGTTTGGCGTGGCTGCTCT	255	20	54.3	218
EST	BQ586457	dinucleotide	90	105	16	14	TC	CCACCTTCTGCTCCCTAC	45	19	55.6	CTTCTCTGATGATGCTGCT	242	18	60.6	198
EST	BQ586458	trinucleotide	110	121	12	9	AGG	AGGTGGACGAGATTGAAAG	18	19	55.2	TAGTACCAAGAACGCAACAC	407	21	54.7	390
EST	BQ586477	trinucleotide	321	332	12	9	ATC	TAACATGATTGGCAGCTACT	150	21	56.7	CGAAGATGAAGAAGATGA	402	19	54.7	253
EST	BQ586483	trinucleotide	101	112	12	9	ACC	AATACTCAAACCTCTCACTTC	1	21	54.9	AATCTCTTTGACCTCTTCTTG	316	21	55.2	316
EST	BQ586500	trinucleotide	237	248	12	9	CAA	ATTGAGGGTAGTGAGGACAG	196	21	55.8	CCTTGATAGTCCCATAGTTCA	451	22	55.9	256
EST	BQ586500	trinucleotide	279	290	12	9	GAT	AACAGCAACAACAACAAGAAC	231	21	55.5	TCCTCCATAAGCGGTCTTAA	477	20	56.0	247
EST	BQ586506	dinucleotide	172	185	14	12	AG	TTTCTCTCTCTCTCCACAC	56	19	55.1	CTTTACAACCTCGGTTCTCT	397	21	55.7	342
EST	BQ586509	tetranucleotide	366	377	12	8	TTGG	ACATCTTGCTCTCTCTCTCT	143	21	55.3	CTCAACCTCTCTCTCATCTCA	530	21	54.6	388
EST	BQ586513	trinucleotide	419	430	12	9	CAG	GCAAAGAAAGAGAGAGGTAGG	310	21	54.9	ATTACAAGGAAGGTTGAAAGT	226	21	54.5	149
EST	BQ586514	trinucleotide	144	155	12	9	ATG	TATGAACAAAGAGAGGTGGGA	78	21	55.9	ATCCAGAGATGAACACACAC	372	21	54.9	310
EST	BQ586526	trinucleotide	130	144	15	12	TAC	CTTGAACCTGCTCACAATC	63	20	55.7	GCTCCACCATAGGAATAGAT	493	21	55.0	343
EST	BQ586533	trinucleotide	210	227	18	8	CTT	CGAATACAACCTACCTTCAGCA	151	21	55.2	CCTTGATAGTCCCATAGTTCT	500	21	55.5	334
EST	BQ586547	trinucleotide	393	410	18	15	AGC	CAACAACAACAACCTTCCT	167	20	55.2	CTTATCTCTCATCGCTTCT	227	19	55.7	208
EST	BQ586547	trinucleotide	168	179	12	9	CAA	CATCTCTCTCTCTCTCTCTCC	20	22	54.1	CGGGAATGATGGTATTGT	464	21	54.9	322
EST	BQ586559	trinucleotide	263	274	12	8	TCG	GAGGGCATCATAGAAACTCA	143	20	55.3	TAGACATAACGAGAATGGGA	299	19	55.4	235
EST	BQ586576	trinucleotide	129	146	18	8	AGG	GCCTTTGATTGGAAGTAATGT	65	21	55.9	GCTGCTTGTGCTCTGTGAG	363	20	53.9	332
EST	BQ586583	dinucleotide	107	116	10	8	CT	CTTCTCACCATCTTCTCTCT	32	21	55.2	AAATGCTCTCTCCATCTGT	186	20	54.3	178
EST	BQ586591	dinucleotide	30	47	18	16	CT	TCTCACTCAACATCATCTCT	1	19	50.8	GACGACCCCATATTAGATT	186	20	54.3	178
EST	BQ586591	trinucleotide	69	80	12	9	TTC	AACATCATCTCTCTCTCTCT	9	21	55.8	AATCTGCTCTCTCTCTCTG	235	21	55.2	181
EST	BQ586608	trinucleotide	128	145	18	15	TCA	TGTTGGTTGGTTGTTCTTAA	55	20	55.2	ACTTAGGGCTCACTTCTTCA	442	21	55.9	390
EST	BQ586612	tetranucleotide	306	317	12	9	CTG	CTTTGTTGTTGTTGTTCTCT	53	20	56.3	CGAACAACCTCTGAAAC	398	18	56.5	317
EST	BQ586612	tetranucleotide	336	347	12	8	TTGG	TTCTCTCTCTCTCTCTCTCT	82	18	54.8	ACCTCAGAAACCTCATACAC	365	21	55.7	265
EST	BQ586620	tetranucleotide	275	290	16	12	ATTG	TATCTCTTACCACCAACGAA	101	21	54.6	GCATCCTCTCTTTACACCTCT	539	21	55.2	125
EST	BQ586635	trinucleotide	449	460	12	9	TAA	TTCTGTTACTGTTGCTCTTTC	415	21						

EST	BQ586638	pentanucleotide	107	121	15	10	TTTCA	TC	TCCTCTACCCACCTTCTT	46	20	55.5	GCCAACTCTGACGGAATAG	206	18	51.4	161
EST	BQ586641	trinucleotide	126	149	24	14	TCT	TAGGTTGGTTCCTTCTCTG	87	21	21	56.1	GTGATTGTACTGCTACTGCC	190	21	55.1	104
EST	BQ586642	trinucleotide	401	427	27	17	CAA	GTGTTGAGTTGATGGGTAATC	233	21	21	54.5	CATTGTTGGGAAGTGTCATAG	487	21	55.6	255
EST	BQ586642	trinucleotide	386	400	15	12	CAG	GTGTTGAGTTGATGGGTAATC	233	21	21	54.5	CATTGTTGGGAAGTGTCATAG	487	21	55.6	255
EST	BQ586647	trinucleotide	311	325	15	12	TGA	CATTGTAAGGCGATTAATG	265	20	20	55.4	CTCTCTCTCTGTAACCTTTGCTC	596	23	54.6	332
EST	BQ586664	trinucleotide	539	550	12	9	CTC	GTGTATGTCGTTTGGAGAAGT	297	21	21	54.3	CAAGGTGCGATAGTTGTCGTG	620	20	56.9	324
EST	BQ586672	trinucleotide	58	81	24	14	CAT	ACAGTTGGCGGAAGAACCA	29	18	18	57.7	AGGAGAGAGACGGAATGAG	165	21	55.3	137
EST	BQ586679	dinucleotide	119	140	22	20	CT	AGGAACCTGAACAAACCCCTT	87	20	20	55.4	CCAATAAGAGAGACGACATAACA	354	22	54.1	268
EST	BQ586690	trinucleotide	442	459	18	15	TGA	ATGATAAAGAGAGAGGTGAGG	266	21	21	55.0	TCAGAGGAGATAGAGAGAGAAA	542	23	54.4	277
EST	BQ586690	trinucleotide	314	325	12	9	TAA	ATGATAAAGAGAGAGGTGAGG	266	21	21	55.0	TCAGAGGAGATAGAGAGAGAAA	542	23	54.4	277
EST	BQ586691	pentanucleotide	391	400	10	5	TCTCA	AAGGAGGTCTGGGTGATCT	234	20	20	55.1	CTCGTATCCAAACAATAGCAGT	471	21	54.6	238
EST	BQ586713	trinucleotide	103	117	15	12	TAC	TACAGGACACCTCAACATTTT	14	21	21	55.5	CCAACCTTAGAGAACCC	406	19	54.6	393
EST	BQ586722	trinucleotide	90	105	16	14	TC	CCCACTTCTCTCCCTTAC	45	19	19	53.8	AGTTTGGTGGCTGCTCT	242	18	60.6	198
EST	BQ586726	trinucleotide	107	118	12	9	TGA	GAGGACTGGGAGGATGATT	29	19	19	56.4	CTTTCTGCTGGGCTTCT	206	18	55.7	178
EST	BQ586753	trinucleotide	449	460	12	9	AGT	GAGTCTATGCCACCTCCC	349	18	18	55.4	GAATCAGAAACCCCTGAAC	617	19	55.4	269
EST	BQ586761	trinucleotide	83	94	12	9	CCT	TCTCTCAGGTCAGCA	19	18	18	55.2	TCACATCTCTCCATCTTTGT	286	21	51.4	268
EST	BQ586764	tetranucleotide	118	137	20	16	TTTG	TAGGAAAGGGAATCAAAAC	25	19	19	54.2	CTCTAAACCCACAAATCC	311	19	52.1	287
EST	BQ586770	trinucleotide	253	270	18	8	TCT	GAATCATCAATCACACCATC	122	21	21	55.2	ACCAACAAGTATCCACAACA	313	21	55.5	192
EST	BQ586773	trinucleotide	60	99	40	36	AAAG	CACCCACAGACACACAAA	32	18	18	54.3	GTGAAGAAGATGAAGAATAAGA	154	22	50.6	123
EST	BQ586782	trinucleotide	331	351	21	11	AAT	TAGAGGTGGAGGAGGAATCT	238	20	20	55.4	TAATAAGCAACCAACCAAC	518	21	55.4	281
EST	BQ586795	trinucleotide	403	423	21	18	TAA	GAGAGAGAGCAGCAGAAAC	96	21	21	55.0	CTCAACCTTACACCATCAC	480	20	55.4	385
EST	BQ586805	dinucleotide	110	119	10	8	TC	TCATTTCTCTTCAACACA	39	21	21	54.3	ACCTTTCTGGAGCATTAG	277	18	55.3	239
EST	BQ586811	dinucleotide	57	72	16	14	CT	ATTGCGCTCTCCCAATC	29	18	18	55.2	AACGCGCTCGCCATTAG	203	18	54.8	175
EST	BQ586831	trinucleotide	166	177	12	9	AAC	CTCTACATTTGACTCTCCCA	38	21	21	53.8	TGTTATTAGGATGATTCACAT	232	23	54.7	195
EST	BQ586831	trinucleotide	178	189	12	9	AAT	CTCTCATTTGACTCTCCCA	38	21	21	53.8	TGTTATTAGGATGATTCACAT	232	23	54.7	195
EST	BQ586837	trinucleotide	115	126	12	9	AAC	CGTTGTTGGGTGTTATGT	22	20	20	56.0	ATTGCTCTGTTGTTGTTGT	410	21	55.0	389
EST	BQ586868	trinucleotide	262	285	24	21	CAA	GTATCTCTCTCCCAACCACT	7	21	21	54.9	GTAGGTGCTCTCGGTTCT	328	20	55.8	322
EST	BQ586868	trinucleotide	217	228	12	9	TGA	GTATCTCTCTCCCAACCACT	7	21	21	54.9	TGTTGTTGTTGTTGTTGT	283	21	54.9	277
EST	BQ586870	pentanucleotide	542	551	10	5	TTTTC	CTCTCATCGTTTCTCCCT	223	21	21	55.4	ATGGGCAATTTGCTGTTCT	603	19	55.5	381
EST	BQ586872	trinucleotide	372	383	12	9	TTC	CTCTCATCGTTTCTCCCT	223	21	21	54.9	GATGATTTGTTGTTGTTGG	557	21	56.2	398
EST	BQ586882	dinucleotide	90	99	10	8	CT	CCTCCACTCTTTCATTC	52	19	19	54.6	TCATCTCTCTGCTCTCTTG	229	21	54.8	178
EST	BQ586884	trinucleotide	464	475	12	9	TGG	AAATCGTTGGAATCGGAA	329	18	18	56.4	TCTCAGCGCTCTCATCAC	557	19	54.7	229
EST	BQ586886	trinucleotide	156	167	12	9	AAT	AGTGAAGAAGACCAACAACA	29	21	21	55.3	ACCGCAAGATGACAAGA	428	18	55.9	400
EST	BQ586888	trinucleotide	334	363	30	27	GCA	CAGTATGAACAGGCAGGATT	256	20	20	55.2	CTGGAAGTTGGTATTGT	516	19	53.3	261
EST	BQ586888	trinucleotide	404	415	12	9	CCA	CAGTATGAACAGGCAGGATT	256	20	20	55.2	CTGGAAGTTGGTATTGT	516	19	53.3	261
EST	BQ586920	pentanucleotide	264	273	10	5	GCCCG	AACACACATCTACAAAGCAA	45	22	22	53.2	GGCAGTTCTCATCTCTCC	441	18	55.5	397
EST	BQ586936	trinucleotide	139	153	15	12	CTT	TCTCCACTCTCTCTCTCAA	74	20	20	55.0	GAAGATAATCCGAACGAAGA	341	22	55.3	268
EST	BQ586952	trinucleotide	534	545	12	9	TGG	CTGGTGGTCTTACATCTTTG	295	21	21	54.9	TGAACCTGCCATCTGTTGT	582	19	55.0	288
EST	BQ586977	trinucleotide	59	70	12	9	CAG	ACCAATACAAAGGACCA	15	18	18	54.8	CTCAAGTTCTCAGCAGTGT	323	20	55.5	309
EST	BQ586989	trinucleotide	515	529	15	12	TAC	TCTTCTCATCTTCACTTCAAC	394	21	21	54.4	GCTGATTGTCACTCCCAAA	636	20	56.2	243
EST	BQ587000	dinucleotide	86	124	39	29	CAA	ACAGCAATGGAAGACAATC	5	20	20	55.2	CTTAGATGAAGCGGAATAGG	362	21	55.9	358
EST	BQ587028	trinucleotide	551	562	12	9	CTG	CTTCTTCTCATCTGCTACTAC	0	22	22	50.3	ACACCAAGCAATCTCCAA	354	18	58.6	355
EST	BQ587049	trinucleotide	92	106	15	12	CAA	ATCTGGTGAGACAATGAGACA	514	21	21	55.8	CAACAGGCATCCATCTAA	635	19	54.6	122
EST	BQ587052	trinucleotide	61	72	12	9	GAA	AGCAACTTCATCTCTCCCAAC	18	20	20	55.9	TAAATCCGTGTTCCGATAA	339	19	54.1	287
EST	BQ587067	trinucleotide	365	394	30	27	AAC	TTTCAATCCCAATGAGAGACA	18	20	20	55.0	CTTCAAGGTAAGCCCTGT	384	18	55.2	367
EST	BQ587077	trinucleotide	135	149	15	12	TCT	AATCCATCACATTTCTCCAC	266	20	20	54.8	CTTCAAGGTAAGCCCTGT	384	18	55.2	367
EST	BQ587083	trinucleotide	195	206	12	9	CCA	AAGTGGGTGTTGCTGTTT	26	20	20	55.7	TTGACCTCTGTTACTCTTG	575	20	54.6	310
EST	BQ587093	pentanucleotide	169	178	10	5	AAATC	CATACCACGACTACCTCAAC	97	21	21	54.8	GCGAAGGAGAGAGAATGG	437	19	57.5	341
EST	BQ587106	pentanucleotide	250	259	10	5	TTTTA	TTTCTTTCTTCTTTTCCCA	122	21	21	55.9	CTCTCTCTCTCTGCTCTCTT	383	21	54.8	262
EST	BQ587112	dinucleotide	178	189	12	10	TC	ACAGTTTATTTGATGGGTT	210	21	21	55.2	GAGATGCCATACCAAGAGACA	557	21	55.5	348
EST	BQ587119	trinucleotide	289	300	12	9	GGC	ATCACAAACCTCTCTCATC	140	19	19	55.2	ACATCTCTCATCTTCCCTGT	484	21	55.3	345
EST	BQ587131	trinucleotide	324	335	12	9	GGA	TTTGTGTATCGGAAGCC	201	19	19	56.2	ATCTGTTCATCTCTCTCAC	519	21	55.7	319
EST	BQ587146	trinucleotide	262	273	12	9	AAT	ACAATGAAGAACCTGCTGTAA	226	21	21	55.1	GCCTACAAGTCGGTAGTAA	447	20	55.5	222
EST	BQ587148	trinucleotide	144	158	15	12	ATA	TTCTTTGCCCTTACACCC	30	18	18	56.1	CTTTGACTTGGCCCTGAAAC	422	19	55.9	393
								TTATTCAAAATGGCGGTTT	54	20	20	55.3	AAGAAAGAAGCACAAAGTAGCC	335	21	55.6	282

EST	BQ587150	tetranucleotide	102	113	12	8	TTCT	TCTTTACATTTCTTCCAG	47	19	52.9	TTCTGTTGTTGAGATTAGTAGGT	176	23	52.6	130
EST	BQ587168	trinucleotide	80	91	12	9	TCA	TTCTTCCACTAACCATTAACA	3	21	54.8	GCTGCTCTACTTAACAATAAA	136	23	53.0	134
EST	BQ587176	dinucleotide	109	120	12	10	CT	GTCGGCTCTCTCTCTCT	19	20	55.5	CTTAGACTGGGTGACTTGTG	259	21	55.0	241
EST	BQ587181	trinucleotide	191	208	18	8	GGT	GTGGACATTTGGAGTGA	115	19	54.1	AAGATCACTGCTGAACATC	253	21	53.7	139
EST	BQ587187	trinucleotide	256	267	12	9	TGA	TTTGGTGATGAAGTAGTGATG	214	22	55.3	TGAAGTAAATGAGGAACCTT	455	21	55.5	242
EST	BQ587188	dinucleotide	149	160	12	10	AG	ATGGAGAGCTGGGTATTG	59	19	54.8	AATGTGGACAAACAACTGAAC	340	21	55.0	282
EST	BQ587189	pentanucleotide	566	580	15	10	TGATT	GTCCTTCATAGTCTCTGTTGT	496	22	55.0	CTCTAAACCCCTTCCATC	609	19	53.7	114
EST	BQ587200	trinucleotide	74	85	12	9	AGA	TTCTCCATCCGAGTTGCT	19	18	56.8	GAAGTTGCTCTAATCTGTGCT	185	21	54.0	167
EST	BQ587213	dinucleotide	63	74	12	10	TC	GTCGGTAACTTTCATCTCT	19	21	55.4	GCACAAGACCACACTCAAC	403	19	54.8	385
EST	BQ587220	trinucleotide	78	87	10	8	CT	GTCCGTAACCTTTCATCTCT	19	21	55.4	GCACAAGACCACACTCAAC	403	19	54.8	385
EST	BQ587265	trinucleotide	369	380	12	9	CTC	AACCTATCACCATCTCTCTCTG	285	23	54.5	GATGTTCTTGACGGGAAA	521	18	54.3	237
EST	BQ587269	tetranucleotide	256	267	12	8	GAAA	GCCACCTTAGACACTTT	161	18	52.5	TTGAGAAAACCTTCTATAGTCA	519	21	54.9	359
EST	BQ587270	pentanucleotide	326	335	10	5	TAAAT	AGTATGTGCCGCTCTCAA	70	18	55.3	TCATCAACCATCCAACTTATC	423	21	55.0	354
EST	BQ587270	dinucleotide	33	44	12	10	CT	TTCAACAACCTCACGCTAA	2	18	55.1	TACTTCTCAAGACTCCAACA	201	21	55.0	200
EST	BQ587282	trinucleotide	397	420	24	14	CAA	CACGGATGGAAGAGAAATG	117	18	54.8	CGGTGGTTGCTGTTGTTG	461	18	59.7	345
EST	BQ587282	trinucleotide	372	386	15	12	CAA	CACGGATGGAAGAGAAATG	117	18	54.8	ATGTTGTAGAGGGTGTGTTG	434	21	55.1	318
EST	BQ587291	trinucleotide	348	365	18	15	TCA	CCCTTCACATCTTATCTCT	297	21	55.0	GTTTCACCACACATTTCTC	585	20	55.4	289
EST	BQ587291	trinucleotide	94	108	15	12	AAC	CCAATGCCCTCTCTCCAA	7	18	57.2	TTAGGGTTAGGGTTCTTTATC	278	22	53.7	272
EST	BQ587296	trinucleotide	168	179	12	9	TCT	CCCTACTTCTCATCTCTCT	70	20	55.0	CACATTCACCATTCACCC	394	19	55.4	325
EST	BQ587306	trinucleotide	223	234	12	9	CCG	GCAGTCCCATCATCTCACCC	83	18	57.2	GTCCATTCAACAAATCTTCCT	455	21	55.7	373
EST	BQ587320	dinucleotide	45	54	10	8	GA	AGACACAGAGGAGGAGACTG	16	19	55.1	CGAAGTTTGGCATAGGT	308	19	55.4	293
EST	BQ587321	trinucleotide	112	126	15	12	AGG	GCGGTGATGAGAGAGATG	83	18	54.9	ATGATTAGGAGGAACAACAAA	298	21	53.9	216
EST	BQ587339	pentanucleotide	248	257	10	5	AAAAG	CTTGCTCTCGCCGTTAGG	1	18	59.7	GTTATTGTTGCTGAACACTT	322	21	54.8	322
EST	BQ587375	pentanucleotide	135	154	20	15	TCAAT	GAAGGAGAGGAGAGAGAGAGA	100	21	54.5	AGACAGAAAGAACAAAGAGCC	392	21	55.4	293
EST	BQ587375	dinucleotide	110	121	12	10	GA	ATCCACCCACTCATCAAA	55	18	54.4	ATCAGTTCACCACTTCTTT	453	21	54.1	334
EST	BQ587377	trinucleotide	183	194	12	9	AAG	TACCGTTTATGCGAGTCA	111	18	53.5	ATTACATAATGGCTCCACTT	281	21	56.2	171
EST	BQ587378	pentanucleotide	248	257	10	5	AAAAG	CTCCGATTAGGGTTGCT	143	18	55.3	TCGTTATTGCTTGCTGAAC	324	19	55.0	182
EST	BQ587422	pentanucleotide	135	154	20	15	TCAAT	GAAGGAGAGGAGAGAGAGAGA	100	21	54.5	AGACAGAAAGAACAAAGAGCC	392	21	55.4	293
EST	BQ587422	dinucleotide	110	121	12	10	GA	ATCCACCCACTCATCAAA	55	18	54.4	ATCAGTTCACCACTTCTTT	453	21	54.1	334
EST	BQ587427	trinucleotide	118	129	12	9	TGA	AGCGTTGATGAACCCAAA	80	19	55.7	ACTTCCCTGGCTGCTATC	223	19	54.2	184
EST	BQ587471	trinucleotide	247	267	21	18	AAC	GAGCACAAAGAAAGCAATC	34	20	55.2	CAAAACAAATAATAATGGTG	320	22	54.2	287
EST	BQ587471	trinucleotide	332	343	12	9	GAA	ACAACAACAACAACAACAACA	247	21	54.9	GTATCTTGTCTCCACATCC	414	19	55.4	168
EST	BQ587476	trinucleotide	292	303	12	9	GAA	TTCAAACCTCTTCTCTCTCT	120	20	55.6	TTACAGATTCAACACCTTCTTT	453	21	54.1	334
EST	BQ587483	trinucleotide	136	153	18	15	ACT	CACCAACTTCTCTCTCTTTG	86	20	55.0	ACCGATCACTGTCTTTCT	268	19	55.7	183
EST	BQ587491	trinucleotide	469	480	12	9	GAA	GTAAGTCCCGAGTCCAA	403	18	57.1	ACAGATCAACACGACGCA	584	19	55.3	182
EST	BQ587498	trinucleotide	174	185	12	9	GAT	TTGGATTGGAAGACTATGATG	41	21	55.2	GGAGGTGAAAGAACACAGTGT	237	20	56.6	197
EST	BQ587523	trinucleotide	285	305	21	18	GCT	TTTGGTTGATGGGTTCTT	183	18	54.4	ATTCTCTCCGACTATGTTTG	557	21	55.9	375
EST	BQ587532	trinucleotide	261	284	24	21	CAA	ATTGGTGGTATCTTCTCTCC	0	20	55.5	TAATCGTGGTAGGTTGCTTTC	335	21	54.4	336
EST	BQ587532	trinucleotide	216	227	12	9	TGA	ATTGGTGGTATCTTCTCTCC	0	20	55.5	TGTTGTTGTTGTTGTTGTTG	282	21	54.9	283
EST	BQ587540	trinucleotide	358	369	12	9	GAA	AACCGTCTTCTCAAAACAC	39	19	55.1	TCAACTCACTATCTCTCTCAA	438	21	54.9	400
EST	BQ587540	trinucleotide	370	387	18	8	GAT	AACCGTCTTCTCAAAACAC	39	19	55.1	TCAACTCACTATCTCTCTCAA	438	21	54.9	400
EST	BQ587552	trinucleotide	450	461	12	9	TGA	AGTCTTGTGCTTGAATCTTG	244	21	54.6	TTCATCATCCACTATATCTCC	532	21	54.1	289
EST	BQ587557	dinucleotide	364	373	10	8	TC	TTAGAAATGTTGGAGAAA	275	19	50.7	GTCGCGGATGAGAGAAA	637	18	55.5	363
EST	BQ587562	trinucleotide	190	201	12	9	ACA	AGGGTTACTTCAATTTCCA	56	18	50.2	GTATTAGGGTTCTCTGTTTC	343	21	54.6	288
EST	BQ587583	trinucleotide	168	179	12	9	TCT	AACACACAACAACCCAGTATC	13	21	54.9	CGACGAAAGGCAACTTATT	212	19	55.6	200
EST	BQ587589	trinucleotide	167	187	21	11	TCT	TCCTCTCTCTCTCTCTTCAAC	111	21	55.3	TTCATATCTTTCACAGACA	384	21	54.4	274
EST	BQ587595	pentanucleotide	135	154	20	15	TCAAT	GAAGGAGGAGGAGAGAGAGA	100	21	54.5	AGACAGAAAGAACAAAGAGCC	392	21	55.4	293
EST	BQ587595	dinucleotide	110	121	12	10	GA	ATCCACCCACTCATCAAA	55	18	54.4	AGACAGAAAGAACAAAGAGCC	392	21	55.4	338
EST	BQ587609	trinucleotide	118	129	12	9	TGA	AGCGTTGATGAACCCAAA	80	19	55.7	ACTTCCCTGGCTGCTATC	223	19	54.2	144
EST	BQ587612	trinucleotide	355	378	24	14	TGA	TAACCTCAACCTCAACCTCAA	72	21	55.0	TTCCGATAACCATATAAAGAC	426	21	55.1	355
EST	BQ587623	dinucleotide	64	75	12	10	TC	CCCTTCTCACTCTCTCAATGG	7	21	55.6	AGACTCAAAATGGCGGTTTC	326	18	56.1	320
EST	BQ587623	trinucleotide	120	131	12	10	TC	CTCTCTCTTCTCCAACTCTAC	89	21	54.8	TAGAACCAAAACCAATACTTT	451	22	54.8	363
EST	BQ587632	trinucleotide	218	229	12	9	TTG	AATGGAAGTCAAAAGGAGAGAG	50	21	55.2	TATGATTGTGGAAGCAGA	388	19	55.0	339
EST	BQ587639	trinucleotide	181	192	12	9	GGC	AAATCAATCCTTCTTCCCA	121	18	52.7	CGACTTACTGTGCTGCTTTT	345	22	53.9	225
EST	BQ587639	trinucleotide	245	256	12	9	CAA	CACCTCACTCACTCTCTCAACA	206	21	53.8	CGACTTACTGTGCTGCTTTT	345	22	53.9	140

EST	BQ587639	tetranucleotide	207	218	12	8	CACT	AAATCAATCCTTCTCCCA	121	18	52.7	CGACTTTACTGTGCTGCTGCTTT	345	22	53.9	225
EST	BQ587647	trinucleotide	602	616	15	12	ACA	AGTAAAGTAGACGGACGAGGT	336	21	54.8	AAGGTGTTGTTGTTGTTGTT	648	20	55.4	313
EST	BQ587647	trinucleotide	181	192	12	9	GGC	AAATCAATCCTTCTCCCA	121	18	52.7	ACCTCGTCGCTACTTACT	356	21	54.8	236
EST	BQ587647	trinucleotide	245	256	12	9	CAA	ATTGACACACTACTCACTC	198	21	55.0	ACCTCGTCGCTACTTACT	356	21	54.8	159
EST	BQ587647	tetranucleotide	207	218	12	8	CACT	AAATCAATCCTTCTCCCA	121	18	52.7	ACCTCGTCGCTACTTACT	356	21	54.8	236
EST	BQ587663	dinucleotide	499	510	12	10	AT	ACGACAAGAATCCCATCTC	419	19	54.9	CCTGTGAGGGCAACCA	570	18	58.0	152
EST	BQ587670	trinucleotide	422	439	18	15	TGA	CATACCAAGATTACCCAGA	154	21	54.4	TAGCAACTCAACATCATCAC	551	21	56.2	398
EST	BQ587672	trinucleotide	321	332	12	9	TCG	TATGATTCCACTCTTTGCTG	244	21	55.6	TTATCTCACCACCAACTCC	445	21	54.3	202
EST	BQ587698	trinucleotide	168	179	12	9	TCT	CCTACTCTCTCATCTCCTT	70	20	55.0	CACATTCACACCAATCAC	394	19	55.4	325
EST	BQ587699	trinucleotide	397	420	24	14	CAA	CACGGATGGAAGAGAATG	117	18	54.8	CGGTGTTGCTGTTGTTG	461	18	59.7	345
EST	BQ587699	trinucleotide	372	386	15	12	CAA	CACGGATGGAAGAGAATG	117	18	54.8	ATGTTGTAGAGGGTGTGTTG	434	21	55.1	318
EST	BQ587709	trinucleotide	348	365	18	15	TCA	CCTTCTCACATCTTATCCTT	297	21	55.0	GTTCCACACCACTTCTC	585	20	55.4	289
EST	BQ587709	trinucleotide	94	108	15	12	AAC	CCAATGCCCTCTCTCCAAA	7	18	57.2	TGAGGTAGGGTTCCTTATC	278	22	53.7	272
EST	BQ587712	trinucleotide	223	234	12	9	CCG	GCAGTCCCATCATTCAC	83	18	57.2	GTCCATTCAACAACTTCTCT	455	21	55.7	373
EST	BQ587726	dinucleotide	45	54	10	8	GA	AGACACAGAGGGAGGACTG	16	19	55.1	CGAGAAGTTGGCATAGGT	308	19	55.4	293
EST	BQ587727	trinucleotide	112	126	15	12	AGG	GCAGTATGAGAGAGAGATG	83	18	54.9	ATGATTGAGGAGGAACAACAA	298	21	53.9	216
EST	BQ587757	pentanucleotide	248	257	10	5	AAAAG	CTTGCTCTCGCCGTTAGG	1	18	59.7	GTTATTGCTGCTGAACACTT	322	21	54.8	322
EST	BQ587791	trinucleotide	50	61	12	9	TCT	GCACCTACCTACTGCTGCT	2	20	55.0	GTAATCCAAATAATCCACCC	345	21	55.1	344
EST	BQ587796	trinucleotide	94	105	12	9	GAT	CTGTAGGCAATAAATGTCAG	34	22	54.4	CTCTCCCTGTTCTCTCATC	194	21	55.6	161
EST	BQ587796	trinucleotide	65	76	12	9	ATC	TTCTCCCAAAACCTTAAC	35	18	54.9	CACCTCCACCATCATCTCT	279	19	54.9	245
EST	BQ587816	trinucleotide	104	142	39	15	GGA	GTGAATGGGTAGGTAATGAA	69	21	54.2	TCGCTTCTTCGCTCTCTCT	174	21	56.0	106
EST	BQ587816	trinucleotide	147	170	24	14	GAA	GGTAATGAAGAGCAGACAGA	80	21	54.7	TAGACAAATGCCACCACTT	287	20	55.8	208
EST	BQ587823	trinucleotide	564	578	15	12	TGC	CTAAGGGAATGGGAGAAATG	265	20	55.0	TTTACTGAGGTGGAAGATTG	660	21	54.6	396
EST	BQ587831	dinucleotide	599	608	10	8	CT	GAATCTCTCTCTGGGCTG	453	18	55.3	GCTCTGCTCTTGCTCAATTAG	647	21	54.4	195
EST	BQ587833	dinucleotide	57	70	14	12	CT	CAAACTCTCTCTCTCCCTC	7	20	55.6	GATACCTCTGCTGCTGCTCAT	330	22	54.8	324
EST	BQ587835	trinucleotide	153	167	15	12	CCG	AAGAAGAGGACAAACAATCC	77	21	55.3	CAAAACCATCAGCAAAATAG	289	21	55.0	213
EST	BQ587836	trinucleotide	426	437	12	9	GTG	AATAACCAAACTTACAACCTC	121	21	50.4	CTTAGTGCCTTCTCTGCC	507	19	55.7	387
EST	BQ587846	trinucleotide	192	212	21	11	CAA	GAACCTGCAACCTTCAACATCA	140	21	57.1	CTACATTGAGAACCACATAA	352	21	55.8	213
EST	BQ587904	tetranucleotide	93	108	16	12	ACAT	AAGCACCAACACACACACT	44	18	55.4	CTATCTTCAACCTTCTCTCT	345	21	52.8	314
EST	BQ587913	trinucleotide	252	263	12	9	TGG	TTCTTTTCATCAGTGGGATTG	127	21	55.2	CTCTTCAACCTTCTCTCTCT	345	21	54.9	219
EST	BQ587913	trinucleotide	304	315	12	9	GCT	TTCTTTTCATCAGTGGGATTG	127	21	55.2	TTCTTCAACCTTCTCTCTCT	346	21	54.9	220
EST	BQ587947	trinucleotide	81	92	12	9	AGT	CGAATACTCAATGTAGCGAA	51	19	57.3	GAAAGAACCAAAAGGAGTAAC	201	21	54.6	151
EST	BQ587957	trinucleotide	236	247	12	9	AGA	TGCTTCTCACTCTCTCTCT	202	18	54.9	CGATTCTCACCTTCTCTATCC	438	21	55.6	237
EST	BQ587983	trinucleotide	309	323	15	12	TGA	CTTGTTCCCAATCTCTCTTAT	166	21	55.0	TCATCTTCTCTCTCTCTCTCT	406	21	54.8	241
EST	BQ587989	trinucleotide	163	174	12	9	TCT	CTCTCGTCTTCTCTCTCTCT	107	21	55.1	ACCTCGTCTGGTACATAA	258	20	55.6	152
EST	BQ588000	trinucleotide	122	133	12	9	CGA	AAGAGAGACTGAGAGAAACCC	38	21	54.3	CTTGCCATAAATCTTGAGA	339	20	55.5	302
EST	BQ588011	trinucleotide	320	331	12	9	TCC	ATAGACTCGGAACAACAACCTC	190	21	55.1	CGCCATTGAAGTAAGTAGAA	378	21	57.1	189
EST	BQ588019	trinucleotide	107	118	12	9	GAA	TGGTCAGTATCAGCAACA	4	18	51.2	GATTTCATCTGGTAGGCTTT	334	21	55.2	331
EST	BQ588023	trinucleotide	171	188	18	15	CAA	AAATCAACAACAACAACAACA	34	21	54.1	CCTGTGAATGAAGGAAGTAAG	290	21	54.1	257
EST	BQ588062	trinucleotide	399	410	12	9	TCC	TTCAAGGCCCAAGAACAG	160	18	54.8	CAACGATGCCCCAAGTTATG	522	21	55.8	363
EST	BQ588069	trinucleotide	94	105	12	9	GAT	CTGTAGGCAATAAATGTCAG	34	22	54.4	CTCTCTGTTCTCTCTCATC	194	21	55.6	161
EST	BQ588075	trinucleotide	218	235	18	15	CAC	ATCTTAGTTCGGATGTTG	104	20	55.1	ATCTTCATTGTTGTTGTTG	440	21	55.5	337
EST	BQ588075	trinucleotide	169	186	18	15	AAC	TCCCATTTCTCATCTCTCTCT	56	21	55.5	GAGGGTTGGAATGATGTTTC	327	21	55.3	272
EST	BQ588075	trinucleotide	157	168	12	9	ATC	TCCCATTTCTCATCTCTCTCT	56	21	55.5	GAGGGTTGGAATGATGTTTC	327	21	55.3	272
EST	BQ588079	dinucleotide	69	80	12	10	AG	ACCACCTCTGTTCTCTCTCA	1	21	54.0	AGGGTCTGACTCTGACATT	235	21	53.7	235
EST	BQ588086	trinucleotide	143	152	10	8	TC	AATCAATCCTCTCTCTCTCTC	110	23	53.4	CCTATGACCTCGGAACATAAG	426	21	56.3	317
EST	BQ588089	trinucleotide	212	223	12	9	AGA	GTTACGGTTTAGCATCTCTCA	105	21	54.7	ACAATTCATTAGCATCAAG	273	21	54.6	169
EST	BQ588090	tetranucleotide	371	410	40	29	TTTG	CCACTCTCTTCTCTCTCTTGTG	213	22	55.0	GCACATTCCTCTAATCTTGGT	461	21	55.9	249
EST	BQ588101	trinucleotide	144	176	33	30	CAA	CTCTCTCTTCTCTCTCTCTCT	30	21	54.7	GTTTCTGCTCTTACTTCC	342	21	54.9	313
EST	BQ588114	trinucleotide	132	143	12	9	CAT	CTCTCTCTTCTCTCTCTCTCT	30	21	54.7	GTTTCTGCTCTTACTTCC	342	21	54.9	313
EST	BQ588132	dinucleotide	308	319	12	10	AG	TGATCTTCTCTTCTCAATCC	138	21	55.1	AACCAATAACACCAACCAAG	446	21	55.1	309
EST	BQ588132	dinucleotide	133	144	12	10	AG	CTGTGAAGAGGGCAAGACAC	39	20	56.0	GCAGAGAAGATAACAAGACA	319	21	55.0	281
EST	BQ588138	dinucleotide	648	659	12	10	AT	CTTATCACACGAAGCAACAG	587	20	53.3	TAACCTCATTTGCGACACTC	904	20	56.4	318
EST	BQ588147	dinucleotide	277	286	10	8	TC	ATTGCCACGAAAGGGTT	169	18	60.3	TATTGTAGAGTGTGCTTGA	383	21	53.9	215
EST	BQ588148	trinucleotide	99	109	21	18	CAT	CAGGTTCAAGAGTTTGTTC	38	21	56.4	GCAATGGAGGCTTTAGTGA	158	19	56.4	121

EST	BQ588175	dinucleotide	383	392	10	8	CT	TCTAACAAATCCAAATCCAAA	228	21	54.9	CAATGCCAAGAACAGATAC	421	19	51.4	194
EST	BQ588188	trinucleotide	118	132	15	12	CAA	GTCCGCTTCATTTCTAC	7	18	53.1	GCTACATCAGCAGCAATCTTT	327	21	57.1	321
EST	BQ588196	trinucleotide	149	160	12	9	TAG	TGATGATAGTGAGAGAGAAGA	111	22	55.3	TTATTTGTTGTTGTTGGTTG	216	21	54.6	106
EST	BQ588199	trinucleotide	57	68	12	9	CAA	CTCACTCTCTCCCTCTCTC	3	20	55.6	CTCCTCACAATCTTCCCTTT	386	20	55.9	384
EST	BQ588204	trinucleotide	304	315	12	9	TGA	TATCTTTCCCTCGATTATGT	213	21	54.2	ATTCTTTCCAGCCTTTGAGT	429	20	55.6	217
EST	BQ588220	trinucleotide	264	275	12	9	TTC	ACTTCACCTTCTTCTCCATC	54	21	55.0	ATGAGTAAACAACAGCAGCATC	341	21	55.5	288
EST	BQ588234	trinucleotide	293	304	12	9	CTG	ACTTCACCTTCTTCTCCATC	54	21	55.0	ATGAGTAAACAACAGCAGCATC	341	21	55.5	288
EST	BQ588235	trinucleotide	253	264	12	18	CCA	TTATGATGAGGAAGGCTAA	263	20	52.7	GAAATGAATGTATGGTGTG	540	21	56.3	278
EST	BQ588238	trinucleotide	110	121	12	9	TGT	GGAAGATGAGGAAGGATGAGA	162	21	55.1	ACCAGGAGAAACAAGAAAT	329	20	55.4	168
EST	BQ588239	trinucleotide	151	171	21	18	TCT	TTATCCAACTCCTCCGT	21	18	52.9	TCCATTAATACACCTTACC	223	20	54.8	203
EST	BQ588254	trinucleotide	264	275	12	9	ATG	TTCCAACTTATCTTTCTCT	5	21	55.1	TCCTCAACAATCACATACAT	292	21	54.6	288
EST	BQ588255	pentanucleotide	181	195	15	10	TAATT	CCACCACTTCTCTCATCTTG	19	21	54.0	AGCAGCAGCCTATCTTT	399	18	56.2	381
EST	BQ588261	trinucleotide	618	629	12	9	CTG	CCACCACTTGAAGATGAGA	53	20	55.1	CAAGTTTCTGACGCTGCT	409	18	55.0	357
EST	BQ588268	dinucleotide	183	192	10	8	TC	TTATTTTCGTGACGCTGG	347	19	54.8	AAACAATATTCATCAACAGAC	670	22	51.1	324
EST	BQ588270	trinucleotide	246	257	12	9	TTC	AGTTCTTCATCTTCTTCTCT	140	21	54.8	AGTCCAACTATCTTCCCTG	398	19	55.0	259
EST	BQ588273	trinucleotide	408	417	10	5	CCCTG	GGAAGATGAGGAAGGATGAGA	155	21	55.1	ACCAGGAGAAACAAGAAAT	322	20	55.4	168
EST	BQ588274	trinucleotide	373	393	21	18	CCA	CACCAACGACAAATGAAA	259	19	55.5	GATGAAGCAGTGAGTGTTG	531	20	55.1	273
EST	BQ588282	trinucleotide	263	274	12	9	ATG	AAGTTCAATAGTACCAAGAGG	213	22	54.6	GTGGTGGTGGTGGTGGT	519	18	57.4	307
EST	BQ588287	dinucleotide	204	213	10	8	TC	GCTCTCATACACTACATCCC	97	21	53.9	GCTCAAGAACATTTGTCACT	464	21	54.6	368
EST	BQ588297	pentanucleotide	31	40	10	5	TTCTC	ATGACITTTCCAACTTT	126	18	51.8	TGAACAATAGCAAGAAGAGA	439	20	51.1	314
EST	BQ588302	trinucleotide	107	118	12	9	TGA	ATCTCTCTCTTCTTCTCC	0	18	50.5	ATTGGTTCCTCTCTCTT	354	19	55.2	355
EST	BQ588316	trinucleotide	350	370	21	18	CCA	GCAAGAAAGATGTGGTAGA	25	21	54.7	GGTGAATGCCTGACTG	180	18	54.8	156
EST	BQ588322	pentanucleotide	142	156	15	10	TGCAG	TCITTTCTTCTTCTCTCTCT	179	21	54.1	ATGATCGGACACCTACACC	484	20	54.8	306
EST	BQ588326	trinucleotide	403	417	15	12	CAA	GCTACTCTTACCTTACTGCC	66	21	55.0	GGTGGTGGTGGACATAA	196	19	54.1	131
EST	BQ588331	dinucleotide	52	74	24	8	TC	AATGAAGAGAGGGAATGATG	132	21	55.8	CAGTTAGTTGTTGTTAGTGT	494	23	51.5	363
EST	BQ588334	tetranucleotide	214	225	12	8	CAGG	TCATCTCACTCTCTCTCTTT	16	23	55.0	CTCTTTGCCATCTTGTCT	294	20	55.1	279
EST	BQ588349	trinucleotide	127	144	18	8	CAC	TTTCTATCACTCTCTCATCTC	20	23	55.2	AACTTATTTGTGACGCTGAAC	394	21	54.6	280
EST	BQ588350	dinucleotide	44	53	10	8	CT	ATCAATGTACGCTGGTT	5	18	54.7	CTTGCTTCCTTCCATCAAC	281	20	55.1	262
EST	BQ588354	trinucleotide	39	50	12	9	AAG	CCAACTTTTGAAGAGAGAG	10	19	54.7	GTTGATTGCTGGAGTTG	360	18	54.9	356
EST	BQ588355	trinucleotide	248	259	12	9	TTC	GGAAGATGAGGAAGGATGAGA	157	21	52.3	TAAACGAGAGAGAGACAA	205	18	50.9	196
EST	BQ588364	trinucleotide	294	320	27	10	CAT	AAATGAAGAAGATTTGGT	215	20	55.1	ACCAGGAGAAACAAGAAAT	324	20	55.4	168
EST	BQ588369	trinucleotide	330	341	12	9	CAT	TCATCATCAACAACAACATCA	277	21	55.2	CGTGCTCACTAACAGAGAA	545	20	54.0	331
EST	BQ588369	dinucleotide	155	166	12	10	GA	ATTCACCTCTCTCCGTT	26	21	55.8	CGTCTCACTAACAGAGAA	545	20	54.0	269
EST	BQ588369	pentanucleotide	348	367	20	8	GATTT	CGTGAGCGAGAGAGAGAG	147	18	56.3	CAAAACAATCAAAATCAAAATC	367	21	54.7	342
EST	BQ588370	dinucleotide	170	179	10	8	TC	AGTTCTCATCTTCTCTCTCT	127	21	54.8	TTGTAAGCAATAGAAATCCAAG	509	22	54.1	363
EST	BQ588384	trinucleotide	346	360	15	12	TAT	AACATTTCTCACCATCTACCA	142	21	54.6	TTCAAGTCTGTTCCATAAGTC	386	19	55.0	260
EST	BQ588388	dinucleotide	110	121	12	10	CT	CCCATCTCAGTCTTCTCTCT	54	21	55.6	TCAAGTCTGTTCCATAAGTC	428	22	55.0	287
EST	BQ588399	trinucleotide	274	285	12	9	CAC	ATTCACCAACCCAAAGAAC	170	18	55.7	AGGAGAGAGAGAGAGAAAGTGA	333	21	54.9	164
EST	BQ588401	trinucleotide	275	286	12	9	AGA	ATGCCATTTCTGTTTCTCTCT	119	21	55.1	ACTCCACTAAATCCAAAGCC	350	20	55.9	232
EST	BQ588407	trinucleotide	348	365	18	8	TGG	TACAGCACCAGAACCAAGTAG	94	21	55.6	TGTTAGCCCTTCATTGCC	422	18	57.2	329
EST	BQ588417	trinucleotide	92	109	18	9	CT	AAACAACAACCTGCATCCT	44	19	55.6	ATGAACAAGCAAAACCCCTAAA	147	20	55.0	104
EST	BQ588455	trinucleotide	128	139	12	9	AGA	AAATCCAAGCAGCAGGAG	13	18	56.4	TGAGGAAGATGGTATGG	270	18	55.1	258
EST	BQ588467	dinucleotide	711	722	12	10	AC	TCTCTCTCCCAACATTC	95	19	55.1	GACAAGAAACGGAAGGAC	236	18	54.1	142
EST	BQ588476	trinucleotide	184	195	12	9	AAG	TCCTGTCTTTGTGAACCTTT	561	21	54.1	GTCTGTAAATGTGGTGTGGG	852	21	54.6	292
EST	BQ588487	trinucleotide	208	219	12	9	AGA	AGAAGAAGAAAGAGTCGTCA	61	21	55.8	TATGTAAATCTCGGTCACTT	346	21	52.3	286
EST	BQ588499	trinucleotide	175	186	12	9	TGC	GTTCGGTTTACGATCTCTCA	101	21	54.7	ACAACTCTATTAGCATCCAA	269	21	54.6	169
EST	BQ588510	pentanucleotide	174	193	20	15	AATCA	GTCTCGTCTCGTCTCTCT	18	20	54.1	TAATCGTGTATTCTCTCTCT	224	21	54.0	207
EST	BQ588510	dinucleotide	199	212	14	12	GA	TTTCTCGTAAATCAAGGT	70	18	50.4	ATTATCACTATCACTGCC	269	19	50.5	200
EST	BQ588513	trinucleotide	334	345	12	9	TGC	AGAAAGCAGTCAATCAATCAA	163	21	55.1	CCAAATACAAAAGTAAGGGT	467	21	55.0	305
EST	BQ588526	trinucleotide	382	399	18	15	TGA	GTAGCAGTAAATGATGCCAC	240	21	55.0	ACTCTCCGTTCTTCCAAATC	482	20	55.9	243
EST	BQ588530	dinucleotide	440	449	10	8	GA	CTTAGTGAAGAACCAACGCA	120	19	54.9	TATCAACTCAAAACCCAC	427	18	52.2	308
EST	BQ588531	trinucleotide	547	558	12	9	GAG	CTGGTGAATGGAAACAGG	142	18	54.7	CGTGCAATAACATCACTAAT	515	21	55.3	374
EST	BQ588533	tetranucleotide	256	267	12	8	GAAA	TCAGTATCTTCTGGTCTCCA	235	21	55.1	TTCACGCGTCCCAATTGT	597	18	57.3	363
								GTACCCCTGAACACTTTTCCA	33	20	57.0	TCCAACGCACTTCTTCTTT	416	19	56.0	384

EST	BQ588538	pentanucleotide	434	448	15	10	ATATG	GTTCGGAGATGGGGTTC	205	18	61.6	AAGACACAAACATTAGACCA	491	22	54.8	287
EST	BQ588548	trinucleotide	288	299	12	9	AAG	ATGATTTGAGACAGAATCCA	87	21	54.7	CTGATGCTTGGTAAGACGA	364	19	54.8	278
EST	BQ588561	trinucleotide	295	306	12	9	GAA	TGGTCAGTATCAGCAACA	192	18	51.2	GATTCATCTGGTAGGCTTT	522	21	55.2	331
EST	BQ588589	trinucleotide	142	153	12	9	TCT	GTCAACACCTCTCTCAAC	106	21	53.9	CAATAGATGCCAACCTCTTTC	321	21	56.5	216
EST	BQ588597	trinucleotide	107	116	10	8	TC	TTGTAACCTTAACACTCTCA	50	21	54.8	CGATTTGGTCTATCATCTATC	382	21	54.9	333
EST	BQ588599	trinucleotide	299	310	12	9	GAA	AACATTTCCAACAACACTCTAC	207	21	55.0	TTCCTAAGATGAACAAAGAA	546	21	54.2	340
EST	BQ588629	trinucleotide	167	190	24	14	GAT	GCAGAAGTTGAAGAAGAA	138	19	53.0	AGTCTCAGGATGATGCC	291	18	55.8	154
EST	BQ588630	dinucleotide	70	85	16	14	AG	ACGTTGTAGAGAGAAAGAG	24	22	55.0	AGCATCAGGATGACACATAG	342	21	55.5	319
EST	BQ588633	pentanucleotide	106	115	10	5	AGAA	ATGGGTAGGTGGAAATGG	47	19	57.2	CCAGACAAGATGTGAAGACA	266	21	56.3	220
EST	BQ588647	trinucleotide	308	337	30	20	CAT	ATGATGGTATGATGAAGATG	193	21	52.4	GATGGGAAGTTGGTTATGAG	413	21	56.2	221
EST	BQ588649	trinucleotide	267	281	15	12	ATG	TTCAACGCTTCACTTAGCA	216	20	54.8	ATGATATAAGACACCCCTTCA	364	21	56.3	149
EST	BQ588664	trinucleotide	580	594	15	12	CCA	TAGGCAATGAGGATGAT	292	19	55.5	TAATGTATGATGTGGATGGGT	680	21	55.1	369
EST	BQ588669	trinucleotide	300	311	12	9	GCT	AAATGATCGGAATCTGCT	259	19	55.9	TGGTAATCTGCTGTAAGAAGC	493	21	57.0	235
EST	BQ588670	trinucleotide	192	203	12	9	GAG	ATTCTCTAACCCACTTGAC	65	21	54.9	ATTTCTCCACTGTAAGAAAC	306	21	54.9	242
EST	BQ588673	trinucleotide	232	243	12	9	TGC	AGTCATCCACTCTCCAAAG	141	20	55.1	ATTACACCAACTTCTCTCA	379	21	54.8	239
EST	BQ588679	trinucleotide	302	316	15	12	TCA	TTCACTCTCTTCTAAATCCCT	250	21	52.4	TAGTCAAGCAACACGACGAC	533	21	59.3	284
EST	BQ588688	trinucleotide	94	114	21	18	CAT	GCCTTCTCTTCTCTCTCTC	42	20	54.9	AGCATACCAACACATTTCA	441	19	54.8	400
EST	BQ588696	trinucleotide	84	95	12	9	AGC	TCCGTCCTCTCTTCTCTCT	19	21	55.0	CTACGCTTCAATCTCTCTTG	242	20	55.3	224
EST	BQ588702	tetranucleotide	57	72	16	12	CCTC	CGGAGGGTCTTACTTT	16	18	54.2	CTTCTTTGCTCTCTCACT	319	21	55.3	304
EST	BQ588702	trinucleotide	47	56	10	8	CT	CGGAGGGTCTTACTTT	16	18	54.2	CTTCTTTGCTCTCTCACT	319	21	55.3	304
EST	BQ588715	trinucleotide	504	518	15	12	CTG	AGATGGAAGAAATGAAGCA	164	20	55.0	AAACAAGACACAATCAATAA	551	22	55.1	388
EST	BQ588745	dinucleotide	235	246	12	10	CT	CTCCTACTCTTACTCCAC	4	21	54.7	TATTCACGCAATCTCC	359	19	55.2	356
EST	BQ588746	trinucleotide	189	209	21	11	CAA	ATGACAACCACTCCACA	91	18	55.4	CACCACTCTCTTTATCCCT	488	21	55.1	378
EST	BQ588747	trinucleotide	116	125	10	8	TC	CACTTTCAACGCTTGCT	62	18	54.5	GTGCTTATTTCTCTCTCAT	411	21	53.0	350
EST	BQ588757	trinucleotide	260	271	12	10	CT	GTTCGCGCATGTTATT	197	19	55.2	TCTACGCACTCTCTTTCTCT	575	21	55.0	379
EST	BQ588768	trinucleotide	493	502	10	8	AG	GTTCGCGCATGTTATT	394	18	53.7	ACCCGACACATAACAGAG	554	20	56.0	161
EST	BQ588777	trinucleotide	118	138	21	18	GGT	ACAACTCAACTAAACCAAGAA	70	22	53.5	GTAAGAAGACGCGAGAGAGA	206	21	55.7	137
EST	BQ588799	trinucleotide	303	314	12	9	GAA	ATACAGGAAGAGAGCAAAAG	80	21	52.6	ATCTACATTCAGACAACAA	420	20	54.2	341
EST	BQ588811	trinucleotide	132	158	27	11	GTC	GTGCTCACTCTCTCAAGT	72	19	55.1	GTATCTCTGTAACTGCTTGT	276	22	54.4	205
EST	BQ588812	trinucleotide	74	85	12	9	CAT	CTCATCTCTCTCTCTTCTC	14	21	54.8	CTCACATCTGCTCCCTTT	180	18	57.1	167
EST	BQ588815	trinucleotide	237	246	10	8	TC	CATTACCACTTCAACCTC	18	19	56.2	ATCAACCAACCAAGAAACAA	417	21	55.6	400
EST	BQ588822	trinucleotide	201	212	12	9	GCT	AAGAAAGGTGTCAGATGGG	124	19	55.0	CGACCAGAACAAAGAAATGAG	243	21	55.1	120
EST	BQ588844	trinucleotide	76	87	12	10	TC	CCCTTCTTCTCTCTCACTC	35	21	54.9	ATCCACCACTTATCCC	387	19	55.4	353
EST	BQ588848	trinucleotide	194	208	15	12	ATA	ACCATCTTCTCTCTCAAGC	58	21	56.0	AACTGCCATTATCCC	446	18	54.9	389
EST	BQ588872	trinucleotide	603	614	12	9	GCG	TGTGTTGTTGGATGATG	571	20	55.1	GAGAGGAGCGGAGTAGAG	730	20	56.0	160
EST	BQ588880	trinucleotide	106	123	18	8	CCA	TTCCTCACTCTCTCTCTCTC	7	21	55.3	GACAACGACACACACGAA	378	19	55.8	372
EST	BQ588928	trinucleotide	212	232	21	11	CAA	TACTCCACATCTCAATGTC	67	21	55.0	GAGAGAGAAAGCAAGGGTT	331	19	53.6	285
EST	BQ588929	trinucleotide	777	788	12	10	AT	ACCTACTACCATCAACACCT	607	21	55.1	TACAGAGCCAGCGAATCA	839	18	56.4	233
EST	BQ588936	trinucleotide	204	232	30	13	ATC	CCATCTTCTCTCTCTCTCTT	164	21	54.4	ACTATCCCATTCATCATCTT	466	21	55.0	303
EST	BQ588936	pentanucleotide	113	127	15	10	ACAAC	AGAAACCATCTTCGCTTATC	73	20	53.7	ACTATCCCATTCATCATCTT	466	21	55.0	394
EST	BQ588942	trinucleotide	258	267	10	8	CT	AGAAGAGGAAGCAAGAAAGA	117	21	55.1	CGTATGAGGTTGTAGGAGA	346	21	54.5	230
EST	BQ588947	trinucleotide	209	226	18	9	GA	AAATAGATGTACGCCCTTC	114	20	51.4	TAAACCATTCCTCATACCAA	439	21	54.7	326
EST	BQ588948	trinucleotide	168	197	30	13	CCA	CCTCTTCTCTCTCTCTCAAC	85	20	55.6	ATTGAGCCATTTGATTTGAG	251	20	55.3	167
EST	BQ588948	trinucleotide	138	152	15	12	CAC	CCTCTCTCTCTCTCTCAAC	85	20	55.6	ATTGAGCCATTTGATTTGAG	251	20	55.3	167
EST	BQ588948	trinucleotide	109	118	10	8	CT	TTCTCTCCACTCTCTCTCT	76	20	55.6	ATTGAGCCATTTGATTTGAG	251	20	55.3	176
EST	BQ588948	pentanucleotide	87	96	10	5	CTCTT	CCTCTCACTCTCTCTCTCT	58	19	53.4	AGTTGTTGGTGGTGGTTG	202	18	55.0	145
EST	BQ588948	trinucleotide	326	340	15	12	GAT	CATCATCACTCTCTCTCTCT	218	19	55.4	CTCTCTCTCTCTCTCTCTC	411	21	54.8	194
EST	BQ588969	trinucleotide	383	394	12	9	GAT	AAATGACGAGGACGATAA	274	20	52.4	GAGACGAAGCAAGAAATGT	453	20	54.4	180
EST	BQ588994	trinucleotide	142	151	10	8	TA	ACGAGGTGTTGAGGTTATTC	53	21	55.8	CATTTGTTGGTCTCTTT	200	18	50.6	148
EST	BQ588999	trinucleotide	182	193	12	10	GA	ACCAAGTAGCATTTAGCCATT	15	21	55.7	GGAGAAGTACAGAGAAGAAAC	327	21	55.5	313
EST	BQ589042	trinucleotide	535	546	12	10	CA	GGCACACATCATTAACATC	427	19	54.8	CTCCCAACATCTCTCTCTT	639	21	55.2	213
EST	BQ589043	trinucleotide	138	149	12	9	CCA	TACACCCACCAACATCAA	21	18	56.4	ATCACTCTCTCCATAACCCGT	398	21	55.8	378
EST	BQ589051	pentanucleotide	44	58	15	10	TCTTC	ATCTTAGTCTCTCTCTCAGTCC	13	21	51.8	TAATCTCTCATACAGTCTCC	309	21	55.7	297
EST	BQ589055	trinucleotide	109	120	12	9	AGA	GCTCTCTAATCAATAATCC	23	21	54.7	TTCTCTCTCTCTCTCTCT	255	18	54.9	233
EST	BQ589067	pentanucleotide	105	119	15	10	TTCAA	GTCGCGCTTCTCTCTCTCT	19	18	60.7	GTTTGGCTCTCTCTCTCTCT	308	21	55.1	290

EST	BQ589067	trinucleotide	289	300	12	9	GAA	GTCCGCCTTCTTTCGTCC	19	18	60.7	AAATCTTCTCATCGTCAA	361	19	50.5	343
EST	BQ589068	trinucleotide	334	345	12	9	TGC	GTCTCTTCTCTCTCGATC	56	21	55.9	TACCCACTTCTTAGCAGG	402	19	56.4	347
EST	BQ589072	trinucleotide	320	331	12	9	TGC	ATGGTGATGGTGTTATTC	164	22	54.8	CGAGTCTCTCTTCTTGTT	527	21	55.4	364
EST	BQ589094	trinucleotide	141	152	12	9	GAA	TTCTCTCTCTCTCTCTACAA	5	22	55.1	CGTTTCTGCTACCAATCAA	245	21	55.5	241
EST	BQ589107	pentanucleotide	92	101	10	5	AGAAC	ATGGGTATGTGGAATGG	33	19	55.5	AACGCTATGCTGGAGTCTT	278	19	55.1	246
EST	BQ589119	dinucleotide	70	85	16	14	AG	ACGCTTGAGAGAGAGAAAG	24	22	55.0	AGCATACACAGGTAGACATAG	342	21	55.5	319
EST	BQ589125	trinucleotide	154	168	15	12	CCG	TTCTCTCTCTCTCTTTCAC	34	21	55.3	ATGTTGACCTCTGAATCTCTC	316	20	54.0	283
EST	BQ589149	trinucleotide	50	61	12	10	TC	ATTTCACTCTCTCAACTCT	20	20	50.3	GAGCCGACATAAACATAAA	189	19	51.3	170
EST	BQ589159	trinucleotide	163	174	12	9	CAT	CCCCTCTATGTTGCCCTAA	131	20	56.8	ATTCCTCTCTCTGTCGG	427	18	55.1	297
EST	BQ589160	trinucleotide	289	306	18	15	TGG	AAACATCAACCCATCTTCA	101	19	53.7	TCATCTTCCAGAACAAATC	359	20	55.1	259
EST	BQ589171	trinucleotide	313	333	21	18	TTC	CTTCTTGATTGATCTTCCA	275	21	54.6	CAACTTCTTTCAGTAACCTGCT	421	21	54.0	147
EST	BQ589183	trinucleotide	194	205	12	9	ATC	CATCTTCTCTCTCTCTTGCT	125	22	54.9	GCTCTACATGTTTGGTAA	330	20	50.4	206
EST	BQ589195	trinucleotide	153	162	10	5	GAGGT	ATTTCACTTCAACCAACACAG	36	21	55.2	AGCAGAACTCACAAGCAGTAA	394	21	55.5	359
EST	BQ589230	dinucleotide	228	239	12	9	TCT	AATCTTATCCAACTCTCTCTC	180	21	54.0	CCGAAAGTGGCTTCTGCT	320	18	59.1	141
EST	BQ589246	trinucleotide	178	189	12	10	CT	ATCTGCTAATCCAAACCTGA	94	20	54.9	ACGAAACCCGCTAAGTTG	422	18	56.4	329
EST	BQ589255	trinucleotide	56	69	14	12	TA	ATAGGACACACATGGA	22	18	55.0	TGTTGTTGTAATGAAGGGTTT	170	22	53.3	149
EST	BQ589262	trinucleotide	230	241	12	9	CTC	GGAGGAGGAAATCTAACAGAA	52	21	55.1	GTAATGATCGCTTGGCAG	329	18	56.1	278
EST	BQ589264	trinucleotide	304	315	12	9	TGG	AGGTTGAGGAGAGAGAAAGAA	173	21	54.9	TCCAGTATCAGAAATAGCC	350	21	56.0	178
EST	BQ589289	pentanucleotide	80	94	15	12	CGA	AAATCCTAACTTGGCGG	18	18	55.3	TACATCCTCTCATCACTCTG	369	21	55.2	352
EST	BQ589309	trinucleotide	223	232	10	5	TGTGT	ATTGTGTTGCTGATGTCT	172	20	56.6	CGATAGAGAGAGAGAGAGG	285	21	55.2	114
EST	BQ589327	trinucleotide	143	154	12	9	TCT	ATCAACAATGGAACCCCTAAC	84	21	55.6	CGAAGAGAGAGAGAGAGAAAG	318	21	54.0	206
EST	BQ589332	trinucleotide	174	185	12	9	TGC	GTCCTCGCTTCGTCCTCTC	18	20	54.1	TCAATCGTATTCTCTCTCT	223	21	55.4	287
EST	BQ589348	trinucleotide	241	252	12	9	CAC	TCCTCTATGTTGCTACTCTCTC	50	23	54.8	ACCTTGTGGCTATTTGTATT	336	21	55.4	287
EST	BQ589352	trinucleotide	80	94	15	12	CGA	CTAAACTTGGCGGGAAC	23	19	62.9	AACCTATCTCTGACTACTGAA	299	22	54.0	277
EST	BQ589376	trinucleotide	884	895	12	9	TCT	GTTTCTCTGATCTCTCCGCC	835	20	63.1	AACCGACGACAGAACAA	942	18	60.0	108
EST	BQ589395	trinucleotide	143	154	12	9	TCT	ATCAACAATGGAACCCCTAAC	84	21	55.6	CGAAGAGAGAGAGAGAGAAAG	318	21	55.2	235
EST	BQ589405	trinucleotide	242	253	12	9	GAT	TGATAATGGAGCAATGTG	23	20	55.4	ATACCTCTCTTCGCACCTGAC	400	20	54.5	378
EST	BQ589407	trinucleotide	175	186	12	9	TGC	GTCCTCGCTTCGTCCTCTC	18	20	54.1	TCAATCGTATTCTCTCTCT	224	21	54.0	207
EST	BQ589424	trinucleotide	241	252	12	9	CAC	TCCTCTATGTTGCTACTCTCTC	50	23	54.8	ACCTTGTGGCTATTTGTATT	336	21	55.4	287
EST	BQ589430	trinucleotide	399	410	12	9	TGC	TCCTTGTCTTGAGATAATGGT	191	21	54.2	CTTGATGGAGATGGTATAGT	471	21	54.1	281
EST	BQ589445	trinucleotide	133	150	18	8	CTT	ACAACCTTCCATCACCTTC	75	19	54.8	AACATCATCTTCCCTACCTTT	440	21	56.0	366
EST	BQ589446	trinucleotide	302	313	12	9	GTG	AGGTTGAGGAGAGAGAAAGAA	173	21	54.9	TCCAGTATCAGAAATAGCC	349	21	56.0	177
EST	BQ589457	trinucleotide	318	335	18	15	TGG	AAACATCAACCCATCTTCA	127	19	53.7	TCATCTTCCAGAACAAATC	388	20	55.1	262
EST	BQ589463	trinucleotide	405	419	15	12	TGG	CCACAAAGAGAGATGATAGT	105	21	53.5	TGATAGTCTCTCCAAAGAGA	495	21	54.9	391
EST	BQ589467	trinucleotide	81	95	15	12	CGA	AAATCCTAACTTGGCGG	19	18	55.3	TACATCCTCTCATCACTCTG	371	21	55.2	353
EST	BQ589467	trinucleotide	393	404	12	9	GAA	AGCGTATCTCTTCAACCAT	202	19	54.8	ACTCTGACCTTCTCATCATC	491	21	55.7	290
EST	BQ589467	trinucleotide	467	478	12	9	ATG	TCAGGAGACGAAAGCGTATT	191	19	56.0	ACACACCATCTTTTGAACCT	565	18	54.5	375
EST	BQ589471	trinucleotide	132	143	12	9	AAC	CTTCATCCTCTTAAACCCAGATT	47	21	55.0	ACCCAGACATAGCGTCTG	358	18	56.5	312
EST	BQ589475	trinucleotide	378	395	18	15	TCA	CGATAAAGAAACCCCTAACCC	286	20	55.4	CGAGTTGTTGAGAGAGAAAC	487	21	54.3	202
EST	BQ589475	trinucleotide	123	137	15	12	AAC	CTCCTCTCTTCTCTCTCT	8	19	55.1	ATTAGGGTTAGGGTTTCTTT	310	21	53.1	303
EST	BQ589481	trinucleotide	300	311	12	9	GCT	TATGGAGGAACAGCAACC	226	18	54.3	CATTAGCACACGGGAACA	371	18	55.4	146
EST	BQ589491	pentanucleotide	223	232	10	5	TGTGT	ATTGTTGTTGCTGATGTCT	172	20	56.6	GAGAGAGAGAGAGGTGCTGAGT	277	21	55.4	106
EST	BQ589503	trinucleotide	400	411	12	9	GAT	TGATGTCCTCAAGCAATAAGGT	330	21	55.0	CAGCGTATCTAAGTGGGTC	454	19	53.2	125
EST	BQ589524	trinucleotide	142	162	21	18	AAC	CCAACAACACTATTACAAACC	28	21	54.6	TACCTGCTTCTTCACTGCT	317	20	55.4	290
EST	BQ589524	trinucleotide	247	258	12	9	CAT	CCAACAACACTATTACAAACC	28	21	54.6	TACCTGCTTCTTCACTGCT	317	20	55.4	290
EST	BQ589533	trinucleotide	242	253	12	9	GAT	TGATAATGGAGCAATGTGTG	23	20	55.4	ATACCTCTCTTTCGCACTGAC	400	20	54.5	378
EST	BQ589537	trinucleotide	143	154	12	9	TCT	ATCAACAATGGAACCCCTAAC	84	21	56.3	CAACCAAAATCAAAATCAATC	419	21	54.7	342
EST	BQ589573	trinucleotide	207	218	12	10	GA	ATTCAACTGTCTCTCCGTGTT	78	21	54.6	TTGTAAGCAATGAAATCCAAAG	561	22	54.1	363
EST	BQ589573	pentanucleotide	400	419	20	8	GATTT	CGTGAGCGAGAGAGAGAGAG	199	18	54.6	TTGTAAGCAATGAAATCCAAAG	456	21	56.3	400
EST	BQ589574	trinucleotide	104	115	12	9	AGA	CCCTCAATCCCTATCTCTCT	57	21	55.1	TCCTCTCAACCTTCTTCTTG	333	22	54.1	329
EST	BQ589602	tetranucleotide	198	263	64	41	GATT	GCGTGGGAAACCCCTAACT	5	18	57.6	GTGTTTACCTGAAAGTCTCTTG	408	21	55.0	272
EST	BQ589612	trinucleotide	198	209	12	9	ATG	TAGAAGAATCAAAACCCCTCTCT	137	21	52.4	ACTACGACCAAGACAAAGACA	255	21	54.5	250
EST	BQ589632	pentanucleotide	95	114	20	8	AAAAG	CAGATAAGAAAGGTTGCCCTC	6	20	54.2	TTACATCAAGAACTCCGTTTC	444	21	54.0	196
EST	BQ589639	trinucleotide	327	341	15	12	GAT	CTGTTGGTGTGAGGTTCTCT	249	20	55.2	TTCCACTTCTTCTTCTCTTG	444	21	54.0	196
EST	BQ589662	trinucleotide	240	254	15	12	TAG	TTGGTTCATCTTGTGATTTCC	168	20	55.1	CAGTTTGTAGTAAGAGCAGA	346	20	54.4	179

EST	BQ589664	tetranucleotide	322	333	12	8	TCCC	CTATTATGACGGCGGT	140	18	56.1	AAAGAAACAAGAGGGTTACA	392	21	53.4	253
EST	BQ589666	tetranucleotide	320	331	12	8	TCCC	CTATTATGACGGCGGT	138	18	56.1	AAAGAAACAAGAGGGTTACA	390	21	53.4	253
EST	BQ589726	trinucleotide	383	394	12	9	TAC	AGAAGATTGGTGAGAAATAGTG	244	22	55.1	CAATTGAGCCACATACGA	441	18	56.4	198
EST	BQ589731	trinucleotide	51	71	21	11	CCA	GACGAATCAACCCCTCCT	0	18	54.9	TGTCGCCCTGAGAAATGAA	382	18	56.2	383
EST	BQ589733	dinucleotide	74	85	12	10	CT	TCCTCTCTGTCTACCTTCCG	11	21	55.2	GCTTCAATCTCTCAGTTGT	358	21	54.0	348
EST	BQ589742	dinucleotide	100	113	14	12	TC	TTCTACTGTTCGCTTTACCTG	53	21	55.0	TCCTCATCTGTATCTCCTG	434	20	52.4	382
EST	BQ589752	pentanucleotide	281	290	10	5	CCCCG	CGATTACCGCAACGGGAC	139	18	63.6	GGAGCCAAATACAGAGG	357	18	55.6	219
EST	BQ589763	tetranucleotide	377	388	12	8	CCCT	CGTTCTCACTTTACCTCTT	274	21	55.3	TTCTCTCATCTACTGTCGCTG	621	21	55.5	348
EST	BQ589772	tetranucleotide	299	310	12	8	TTAT	TCATCAAAATCTTCACTTACT	27	22	54.0	TCCGAAACCTTCAAACATC	373	19	56.1	347
EST	BQ589814	dinucleotide	340	349	10	8	AT	CCAATCAAACTTATCAACAAC	211	22	54.7	ACCGCTGCCCTCCATTT	382	18	60.8	172
EST	BQ589818	trinucleotide	353	364	12	9	TGT	CTCATCTACTGCTCCTCTCT	82	21	56.0	ATTCAACCAATGAACACGA	476	19	54.7	395
EST	BQ589823	dinucleotide	263	272	10	8	AT	TTCTCTCTCCTCGACACT	124	19	54.8	ATCATTCCTCAACATCAAC	469	20	54.8	346
EST	BQ589823	pentanucleotide	198	207	10	5	AAAAC	TTCTCTCTCCTCGACACT	124	19	54.8	ATCATTCCTCAACATCAAC	469	20	54.8	346
EST	BQ589823	tetranucleotide	133	144	12	8	TTTC	GTTGAGGAAGAGGAAGAAAG	29	21	54.9	AAGAGCAGCAGAGGAGAAC	317	18	55.7	289
EST	BQ589875	trinucleotide	221	232	12	9	CCT	GCCTCATTTCTTCTCTCT	60	19	52.2	ATCCTTTGTTCTATGCCAATC	354	21	55.8	295
EST	BQ589876	trinucleotide	288	299	12	9	GAA	CCAATAACCCCAAGCGGTG	40	18	59.9	CATCATCTTCAATGGTCTCTC	391	21	54.6	352
EST	BQ589879	dinucleotide	237	254	18	16	CT	TCCTCTCTCTCGTGCTCTCT	25	21	55.8	GATGACGAAACAACTGTC	310	20	55.9	286
EST	BQ589883	trinucleotide	79	93	15	12	CAA	CGTTCACAACCTTCCATTT	31	20	55.3	GCATCTCACCTTCTCTCATTT	327	21	56.0	297
EST	BQ589889	tetranucleotide	28	43	16	12	CACCT	CAACGCTCCTCTCTCTTT	0	18	55.5	ATCTGCCATTTGTTATTTT	245	21	51.0	246
EST	BQ589892	trinucleotide	195	206	12	9	CTT	TAAACCACTTACACTCCACGA	152	21	54.9	CTCCTCCATACCAACGACT	487	19	55.0	336
EST	BQ589911	trinucleotide	252	275	24	14	ACC	ACCCACTTACACTATCCACT	45	21	55.1	GAAAGCGGCGAGAGAGAA	303	18	56.6	259
EST	BQ589911	dinucleotide	159	172	14	12	TC	TACCCACTTACACTATCCACG	44	21	54.1	AAGAGCGGAGAGAGAAAG	302	18	55.7	259
EST	BQ589921	trinucleotide	69	80	12	9	TCT	AGAGAGGAGAGAGAGAGACGA	35	22	54.2	AAGAGACTACAAACCACTCAA	431	22	54.1	397
EST	BQ589925	trinucleotide	482	496	15	12	TGC	GAAAGCAAGTCAGAGAAACT	325	20	53.7	ATCAAATCCAGAAACACCAC	529	20	54.8	205
EST	BQ589928	tetranucleotide	63	74	12	8	ACTC	CACAGCAATATACCACTAC	28	21	56.5	CAAACTCATCTTCACTCTCTTG	186	22	54.2	159
EST	BQ589956	trinucleotide	353	367	15	12	GAT	ATGGTTTCAATATGACGAA	34	20	56.0	TCTTCAACTCCTTGTTCATC	425	20	52.7	392
EST	BQ589959	trinucleotide	165	176	12	9	GAT	AAATCCTTGATGCTCCTTACA	5	21	54.1	TAGTCCCTCCTCGTTTGA	272	18	55.3	268
EST	BQ589989	trinucleotide	288	299	12	9	GAA	CCAAATAACCCCAAGCGGTG	40	18	59.9	CATCATCTTCAATGGTCTCTC	391	21	54.6	352
EST	BQ589998	tetranucleotide	379	390	12	8	AGCA	ATGGTAGAAGTGGCTTGATG	329	20	55.2	TGGTCATTAGTTTGGTGT	457	19	51.1	129
EST	BQ590004	trinucleotide	282	293	12	9	ACT	ACAACGAGGATGGGATGAA	138	19	55.4	TAACCTGTGCTCTTCTTCACT	502	21	54.3	365
EST	BQ590010	trinucleotide	92	109	18	8	ACA	AGCACAGAGAGAGAGAGAGTGA	19	22	55.0	GAAAGTGTGAGGAGGAGAG	211	21	55.6	193
EST	BQ590017	dinucleotide	67	80	14	12	CT	TCCTCTCTCTCATCTCACA	19	21	55.0	TAAGACATACCAAGACCTGA	254	21	54.8	236
EST	BQ590017	dinucleotide	93	102	10	8	CT	TCCTCTCTCTCATCTCACA	19	21	55.0	TAAGACATACCAAGACCTGA	254	21	54.8	236
EST	BQ590031	trinucleotide	414	434	21	18	TGC	CTCTGTTCTTCCACTCTCT	127	21	54.7	ATAGTCCCAATGCTGTTTG	526	20	55.3	400
EST	BQ590032	dinucleotide	227	236	10	8	CT	CTCACCTCTCTCTTCTTCTC	180	21	54.9	ATTCACTCCTCTCAACCCCTAC	577	21	54.9	398
EST	BQ590032	pentanucleotide	205	214	10	5	CTCTT	TATCTCCAAATCCTTCAACAA	155	21	54.9	CAACTCCATAAACTTCTCCA	510	21	54.6	356
EST	BQ590038	trinucleotide	221	232	12	9	CCT	GCCTCTCATTTCTTCTTCTT	60	19	52.2	ATCCTTTGTTCTATGCCAATC	354	21	55.8	295
EST	BQ590048	trinucleotide	330	341	12	9	TCT	ATGCCCACTAAATAAGAAATGG	144	21	55.9	AAGGTGTGTGAAGGATGG	516	19	55.8	373
EST	BQ590059	trinucleotide	421	438	18	15	GAG	CTTTCTCTCTCTTCCCGT	152	20	55.3	AATAGTCTTGGCATCCTCCT	497	20	55.4	346
EST	BQ590059	trinucleotide	439	450	12	9	GAA	CTTTCTCTCTCTTCCCGT	152	20	55.3	AATAGTCTTGGCATCCTCCT	497	20	55.4	346
EST	BQ590059	dinucleotide	156	165	10	8	TC	CTGGCGCTCTCCATAAATAA	60	20	55.5	TCATCTCTCTCTTCTCTCTC	454	21	55.2	395
EST	BQ590075	trinucleotide	58	69	12	10	AG	CATCACCAAGATACCCACGA	26	20	56.0	ATTTCCACGAAGAGTTTCATT	319	21	55.5	294
EST	BQ590076	trinucleotide	385	399	15	12	GCA	AACACACTCCATAGTTGCC	53	19	53.3	AAGAAAGGTCTGCTGGTGC	430	18	52.5	378
EST	BQ590082	dinucleotide	159	170	12	10	CT	GTGGAAACGAGTGATGATA	19	20	56.0	AATGGAAGAGGAGAGGAGG	267	20	55.1	249
EST	BQ590093	trinucleotide	254	271	18	15	TCA	TTTCTCTCTCTCTTCCCA	12	19	52.4	GACGCCATTGTTGTTATGT	322	19	54.3	311
EST	BQ590093	pentanucleotide	182	196	15	10	AAAT	TTTCTCTCTCTCTTCCCA	12	19	52.4	GACGCCATTGTTGTTATGT	322	19	54.3	311
EST	BQ590101	tetranucleotide	130	141	12	7	CCTC	ATAACTCTCCTCCGCAAA	14	18	55.7	AAAGCAACATATCATCCAC	181	20	55.8	168
EST	BQ590123	pentanucleotide	563	572	10	5	GGGGC	CTCACCATACACTTCTCT	508	19	55.9	TCAACACTATTCATCCAC	777	20	55.8	270
EST	BQ590142	trinucleotide	587	598	12	9	CAG	ATTCTCGCTGCTGAGTTTGT	253	21	54.8	ACTGTTGCTGTGCTGCT	634	18	55.4	382
EST	BQ590158	trinucleotide	362	382	21	18	CCA	TCCTTCTCTTCTCTCTCT	191	21	54.1	ATGATCGGACACCTACACC	496	20	54.8	306
EST	BQ590200	trinucleotide	50	73	24	14	CAT	ACAGTTGGCGGAAGACA	21	18	57.7	AGGAGAGAGAGAGAAATGAG	157	21	55.3	137
EST	BQ590218	trinucleotide	353	367	15	12	GAT	CTTATGCCGTTTGATGATG	226	19	55.1	TTTCTCTCTATGCTGAACC	513	21	53.6	288
EST	BQ590218	trinucleotide	400	411	12	9	TGA	CTTATGCCGTTTGATGATG	226	19	55.1	TTTCTCTCTATGCTGAACC	513	21	53.6	288
EST	BQ590220	trinucleotide	253	267	15	12	CAG	TAACCCCTAACCCCTAACCCCTAA	29	21	54.7	ATCAAGACACAGGAGGAGAG	366	21	56.0	338
EST	BQ590226	trinucleotide	182	193	12	9	GTA	TTCAACTCTTCTCTGCTCTAA	26	21	54.8	GCTCAACTACTACTGCTCTCA	363	21	55.0	338

EST	BQ590226	trinucleotide	210	221	12	9	TAC	26	21	54.8	GCTCAATACTACTCGCTCTCA	363	21	55.0	338
EST	BQ590232	trinucleotide	296	307	12	9	AAG	18	21	55.8	TTCTCCCTCTTCACTCTTCTC	338	21	55.2	321
EST	BQ590259	trinucleotide	294	317	24	14	AAC	249	21	55.5	TGGACAAGTAACAATCTCTGG	530	21	55.3	282
EST	BQ590259	trinucleotide	426	440	15	12	AGA	297	21	54.9	TGGACAAGTAACAATCTCTGG	530	21	55.3	234
EST	BQ590259	trinucleotide	265	276	12	9	AGA	136	20	53.8	TCTCTCTCTCTCTCTCTCTCAA	437	23	54.5	302
EST	BQ590265	trinucleotide	75	89	15	12	TCA	45	20	53.4	ATTAGGTCCAGATCAAGGTC	368	21	52.4	324
EST	BQ590301	trinucleotide	302	313	12	9	AGC	126	21	54.3	ATGAAAGAGATGAAGGCTGG	412	20	56.9	287
EST	BQ590306	trinucleotide	107	133	27	24	CCA	19	20	54.6	TCATCCCTCAGCAACAAC	363	18	55.3	345
EST	BQ590306	trinucleotide	423	441	20	11	TC	392	21	54.8	TTTCGTATCTTCAAACTTTTC	544	22	53.2	153
EST	BQ590313	trinucleotide	339	416	78	19	GAT	256	21	55.0	ATCGGACATACACCGCC	466	18	59.5	211
EST	BQ590313	trinucleotide	102	113	12	9	TGC	36	19	55.0	CATCGTGTCTACTTTGTTCTT	341	21	54.8	306
EST	BQ590361	trinucleotide	317	328	12	9	CAG	208	21	54.0	GGGTAGCAGAGTGATAATG	519	21	54.1	312
EST	BQ590383	trinucleotide	82	93	12	9	CTT	5	21	55.3	TCTCTCTGCTATTACCCATAA	255	22	53.1	251
EST	BQ590390	dinucleotide	88	97	10	8	TC	32	21	54.8	CACACTACTAATCAACAACA	186	21	54.5	155
EST	BQ590391	trinucleotide	266	277	12	9	TGC	218	21	55.1	ATCCAAGTCTCTGTTTATTC	332	21	54.8	115
EST	BQ590401	trinucleotide	68	81	14	12	TC	11	21	55.2	ATTCCACTTCTCAACCAC	363	19	54.8	353
EST	BQ590407	trinucleotide	163	174	12	9	AAT	106	21	54.2	CATGAGGAAGGAGGAAGAAG	324	21	55.1	219
EST	BQ590443	tetranucleotide	246	257	12	8	ATTA	87	19	55.9	TCACACTCTTATCTTACCCCTC	373	22	55.1	287
EST	BQ590470	trinucleotide	195	218	24	14	TAA	148	18	54.7	ACTTTGGGCTTAGAACTGAC	481	21	55.3	334
EST	BQ590475	trinucleotide	273	284	12	9	TAA	148	18	54.7	ACTTTGGGCTTAGAACTGAC	481	21	55.3	334
EST	BQ590475	trinucleotide	105	124	20	11	CT	10	21	55.4	CTCGTTTGTAGTCTTGATGT	324	21	54.5	315
EST	BQ590508	pentanucleotide	264	273	10	5	AAAAAG	165	19	55.3	ATAATGAGGCGCAGCATGT	314	20	54.9	150
EST	BQ590555	trinucleotide	100	126	27	24	ATG	14	20	56.8	GCGACTCTCTATCTTCTATC	402	21	55.7	389
EST	BQ590558	trinucleotide	266	280	15	12	CCT	107	22	55.2	ATAAGGCCAGTATCAGGAAG	406	21	55.2	300
EST	BQ590558	trinucleotide	212	223	12	9	CCT	107	22	55.2	ATAAGGCCAGTATCAGGAAG	406	21	55.2	300
EST	BQ590558	trinucleotide	242	253	12	9	CCT	107	22	55.2	ATAAGGCCAGTATCAGGAAG	406	21	55.2	300
EST	BQ590596	trinucleotide	418	429	12	9	GAT	272	19	54.1	CAGCAAGAAGATGGAGT	587	19	55.4	316
EST	BQ590597	trinucleotide	332	346	15	12	CGC	271	21	56.7	AACTCGTCTCTCTCATCTC	573	20	54.9	303
EST	BQ590618	trinucleotide	326	346	21	18	CGA	113	21	55.6	CTCTCTCTCTCTCTCTCTCTC	436	21	54.9	324
EST	BQ590618	trinucleotide	464	490	27	17	TGA	416	21	54.9	TCAGCAACAGTAACAGAAAGT	600	21	55.1	185
EST	BQ590620	tetranucleotide	113	124	12	8	CAAT	29	21	55.0	TACCAACCTTGAACATCC	246	19	55.8	218
EST	BQ590624	trinucleotide	213	227	15	12	GTG	20	20	54.7	AAGAGTGAGAAAGGAGGATGT	304	21	54.6	285
EST	BQ590624	trinucleotide	385	405	21	11	CGC	332	21	54.9	AACCTCCACCAACCCCTC	490	18	55.6	159
EST	BQ590627	trinucleotide	115	129	15	12	TAA	71	22	55.2	ATCTCTTGTATTTCTTTGAG	179	21	55.1	109
EST	BQ590631	trinucleotide	371	385	15	12	TGG	109	21	54.7	TAAAGTTGAAGCGGAGGAGT	495	20	56.7	387
EST	BQ590633	trinucleotide	311	322	12	10	CT	194	21	55.0	AGAGAGCGAAGGAGGATAGA	481	21	55.2	288
EST	BQ590644	trinucleotide	565	576	12	9	AAC	286	21	55.1	GGAACAGGAGGAAGTAGAGTG	612	21	55.5	327
EST	BQ590645	trinucleotide	224	259	36	12	AGT	188	21	54.6	TGACTTATCAACAACCCCTGA	333	21	55.7	146
EST	BQ590651	pentanucleotide	182	191	10	5	TCAAT	130	19	50.2	GCTTCGCATCTATTTTGAGG	449	20	55.3	320
EST	BQ590664	dinucleotide	410	421	12	10	AG	285	21	54.9	ATTATCAGAAGACATCCCAT	510	21	52.8	226
EST	BQ590684	pentanucleotide	248	262	15	10	ATAAA	144	19	54.5	CAACCAAAAGTTCAAAGAAGAA	394	21	54.8	251
EST	BQ590684	trinucleotide	371	382	12	9	CTT	143	19	55.0	CAAGCAAAAGGTAACAC	484	20	55.0	342
EST	BQ590684	trinucleotide	206	215	10	5	AAATC	144	19	54.5	CAACCAAAAGTTCAAAGAAGAA	394	21	54.8	251
EST	BQ590704	trinucleotide	149	163	15	12	AGA	108	23	51.1	TTACGCATCTTGAGGCC	433	18	55.7	326
EST	BQ590707	trinucleotide	58	69	12	9	AGA	22	21	54.2	GATGAAGAGTATCAGCGAGG	505	20	55.0	238
EST	BQ590715	trinucleotide	399	413	15	12	TGC	106	21	54.7	ATAGTTCCCAATGCTGTTTG	449	20	55.3	400
EST	BQ590751	pentanucleotide	182	191	10	5	TCAAT	130	19	50.2	GCTTCGCATCTATTTTGAGG	449	20	55.3	320
EST	BQ590767	trinucleotide	197	208	12	9	ACC	112	19	54.2	TAAAGCATCAACAAGCCATAC	480	21	55.6	369
EST	BQ590770	pentanucleotide	257	266	10	5	ATCAA	1	21	54.8	CTTGAGCAAAAGCCCTCATTT	359	21	55.2	359
EST	BQ590782	trinucleotide	51	66	16	12	ATAC	2	20	54.4	GTATCCTCAAAATCCATCAACC	360	21	55.9	359
EST	BQ590788	trinucleotide	199	213	15	12	ATC	142	21	56.3	ATCAATCCACCAACGAGTC	358	19	55.6	217
EST	BQ590827	trinucleotide	182	193	12	9	TGG	126	18	52.6	GACCAACTATCTCTCTCAAA	297	21	55.3	172
EST	BQ590831	dinucleotide	292	311	20	18	TA	1	20	56.0	TGAGTGATGTTGATGGGT	400	21	55.4	400
EST	BQ590832	dinucleotide	269	278	10	8	CT	110	19	54.2	GAGAAAGTGGTAAAGGAGGA	376	21	55.1	267
EST	BQ590833	trinucleotide	430	441	12	9	CAG	353	21	54.7	CTCTCATCCCAACCTTATC	531	20	54.5	179

EST	BQ590851	trinucleotide	381	401	21	18	AAG	GGAACCTGAGAAAGAAATGTAGAA	286	22	55.2	ATAGCATAAACCCACAGCAAC	597	20	55.3	312
EST	BQ590854	dinucleotide	536	545	10	8	TA	ATCAAGACAGTGGATGAGAT	206	21	53.6	AGACAAATACAAACAGAAACAA	591	22	51.9	386
EST	BQ590867	trinucleotide	142	192	48	27	AAC	TGAAGACGAAGGACAAATGA	73	19	55.0	CCCAATAGGACTTAGAGAG	250	21	54.8	178
EST	BQ590867	tetranucleotide	331	346	16	12	TTCA	ACAACAACAACAACAACAACA	169	21	54.9	ACAACAATCTCTCTCTCTCT	461	21	55.0	293
EST	BQ590867	trinucleotide	40	51	12	9	AGC	CTCTAACTTCTCTCTCTCTCA	8	22	54.7	TGTTGTTGTTGTTGTTGTTG	186	21	54.9	179
EST	BQ590876	trinucleotide	126	152	27	17	CAA	GAAGAGAAGGAAGAAATGG	7	21	54.8	TAGTGAGAAGTGTAGGAGAA	330	21	54.9	324
EST	BQ590880	trinucleotide	96	113	18	15	ACC	GTCACAACTTCTCTCTCTCT	41	21	55.1	ACAATCCATCTCTCTCAACT	373	21	55.4	333
EST	BQ590880	dinucleotide	76	85	10	8	CT	GTCACAACTTCTCTCTCTCT	41	21	55.1	ACAATCCATCTCTCTCAACT	373	21	55.4	333
EST	BQ590896	trinucleotide	266	277	12	9	TGA	CTCTCTCTCTCTCTCTCTCA	0	21	56.0	CATCCCTATCTCTCTGGTT	374	21	55.0	375
EST	BQ590906	trinucleotide	192	203	12	9	ATC	CATCCATCTCTCTCTCTCTCA	32	21	55.1	GTGTTCTCTCTCTCTGGTCT	429	20	56.0	398
EST	BQ590910	dinucleotide	161	172	12	10	TC	GTCCTATCCGACGCTTGT	95	19	55.4	AGATGAGAAGGCGAAGTTG	241	20	54.7	147
EST	BQ590911	trinucleotide	106	117	12	9	TGC	TCTTGAACCGACTATGACTT	12	21	54.1	GCAGGCTCTCTCTCTT	170	18	54.7	159
EST	BQ590915	dinucleotide	128	137	10	8	CT	TCTCTCTCTCTCTCTCTCT	42	21	54.8	CCAGGATGTAAGTAAGTCT	311	20	54.7	270
EST	BQ590927	dinucleotide	49	58	10	8	GA	GCAAGCGAAAGACTGAA	20	18	55.1	GAAGTGATGAAGAGATGGA	268	21	55.2	249
EST	BQ590933	trinucleotide	199	213	15	12	GAT	AAATGGTGAGAAGAAAGATGAA	26	21	54.0	AATCAGAAGAGGCAAGAGAAA	333	21	55.9	308
EST	BQ590933	trinucleotide	93	104	12	9	GAC	AAATGGTGAGAAGAAAGATGAA	26	21	54.0	AATCAGAAGAGGCAAGAGAAA	333	21	55.9	308
EST	BQ590933	trinucleotide	176	187	12	9	AAG	AAATGGTGAGAAGAAAGATGAA	26	21	54.0	AATCAGAAGAGGCAAGAGAAA	333	21	55.9	308
EST	BQ590934	trinucleotide	155	169	15	12	CCT	CACCTACACCAACCAAC	101	18	55.3	ATTGTTATCTCTCTCAATTC	234	21	50.1	134
EST	BQ590934	trinucleotide	108	119	12	9	CAC	ATCTCTGCTCTACCGCT	21	18	57.9	GCATTGTTATGTTATCTCTCT	242	23	52.7	222
EST	BQ590938	pentanucleotide	297	306	10	5	TTTTG	TCCCAATATCCAAATAGAAA	50	21	54.0	TCCAAGCACCTTAAGAGTAAGA	362	21	54.5	313
EST	BQ590947	pentanucleotide	177	188	12	10	TC	TATTGGCATGTAGGAGAGCC	101	21	59.2	CCGTCAGGAGGACATAA	325	18	60.8	225
EST	BQ590967	pentanucleotide	154	168	15	10	ATTCA	ATCCAAACCTCTATTCTCA	122	21	55.4	CTTTCAAGCTCTCTCAACA	498	21	55.1	377
EST	BQ590970	trinucleotide	146	157	12	9	CCA	ACCTAATGAAGCGGACTAAC	58	21	55.3	TTTGAAGAAGCAAGAGATGAG	421	21	55.0	364
EST	BQ590987	trinucleotide	118	129	12	9	AGA	TGTTTCTCTCTCTCTCTCT	73	19	54.9	CCTCACTCATCTCTCAAACT	349	21	54.3	277
EST	BQ591014	trinucleotide	466	477	12	9	TGA	AATCCTTCGCTTTACCT	152	18	54.8	CTGCCCAATCTTCTCTCT	524	18	55.4	373
EST	BQ591024	pentanucleotide	201	215	15	10	TCACA	AGAAAGCCCAATCAATCGTC	53	21	55.9	AACCTCCACGAGCAAC	421	18	55.6	369
EST	BQ591024	tetranucleotide	242	253	12	8	AAAG	CTCACTTCACATCAATCAACA	194	21	55.4	AACCTCCACGAGCAAC	421	18	55.6	228
EST	BQ591058	dinucleotide	111	122	12	10	TC	TGACTTCTCTCTCTCTCTCT	48	21	55.3	TTATCTCTGATGGGTGTTG	265	20	55.9	218
EST	BQ591072	dinucleotide	205	214	10	8	TC	ATTCACTCTCTCTCTCTCTCT	32	21	56.0	CGTGTGATTCGTAATCTTGT	292	21	54.6	261
EST	BQ591073	trinucleotide	250	261	12	9	AGT	TCACTTCTCTCTCTCTCTCT	140	21	55.3	TGTTCTCTCTCTCTCTCTCA	387	21	55.0	248
EST	BQ591084	dinucleotide	52	65	14	12	AG	CCAGATTCAGACTTTTCTCT	19	21	55.4	ATTGCTCCGTAATCTCTCT	265	19	58.8	247
EST	BQ591096	trinucleotide	472	483	12	9	TGT	TCTGGTGAAGATGTCAGTCC	178	20	56.0	ATAGAATCAAGAGCAACAAA	520	20	55.2	343
EST	BQ591104	trinucleotide	273	284	12	8	GCGA	TAAGTTCGACAGTGAAGT	13	19	53.2	CGCACAAATGAAGCAATC	380	18	54.2	368
EST	BQ591109	trinucleotide	199	210	12	8	GCGA	CTCTCTCTCTCTCTCTCTCT	11	21	54.8	ACACTCAAGCACTCAACACT	301	20	55.7	291
EST	BQ591111	trinucleotide	226	240	15	12	TCT	GAAGACGATATGAGGTAG	164	21	54.0	ATTGATGGAAGAGAGAAAG	421	21	55.1	258
EST	BQ591117	trinucleotide	396	407	12	9	ATC	ATTCACTCTCTCTCTCTCTCT	264	21	53.8	TCTTCTCTCTCTCTCTCTCT	540	21	54.7	277
EST	BQ591120	trinucleotide	513	542	30	20	TGA	TTCAACATCTCTCACTTTCTCA	229	22	55.2	GTCAACATTTCCCTCCAAG	581	19	55.5	353
EST	BQ591147	trinucleotide	144	167	24	14	ACG	ATCAACTCTCAACACCAACA	79	21	55.6	AAGAACCCTGTACGACAAAG	361	20	55.2	283
EST	BQ591167	tetranucleotide	306	317	12	9	CTT	TGCTCACTTCAAACTCTCTG	88	21	55.8	AGCTTCCCTATTTCATT	423	19	54.1	336
EST	BQ591167	tetranucleotide	149	160	12	8	ACAA	ACATCGTCTAAGTGTGAGGT	72	21	53.8	TAATGAAGAAATGAGCCAAAG	463	21	57.0	392
EST	BQ591171	trinucleotide	302	331	30	20	CAT	AAAGATGTAGAGAAAGGCA	222	22	55.1	TATGGTGAAGATGATGTTG	364	21	55.3	143
EST	BQ591228	tetranucleotide	94	105	12	8	AACA	AAACCAACCACTAACCACA	43	19	53.0	ACTTCACTTCTCTCTCTCT	399	21	54.3	357
EST	BQ591246	trinucleotide	139	150	12	9	AGG	CAATGGAGGAGGAGGAGG	111	18	58.1	AGGACGAGATCATCATCT	449	20	55.0	339
EST	BQ591249	dinucleotide	353	362	10	8	GT	TTACAAGTTTCGTTGCTGT	277	20	55.0	GATGAAGGAGATGATGTTG	410	20	55.4	134
EST	BQ591273	trinucleotide	307	318	12	9	TGC	TTCACTCTCTCTCTCTCTCT	2	21	55.1	TCAATCGTGTATCTCTCTCT	356	21	54.0	355
EST	BQ591276	pentanucleotide	607	621	15	10	ACAAC	TATTGCCCTATCTCTCTCT	465	19	56.5	GTAGATGCGGTGGAAGG	802	19	58.3	338
EST	BQ591285	dinucleotide	128	137	10	8	CT	CCTCATTTCTTCTCTCTCTCT	64	22	53.9	GCTCTCATTTCCACTCAACT	436	21	53.6	373
EST	BQ591290	dinucleotide	55	68	14	12	TC	TTTGGTAAGTGAGGTTTCT	2	19	52.6	TATTGCCCTTCTTCTCT	283	18	55.1	282
EST	BQ591294	tetranucleotide	372	383	12	8	CGCC	CACACAAGAGGAGAGAGAG	225	20	54.8	ACAGACCAACAATAGAACGAG	502	21	54.5	278
EST	BQ591327	dinucleotide	295	308	14	12	AT	ATCCAATCTCTTACATCCCA	58	20	56.8	AGAAACCAACCAACCAAGG	445	18	53.3	388
EST	BQ591327	tetranucleotide	275	294	10	9	ACAT	ATCCAATCTCTTACATCCCA	58	20	56.8	AGAAACCAACCAACCAAGG	445	18	53.3	388
EST	BQ591329	pentanucleotide	405	419	15	10	GAAGG	TCAAATAATAAACAACGACAC	97	22	54.6	TGAACCTCAACATTAAGTCAGT	481	21	52.3	385
EST	BQ591356	trinucleotide	215	229	15	12	GAA	TAGCACACCAAGTCAACCA	94	19	56.1	ATGAACCACTCCATCTCTCT	484	21	55.3	391
EST	BQ591400	trinucleotide	290	301	12	9	AGC	ACATCAACTCTTAATGGAACA	148	21	54.6	GCTATCTCTTACCGACTTT	468	20	55.2	321
EST	BQ591423	trinucleotide	174	185	12	9	TGG	GGGTTCACTTCTTTTGACCT	81	20	55.8	AGTTTATTGCCTCTTACACC	277	20	53.5	197

EST	BQ591442	trinucleotide	185	199	15	12	CTT	CTTGCCCTTTCTTACTTGTTGA	154	21	55.0	ATTTAGCGTAGTGTTGAATGA	337	21	55.0	184
EST	BQ591478	tetranucleotide	274	285	12	8	CCCG	GGGTGGGAAGATAGATG	109	19	54.6	CGAAGGAGATACATTGA	420	20	55.3	312
EST	BQ591484	tetranucleotide	145	156	12	8	CTTA	AAATCCTTATGTCCAATCTACT	49	22	51.5	AAGTGTGGTGGTGGTGG	411	18	61.7	363
EST	BQ591509	pentanucleotide	318	327	10	5	TTCCT	AAAGAAGGAAGTGAAGGAAA	107	21	54.9	AAAGGAAAGGAAAGGAAAGAA	363	21	54.2	257
EST	BQ591521	trinucleotide	155	164	10	8	CT	TCTCCTAAACTCGTCTCTCC	69	21	55.3	CTTCAGTGTGCTGTAATCGT	259	21	55.4	191
EST	BQ591532	trinucleotide	149	169	21	18	ATC	GTCTTCAATGGCACAACCT	115	19	53.9	GAATCTCACCACTCCAACT	372	19	55.3	258
EST	BQ591532	trinucleotide	339	356	18	15	GGT	ACAACCTCGTACTCTCTCTT	127	21	54.7	GCAAGAACTACACACCAACA	520	19	55.5	394
EST	BQ591533	trinucleotide	155	169	15	12	CTT	TCTTCTACCTCTCAAAACCC	5	21	56.0	TGGCATCTCTTATTTCTCTT	246	22	55.1	242
EST	BQ591579	trinucleotide	239	250	12	9	TTC	CACCCTCTTCTCTCTCTCTC	118	21	54.9	ATCCTGTCCCTTATCTGTCTG	462	21	55.8	345
EST	BQ591601	trinucleotide	179	190	12	9	TGT	GCTGTGTATGTTCTCATTT	134	19	53.4	TAGGAGGGAGTTAGGTT	263	18	54.7	130
EST	BQ591603	trinucleotide	127	138	12	9	ATC	GTAGCAATAAGGCTCGAGT	95	21	56.3	ATTTCCATCCATCCCATC	389	19	57.0	295
EST	BQ591605	trinucleotide	365	379	15	12	GAT	AGTCAAACTCAACCCGACAC	155	20	55.4	AATCAGCCTCTCATCTTCA	460	20	55.0	306
EST	BQ591617	trinucleotide	296	307	12	9	CCA	AGTCTTCCACCACTCAACAA	129	20	55.6	GTCTCTTACTCTGGCAATCTC	434	22	54.9	306
EST	BQ591620	pentanucleotide	87	101	15	10	TTCAA	GCCTACCTCTTCTTCTGTC	1	18	54.8	TGTCTCTCTTCTCTTCTCCC	287	21	55.3	287
EST	BQ591620	trinucleotide	270	281	12	9	GAA	CAAAGATTAGTGAAGAAAGA	191	23	52.6	CATACCACGACGATAGAAAG	416	21	55.1	226
EST	BQ591641	trinucleotide	434	449	16	14	GT	CCCTCTCTGTCCTCTGAA	149	18	56.3	TACAACCTTCGCCACC	537	18	58.0	389
EST	BQ591641	trinucleotide	490	501	12	9	GCT	CCTCTCTTGGTCCCTGAA	149	18	56.3	TACAACCTTCGCCACC	537	18	58.0	389
EST	BQ591654	trinucleotide	271	282	12	9	GGT	CATCAGTAGAGTTGCGAG	83	20	55.0	CGTAGTTGAGGGGAAAGGA	317	19	55.4	235
EST	BQ591657	trinucleotide	719	730	12	10	GC	ACACAACAGCATCGTAAA	865	19	55.0	GGGAGTGGGAAAGAGGT	879	18	56.5	215
EST	BQ591689	trinucleotide	278	287	10	8	AT	TCTTACTTCTTCTGGCTACAA	107	21	54.7	GTGTGCTATGCTGATGTGTG	206	21	54.2	100
EST	BQ591694	pentanucleotide	110	119	10	8	GA	CCCATAACTTACCAACAACA	209	21	55.2	CTCTCTTACCATCATCTCTCA	422	21	54.4	214
EST	BQ591702	trinucleotide	239	250	12	9	AAG	GTTCATTTCTTCAATCCAAA	204	21	54.5	TAGGTGCTCTCTCTCGG	384	19	55.7	353
EST	BQ591717	trinucleotide	113	124	12	9	CTA	TGAAAGGCCATAAATACCTCC	11	21	56.0	CCAATCAGTTGTCATCTTAC	484	21	54.6	281
EST	BQ591724	trinucleotide	57	66	10	8	TC	TCTTTTGTCTCTTTAGGCC	1	19	55.5	TTAGAAAGTTGGATTGGTGA	192	21	55.0	192
EST	BQ591737	trinucleotide	100	111	12	9	GAT	TGAGAAGGAAGGAGGAAAG	53	21	55.3	ATACACAACCCACCCAGAA	451	19	56.2	399
EST	BQ591738	trinucleotide	276	293	18	8	CCT	CACCTCAATCCTCTCTCTCT	132	21	55.2	ACCTCCATTACTTCTCTCCAC	365	20	55.6	234
EST	BQ591743	trinucleotide	451	468	18	15	AGT	TCACACAACCTTCAATTTCA	154	21	55.0	ACTAATCTTCTCTCGCCAA	520	20	56.7	367
EST	BQ591748	tetranucleotide	199	210	12	8	GC GA	CTCTCTCATCTCTCTCCCTC	11	21	54.8	ACATCAAGCACTCACCACT	301	20	55.7	291
EST	BQ591756	trinucleotide	52	65	14	12	AG	CCAGATCCAGACCTTATTC	19	21	55.4	ATTGCTGCGTATCGCTC	265	19	58.8	247
EST	BQ591758	trinucleotide	333	350	18	15	GAT	ATCAGTTCTTGTCTGCTGCT	276	20	54.8	GATTTCTGCTCTTCTATCATC	396	20	52.0	121
EST	BQ591758	trinucleotide	201	212	12	9	AAC	CTACAATCCTCTGCTTCAAC	152	21	55.0	ATCATCTCTCTCTCATCTCC	337	21	54.8	186
EST	BQ591772	trinucleotide	210	224	15	12	CAT	TAATCGCTCTCTCTCTCTCT	92	21	55.6	TCTCTCTGTTGTAGTAGTG	273	22	53.8	182
EST	BQ591772	trinucleotide	77	88	12	10	TC	AAGTCTCATCTCCCTCTCTC	3	19	53.1	TCTCTCTGTTGTAGTAGTGT	271	22	55.5	269
EST	BQ591785	trinucleotide	112	129	18	9	CT	TATGATGATGTGGAAGTGA	57	21	56.5	ATAATGGTGTAAAGCCAA	302	19	53.1	246
EST	BQ591787	trinucleotide	218	232	15	12	TAG	TTGGTTCATCTTGATTTCC	146	20	55.1	CAGTTTGAGTAAGCAGAGA	324	20	54.4	179
EST	BQ591792	trinucleotide	350	361	12	9	AGA	TACCTACCAACAACCTCCGAC	70	20	55.2	TTCAATTCACAGATACGACA	405	21	55.0	336
EST	BQ591804	trinucleotide	209	223	15	12	CAT	TAATCGCTCTCTCTCTCTCT	91	21	55.6	TCTCTCTCTGTTGTAGTAGTG	272	22	53.8	182
EST	BQ591804	trinucleotide	76	87	12	10	TC	AAGTCTCATCTCCCTCTCTC	2	19	53.1	TCTCTCTGTTGTAGTAGTGT	270	22	55.5	269
EST	BQ591820	trinucleotide	41	50	10	8	TC	GCTTACTTAACCACTCTCATTT	0	23	53.9	AGGATTTCTTGCTTGCTGT	199	20	54.0	200
EST	BQ591826	tetranucleotide	98	125	28	17	AATC	TACTCCAACATCACACAACA	8	21	55.0	GAGACTGAACGCCCTGTAA	246	20	55.5	239
EST	BQ591836	trinucleotide	485	498	14	12	TA	TGTAAACTTGGCATTCACTTC	323	21	55.5	ATAATCTCTGGAACACCA	578	20	54.5	256
EST	BQ591865	pentanucleotide	349	358	10	5	AAAGC	ATTGTGAAGGAGAAGGGAAG	281	21	55.2	TGGGATTTGGAAGACCACTC	541	19	55.9	261
EST	BQ591871	trinucleotide	404	418	15	12	CAG	AACCCCTAACCCCTAACCTAAC	181	21	55.5	CACCAATAACCAAGAAACAA	580	21	55.3	400
EST	BQ591874	pentanucleotide	123	132	10	5	AATCA	GGGTCAAGCCCTCAACT	59	18	59.0	ATCTTCTCCCTCAGTCTACCA	339	21	55.5	281
EST	BQ591901	trinucleotide	117	128	12	9	AGA	CCAGTGTTCATCTTGTGTTG	44	21	55.3	AGCGAGTTCTTCAGTTTCTT	198	21	55.2	155
EST	BQ591921	tetranucleotide	538	549	12	8	GCTG	GCTGAAGCTCCCATTTTG	459	19	52.2	TCAACAAGCGTCTCATCAA	589	19	56.3	131
EST	BQ591943	trinucleotide	160	171	12	9	CAT	TTTCAACAGTCCCAACT	34	18	51.8	AATGACGAGAGATGAATGG	306	21	55.2	273
EST	BQ591955	trinucleotide	266	277	12	9	TGA	GTATGGATTGGACTCTGGAA	151	20	54.9	GTCTCTCATCTCTGTCTC	504	20	55.3	354
EST	BQ591956	trinucleotide	290	304	15	12	AGA	GATGAGAGTGACGACGATG	233	19	54.9	ATGGATTGAGTGTATTGCTG	518	21	55.3	286
EST	BQ591963	trinucleotide	508	531	24	14	TGA	AGATGCTGATGATCTGATGT	462	21	54.7	CCCTTCTCTCTTATTTGTT	582	20	55.0	121
EST	BQ591965	trinucleotide	117	130	14	12	TC	CCCATTCTTACTTATTCCTC	79	21	54.6	AAATCTCCAAAGCCACTGTT	367	19	54.7	289
EST	BQ591966	trinucleotide	289	321	33	30	AAC	ACATCAACAACAACAACAACA	253	21	54.9	GAGACAAGAGTCCAAAGGT	402	21	55.1	150
EST	BQ591966	trinucleotide	247	273	27	17	AAC	AACCCCTTCTTCTCTCCACT	38	19	55.3	TGTTGTTGTTGTTGTTGTTG	309	21	54.9	272
EST	BQ591982	pentanucleotide	256	265	10	5	ATCAA	AACAATCCACATTCATACAC	1	21	54.8	CTTGAGAAGAAACCTCCATTT	358	21	55.2	358

EST	BQ591994	trinucleotide	384	395	12	9	CGA	TATGATTCCTCTCTCTCTCC	207	21	55.0	ATTGTCGTCGTTGTTATT	431	21	54.8	225
EST	BQ592021	dinucleotide	39	50	12	10	TC	CACCTCTCATCCTCTCTCAA	9	20	55.4	AACCTGAATGGCTGAATGATG	340	21	54.0	332
EST	BQ592028	trinucleotide	78	92	15	12	TAA	AGAGAAATGAGTGAATACAA	23	23	54.8	AGTTACGGAAGTTGAGGA	415	19	54.7	393
EST	BQ592044	trinucleotide	325	348	24	14	CAA	GATGACGACGCTAATAACAC	208	21	55.0	GTGCTCTCAATGCTCTTCT	496	19	52.9	289
EST	BQ592044	trinucleotide	349	360	12	9	TAA	GATGACGACGCTAATAACAC	208	21	55.0	GTGCTCTCAATGCTCTTCT	496	19	52.9	289
EST	BQ592068	dinucleotide	281	290	10	8	CT	CCATCTCATCTACCTCCAGAG	250	20	55.6	GAACATCAGTTTCAAGTCTCCA	425	21	55.3	176
EST	BQ592070	trinucleotide	423	434	12	9	ATG	ATCGTTGATTCGAGGGT	373	18	57.8	TCTTGCTCATAGTCTCATTC	506	21	55.7	134
EST	BQ592082	dinucleotide	76	85	10	8	GA	GCTCACACACACACATAGA	35	21	55.5	ACTACAGAAACACCAAGGA	183	20	55.7	149
EST	BQ592089	trinucleotide	126	152	27	17	CAA	GAAGAGAAGAGGAAGAAATGG	7	21	54.8	TAGTGAGAAGTGATGGAGGAA	330	21	54.9	324
EST	BQ592099	trinucleotide	66	80	15	12	CAA	AACITTCACACTTCTTCAC	25	20	54.2	GCAGGATAAGCCATTGA	410	18	54.6	386
EST	BQ592100	trinucleotide	259	294	36	26	CAA	AGAGAGAAACAAAGATGGG	202	21	55.2	GGAAGAGCAAGTGAAGACAA	453	21	54.8	252
EST	BQ592103	trinucleotide	77	91	15	12	TCC	CTCATCAACCAACACTTCC	43	20	55.5	GTGTCCAAAGAGCGAACA	195	18	55.6	153
EST	BQ592122	dinucleotide	128	145	18	9	TC	CCITTCCTCTCTCTTCCCT	47	19	55.1	CGAATGTGAAGAGTGAGTT	320	20	55.4	274
EST	BQ592125	dinucleotide	187	196	10	8	CT	GCACCTTCACCTGCTCTCA	158	19	53.7	GATGACTCTAACACCCATTG	374	21	56.0	217
EST	BQ592144	trinucleotide	80	97	18	15	AAG	GGGTATTTGCTCGGTTTC	20	18	55.6	CCCATCTATTACAGATTCA	163	21	55.2	144
EST	BQ592178	trinucleotide	87	98	12	9	GAA	GCTGAGGAGGAGGAGAGAA	4	20	56.4	CAGGGTTGCTTTGTAATC	134	19	55.7	131
EST	BQ592182	trinucleotide	34	48	15	12	TTC	GCITTCCTCTCTCTCAAATC	0	20	53.3	CCACAACACTCCCTTTATTG	376	21	54.1	377
EST	BQ592197	trinucleotide	115	126	12	9	CTT	CACITGTTCTTCCACCATC	58	20	55.6	ACATGCTTTGCTTGCTT	405	21	54.1	348
EST	BQ592204	trinucleotide	89	100	12	9	ATC	TCTCTCTCTCTCTCTTACTTC	44	23	53.9	TTCATCTCTCTCTTTGACT	343	21	56.0	300
EST	BQ592208	trinucleotide	370	381	12	9	GAG	CCAAACGACCCACCTAAA	258	18	56.9	ATAAGCCTCTCATCTTCACT	422	21	54.7	165
EST	BQ592223	dinucleotide	39	50	12	10	TC	CTCTCATCTTACCCAAAGG	0	20	54.0	GTATTCCCAACCAACTCA	247	20	56.0	248
EST	BQ592272	dinucleotide	285	296	12	10	CT	TCTCTCTCTCTCTTACTTC	44	21	55.2	TATTCGACGCCAATCTCC	409	19	55.2	366
EST	BQ592282	trinucleotide	261	296	36	26	CAA	AGAGAGAAACAAAGATGGG	204	21	55.2	GGAAGAGCAAGTGAAGACAA	455	21	54.8	252
EST	BQ592293	trinucleotide	115	126	12	9	ACC	CTCTCCACTGTCCATCCTC	15	19	55.4	CGAAGAAAGGTGAGCGTT	276	18	55.6	262
EST	BQ592293	trinucleotide	182	193	12	9	TCC	CTCTCCACTGTCCATCCTC	15	19	55.4	CGAAGAAAGGTGAGCGTT	276	18	55.6	262
EST	BQ592293	trinucleotide	202	213	10	9	CAC	CTCTCCACTGTCCATCCTC	15	19	55.4	CGAAGAAAGGTGAGCGTT	276	18	55.6	262
EST	BQ592322	pentanucleotide	231	240	10	5	AAAGC	ATTGTGAAGAGAGAGAGGAG	163	21	55.2	GATAGACCAAGCAACTAAAC	295	22	54.9	133
EST	BQ592323	trinucleotide	422	442	21	11	AGA	ACCACCTCTTCAATCCCT	359	18	54.2	TCATGCACCAACTAATACGCC	481	20	56.1	123
EST	BQ592340	trinucleotide	173	184	12	9	CAC	GCAAGAGGAGGATAGAGAAAG	53	21	55.0	AAATGGAGTAAGACAGAGGA	321	21	55.8	269
EST	BQ592348	trinucleotide	105	122	18	15	AAG	ACACAACAAACAAACAAACA	72	20	54.9	TGAACACGCTCTCTAATCTC	342	21	54.9	271
EST	BQ592348	trinucleotide	78	92	15	12	AAC	GTTTCTCTGCTGTTCTTCTC	0	20	54.2	ACGCTCTTAATCTCCATCTT	336	21	55.0	337
EST	BQ592361	trinucleotide	198	230	33	30	ACA	CTCTCTCTGCTGCTTCTGCT	54	21	55.9	ATCTCTTCTCTGACATCTT	318	21	54.5	265
EST	BQ592368	dinucleotide	50	63	14	12	TC	GTTCTACTGGTGGCTTAACT	2	21	55.3	ATCTGATCTCTCTGGCTCTC	378	21	55.1	377
EST	BQ592369	dinucleotide	225	234	10	8	TC	TGCTCTCTCTAAACCACTC	123	21	55.2	ACATCCCTCTCATCGTCATC	435	20	54.9	313
EST	BQ592372	trinucleotide	136	147	12	9	CAT	CAGAGATGTTGGTTCCTT	96	19	52.5	GGAGTTGAGAGAGTAATCGTG	302	22	55.7	207
EST	BQ592374	dinucleotide	132	150	20	11	TC	CTTCTCTTCTCTCTCCCAAG	42	21	55.1	AGTTGAGCGGATTTGTC	259	18	56.1	218
EST	BQ592381	dinucleotide	1002	1015	14	12	GC	AAGCACTCGCACATTAATACA	718	21	56.1	AGTCACCATATAGCGTCA	1088	19	54.9	371
EST	BQ592388	pentanucleotide	281	290	10	5	CCCGG	TGCTCACACTACCAATCTCA	64	21	56.9	CAGGACCGTAAACCTCGG	463	18	59.1	400
EST	BQ592389	trinucleotide	426	437	12	9	CAG	GGCAATCGGAGTTTCAGCA	331	18	60.9	TGCTGATCTTATCACTTAGCC	482	23	55.5	152
EST	BQ592426	trinucleotide	270	281	12	9	CGG	TTGCGTCTGTTAGCGATT	153	19	56.0	GCTGCTGGAATATACGAC	333	20	55.1	181
EST	BQ592432	trinucleotide	405	416	12	9	GAT	AGCATCTGGGTATTCTGTTT	306	21	55.5	AGGCTTTGTTGGCTGAC	521	18	56.3	216
EST	BQ592439	trinucleotide	418	429	12	9	AAG	TTGACGATAATGAGAGAGAA	355	21	52.7	TCAGAAACAGACACTTAGG	480	20	50.3	106
EST	BQ592441	trinucleotide	303	314	12	9	TGA	GTGCTTCATTTGGAAGTAGTG	240	21	54.9	GAGACAGCAAGCCCATTT	386	18	55.1	147
EST	BQ592447	trinucleotide	124	147	24	21	AAC	CTTCCACTCTCTCTCTCTC	16	21	54.9	TGGGTTTCTCTCTCTCATC	178	21	56.0	163
EST	BQ592450	trinucleotide	173	184	12	9	TCT	CTTCAACTCTTCACTACCTC	137	21	55.1	ATAACCTCAACCATTTCAACA	443	21	54.7	307
EST	BQ592461	dinucleotide	722	733	12	10	AG	ATCGGACAAACCCAGTAG	596	18	57.0	CGATCTTCATCATTTCTCTC	946	21	54.1	351
EST	BQ592465	tetranucleotide	104	115	12	8	TGGC	TAAAGGTGAGAAACCACTACTG	41	21	55.0	TCATAGTTGGTCGGTCT	223	18	54.6	183
EST	BQ592465	dinucleotide	195	204	10	8	CT	CTGAAGTCCCAACCACTACTC	62	21	54.0	CGATGTAATGTGAGATAAAG	239	21	55.0	178
EST	BQ592469	trinucleotide	102	111	10	8	TC	TCTCTCTCTCTTGTCTTCTG	27	21	55.1	GCTACTACCCGCTATTCTCT	350	21	55.4	324
EST	BQ592470	trinucleotide	288	302	15	12	TGC	CCGCATAAGATTCAAGAC	132	19	55.7	AAGTGAGAAAGACCAAGTGA	510	21	54.1	379
EST	BQ592489	trinucleotide	437	448	12	9	AGA	ACAACATATCCAACTGTCCAA	109	21	54.7	GTGAACACCACTTACTCC	504	20	54.5	396
EST	BQ592491	trinucleotide	327	338	12	9	CAA	AACATGATGAGGGGAA	244	18	50.0	ATTAGAAGGGTGTGTTGGG	397	20	56.5	154
EST	BQ592493	trinucleotide	70	88	20	11	TC	ACATCAATCTCCCAACCT	28	18	55.0	ACGAATAAATGCCTGGAAAC	352	20	56.7	325
EST	BQ592507	dinucleotide	57	68	12	10	TC	CAACATTCATATCCAAACA	22	22	55.3	CGTCCCAAGGACATAG	383	18	53.9	362
EST	BQ592513	trinucleotide	194	205	12	9	ACC	CCTCTCTCTCTGCTCTCCACTT	62	21	55.2	AAGGTCCTCTACCAAACTCAGG	396	21	55.1	335

EST	BQ592521	trinucleotide	171	182	12	9	AAC	CATCCATCTCAACACACAAATAAG	80	22	54.9	TTCCATTCCACAAATAATAAC	278	21	54.2	199
EST	BQ592523	dinucleotide	191	202	12	10	TA	ATTATGGCGATAGTAAGAA	108	21	52.9	CTGATGGAAGTTGTAGTGGAG	260	21	54.9	153
EST	BQ592537	tetranucleotide	99	110	12	8	CCAC	CCCGCTACTACAAGTCTACAA	7	21	54.9	CAAAAGTTACCAACCCCAATAA	328	21	54.5	322
EST	BQ592546	trinucleotide	90	104	15	12	TCT	ACAACTTCTTCAACATCTCA	58	21	54.7	GGATAAACCTCTCCACATAA	296	21	55.1	239
EST	BQ592547	trinucleotide	210	221	12	9	CGA	TTCTTGCTTTCATACACTCC	74	21	55.5	GTTAGGGTTAGGGTTAGGGTT	389	21	55.5	316
EST	BQ592547	trinucleotide	274	285	12	9	GAC	TTCTTGCTTTCATACACTCC	74	21	55.5	GTTAGGGTTAGGGTTAGGGTT	389	21	55.5	316
EST	BQ592561	trinucleotide	80	91	12	9	TCT	TTTAGGAGAGAGAAGAAGAAA	18	21	50.5	CGTCACAAGAAGAAGAATGAG	300	21	55.2	283
EST	BQ592569	trinucleotide	182	193	12	9	TCT	TGGTGGTCCCTACACTGG	96	18	57.8	GCAATTGGTGAATATACAAGG	394	20	52.9	299
EST	BQ592572	pentanucleotide	203	212	10	5	AAAAC	TTGCCAGACCATAGATACAC	97	20	53.5	TGAAGTAGTGAACATCCCAATC	252	22	54.4	156
EST	BQ592577	dinucleotide	868	879	12	10	AG	GAGTGTATGGTATCGGAGA	818	20	56.1	CGACTCCGCTCTTACTATTT	925	21	55.6	108
EST	BQ592591	pentanucleotide	208	217	10	5	AAAAG	TAATCAACTAATAACGCGCC	12	21	54.9	GAACGCGAGAACGCGACA	336	18	62.3	325
EST	BQ592620	trinucleotide	33	53	21	18	CCA	TCACACACACACAATCT	0	19	50.6	GCTTTCAGAGAGGTTAGGA	313	21	55.2	314
EST	BQ592620	trinucleotide	54	65	12	9	CAA	CCTAAACATCCACCAACA	23	18	55.0	ATCGGAGAAGAGAGAGAGA	223	20	55.7	201
EST	BQ592620	trinucleotide	92	103	12	9	CTC	ACCAACACACAAACACAA	46	19	55.6	AGGAGTTACAGAGAGAGAGAA	296	21	54.9	251
EST	BQ592635	tetranucleotide	421	432	12	8	CGGA	GGAAGAGGAGAAGAGGA	288	19	55.9	GAAGAGTGAAGAGAGACAGA	684	20	55.4	397
EST	BQ592659	tetranucleotide	206	217	12	8	ACTT	ACAAGCAACCTTCTCACACT	20	20	54.9	TTTATGTACCTCCACAAGA	337	20	50.7	318
EST	BQ592672	dinucleotide	185	196	12	10	AC	GTTTCTTGTTGGCTTGAATAA	39	21	54.7	CGTTGTAATGTGTCTCGG	342	18	54.0	304
EST	BQ592692	trinucleotide	303	314	12	9	TGA	CGTGGTAAAGTCGTTCAAT	231	20	55.3	CATAAGTGAATCATCATCTT	614	21	54.2	384
EST	BQ592702	trinucleotide	418	429	12	9	AAG	CGATGATACGATAATACTGCT	290	22	56.9	GTCTTACCCACGGAACCT	619	19	54.2	330
EST	BQ592708	trinucleotide	288	302	15	12	TGC	CCGCTAAGATTCAAGGAC	132	19	55.7	AAGTGAGAGAAGACCAAGTGA	510	21	54.1	379
EST	BQ592732	tetranucleotide	99	110	12	8	CCAC	CCGCTCTCTCTCTCCACTT	62	21	54.4	AGGTCCTACCAAACTCAGG	396	21	55.1	335
EST	BQ592758	trinucleotide	452	472	21	11	AGT	CCCGCTACTCAAGTCTACAA	7	21	54.9	CAAAAGTTACCAAAACCAATAA	328	21	54.5	322
EST	BQ592766	trinucleotide	339	353	15	12	AAC	CAATGAGGAGTAGAAATGAA	168	21	54.5	TGAATAGACGAAGGAGACAGA	542	21	55.1	375
EST	BQ592768	pentanucleotide	240	254	15	10	TTGAG	CACCTCATCTCACATCATCTC	221	21	54.7	CTTCAATAACATCACAATTCT	386	22	53.9	166
EST	BQ592768	trinucleotide	230	239	10	5	TTGAA	CCTTGACGAGTGGTGTGA	205	18	55.4	GCTAAGTTGGAGAAGAAGAG	491	21	55.3	287
EST	BQ592782	trinucleotide	270	281	12	9	GCG	CTTCTCTCAACCTTCAAC	92	19	54.7	GCCACGATAAAGTCCTAC	434	20	53.9	343
EST	BQ592792	trinucleotide	406	417	12	9	GAT	TTTGTTTGGTCTTCTCAGT	208	20	55.0	AAATACACGCCAAGGTAAA	324	20	52.0	117
EST	BQ592797	trinucleotide	174	185	12	9	TCT	AGCATCTGGGTATTCTGTGT	307	21	55.5	TTCCTCTCTCTCTTAAGTGTG	555	22	53.1	249
EST	BQ592805	trinucleotide	122	145	24	21	AAC	CTTCAACTCTTCACTACCTCT	138	21	55.1	ATACCAAGCAATTTTCAACA	443	21	54.7	306
EST	BQ592815	dinucleotide	102	111	10	8	TC	CCTCCTCTCACTCCACTCTC	6	21	55.7	GCGTAGGATTAGGTATTGGTT	293	21	55.1	288
EST	BQ592824	trinucleotide	433	444	12	9	AGA	CTTCAATTGTTTCTTGACATT	32	21	54.4	GCTACTACACCCGCTATTTCT	349	21	55.4	318
EST	BQ592827	trinucleotide	129	152	24	14	TCT	CCAAACAAGTCTCAACAATCTC	273	21	54.8	CAATCTGTCTCTCCATCC	595	19	55.4	323
EST	BQ592833	dinucleotide	57	68	12	10	TC	ATTCCCTATTGCCTTCA	93	19	54.8	TATCTCTTGTTCACATAACCA	254	21	54.8	162
EST	BQ592841	dinucleotide	164	173	10	8	AG	CAACATCTACATTTCCAAACA	22	22	55.3	CGTCCCAAGGACACATAG	383	18	53.9	362
EST	BQ592857	trinucleotide	171	182	12	9	AAC	TGGTGGGAAGGTGAAGAA	61	18	57.4	AAACGCAAGCAAAATCTC	218	19	55.3	158
EST	BQ592858	dinucleotide	191	202	12	10	TA	CATCCATCTCAACACAAATAAG	80	22	54.9	TTCATTTCCCAATAATAAC	278	21	54.2	199
EST	BQ592868	tetranucleotide	424	439	16	12	TTGT	ATTAGGGGATAGTAAGAAA	108	21	52.9	CTGATGGAAGTTGTAGTGGAG	260	21	54.9	153
EST	BQ592874	trinucleotide	210	221	12	9	CGA	TATCCCTCCCTATCTTCAAC	154	21	54.9	GTAGCCATTTCTTTCATTC	501	20	54.8	348
EST	BQ592874	trinucleotide	274	285	12	9	GAC	TTCTTGCTTTCATACACTCC	74	21	55.5	GTTAGGGTTAGGGTTAGGGTT	389	21	55.5	316
EST	BQ592878	trinucleotide	128	139	12	9	TGG	GCAATCTTCTCTTCTCTCTC	26	21	55.0	AACCCCTAACCCCTAACCCCTACT	249	21	55.1	224
EST	BQ592878	trinucleotide	349	360	12	9	ATG	AGTAGGTTAGGGTTAGGGTT	229	21	55.1	GACCAGTCTTTCATTGTGT	500	21	54.2	272
EST	BQ592886	trinucleotide	81	92	12	9	TCT	TTTAGGAGAGAGAAGAAGAAA	17	21	50.5	CGTCAACAAGAAGAAGAATGAG	301	21	55.2	285
EST	BQ592892	dinucleotide	365	374	10	8	CT	TTAGACTTGATTGGATTTCAG	222	22	54.6	TGAGTTGGTGTGTTGAGA	471	19	55.0	250
EST	BQ592892	trinucleotide	378	395	18	8	CCA	TTAGACTTGATTGGATTTCAG	222	22	54.6	TGAGTTGGTGTGTTGAGA	471	19	55.0	250
EST	BQ592899	trinucleotide	589	606	18	15	CTG	TACTGTCTCTCGGTCATAA	379	21	55.0	AGTTGTGCCCTCCACATC	637	18	56.8	259
EST	BQ592903	trinucleotide	363	374	12	9	GAT	GCTGCTATTCTCTCTCTCT	224	21	54.8	TTTCTTCTTCTCTCACGCA	519	19	55.4	296
EST	BQ592918	trinucleotide	185	196	12	9	TAG	TACCTTCACTACTTCCACCAG	142	21	54.5	TGGGTCACACTTCTGCTAC	516	21	54.6	375
EST	BQ592922	dinucleotide	95	106	12	10	GT	ATAAAGAAGACGAAGAAGA	64	21	50.3	CATCAGAACCACCCAGGAA	398	18	55.2	335
EST	BQ592927	trinucleotide	44	64	21	18	CCA	TTTCACACACACACAATCT	9	21	54.8	GGGTTTCAGAGAGATTAGGA	324	21	55.2	316
EST	BQ592927	trinucleotide	65	76	12	9	CAA	TTTCACACACACACAATCT	9	21	54.8	GGGTTTCAGAGAGATTAGGA	324	21	55.2	316
EST	BQ592927	trinucleotide	103	114	12	9	CTC	TTTCACACACACACAATCT	9	21	54.8	GGGTTTCAGAGAGATTAGGA	324	21	55.2	316
EST	BQ592935	trinucleotide	488	499	12	9	TGC	CTACCAAGACACTCAACTCCA	291	21	55.4	AACTCCGTAACCTCAATCT	562	20	55.3	272
EST	BQ592946	trinucleotide	377	388	12	9	TGG	CTACCTCTACCTCTACCTCA	115	21	54.1	CAACCATATTACCACTTCTT	452	21	55.0	338
EST	BQ592952	tetranucleotide	207	218	12	8	ACTT	AAGCAACCTTCTCACACTTTC	23	21	56.2	GAGTCTTTATGTACCTCCACAA	343	23	55.2	321

EST	BQ592966	trinucleotide	103	114	12	9	CAT	CATCGGATTCTCAGCCC	74	18	62.8	AATACTTTGACCTTGCTCTCA	426	21	51.6	353
EST	BQ592988	dinucleotide	54	63	10	8	AG	GGGCTATTGAGAAAGATG	25	19	53.4	CTGTTGATTACCCCTCGCT	398	19	55.4	374
EST	BQ593004	trinucleotide	359	370	12	9	TGC	TGAAACTCTTACTGTCTTGG	290	21	54.9	CTTATCTCAAACTCCTCCTC	556	21	54.9	267
EST	BQ593011	trinucleotide	439	450	12	9	GGT	CAAGTTCTGGATTGTTCTTGG	120	21	55.0	TTATGATTACGCTTTTCC	492	18	51.1	373
EST	BQ593028	trinucleotide	155	169	15	12	TCC	CATCAAGAGAGAGAGAGGGAG	27	21	55.8	GCTAAGAGTGGCAGATAACC	213	20	54.2	187
EST	BQ593050	dinucleotide	141	154	14	12	CT	ACTCCACCTTCAACACTCTCT	73	21	55.5	TCCTCTCTCTTAGCAACTCC	421	22	54.9	349
EST	BQ593050	trinucleotide	410	424	15	12	AAG	AAAGTCATCTCAAGAGACAA	271	20	55.9	CAGAAGTCACCTCCATAAGT	568	21	55.8	298
EST	BQ593061	trinucleotide	366	377	12	9	ATG	ACTCCACCTTCAACACTCTCT	73	21	55.5	TCCTCTCTCTTAGCAACTCC	421	22	54.9	349
EST	BQ593118	trinucleotide	102	113	12	9	GCA	TATTGAAAGGTGGCAGAG	35	19	53.9	GTGGTAGTGGCTCAGGTAG	343	20	54.9	309
EST	BQ593118	trinucleotide	295	321	27	17	CCT	ATTCCTCTCTCCCTCTCC	213	19	54.8	CTTCACATCTTCATCACCTC	500	21	54.7	288
EST	BQ593132	trinucleotide	398	409	12	9	TGA	ATTCCTCTCTCCCTCTCC	213	19	54.8	CTTCACATCTTCATCACCTC	500	21	54.7	288
EST	BQ593132	dinucleotide	49	66	18	15	TCA	TTCTCTCTCATCATCACCATC	18	21	55.1	TCCTCGACAAATACAACTCT	159	21	54.1	142
EST	BQ593132	trinucleotide	351	360	10	8	CT	CAAGAAGTTGATTGTCGGAG	138	21	55.1	TCGTTGAGGAGTATTAGTGA	404	21	55.0	267
EST	BQ593134	trinucleotide	485	496	12	9	AGA	CTCATCTCTCTCTCTGGTTTC	244	21	55.6	AATGCTGCTTGGCTCTCT	566	18	56.2	323
EST	BQ593137	trinucleotide	352	363	12	9	GAT	AAACTGAAACAACAGGTCAA	240	21	54.9	CATAGGTATGAAAGCCCA	407	19	53.7	168
EST	BQ593142	tetranucleotide	134	149	16	12	CATT	TATTATTGGCTTCACCTTCC	31	21	56.0	AATGCTGCTTGGCTCTCT	244	21	55.0	214
EST	BQ593149	trinucleotide	169	180	12	9	CTC	CAAAGTCAATCAGAGAGAGA	15	21	54.6	GGTATCATCAGGGAGGGA	395	18	55.6	381
EST	BQ593198	trinucleotide	278	295	18	15	TTG	CGTTTCATCCCTCTTTCCA	128	18	57.0	GCATCACTAAGGACCACAAA	400	20	56.2	273
EST	BQ593202	dinucleotide	59	70	12	10	GA	GAGAGAAACAGAGAGCAGA	25	21	54.0	GGTCATCCATAAATCCCAA	324	19	55.6	300
EST	BQ593239	trinucleotide	100	117	18	15	AAC	CATCCAACCTACGCTGTT	63	18	55.5	TTTCAAGATTACGGTTTACGA	318	21	55.2	256
EST	BQ593242	trinucleotide	174	191	18	15	CAT	TGCTGAAACCAATAAGAAAC	126	21	54.4	GGGAGAGAGAAAGTAAGGAGA	246	21	54.4	121
EST	BQ593245	trinucleotide	243	254	12	9	TCT	TTGCGGTGAACAGTATGAA	156	19	56.1	GATTGATTGAAGATGGTGAAA	289	21	55.1	134
EST	BQ593271	trinucleotide	158	172	15	12	GGA	CCACTCTCTCTCTCTCC	22	18	54.6	GGGTGCATCAACACCTAATC	359	21	54.4	338
EST	BQ593273	trinucleotide	213	224	12	9	AAC	AAGAAACTCATGTCCTGG	142	21	56.0	AGGGTGCAATCAACCATCA	483	18	57.2	342
EST	BQ593280	trinucleotide	344	355	12	9	TCC	ATAATCAATGTCGCCACAC	253	21	57.5	TACAAAGCGAAGAGAGATG	560	20	53.3	308
EST	BQ593315	trinucleotide	202	213	12	9	CGC	TCTTCATCTCATCTCTCTCA	122	21	55.0	AATCCCTTCTATAATCCTTAC	348	21	54.8	227
EST	BQ593316	trinucleotide	75	92	15	10	CTA	CCGCTCTTGTCTCTTCTT	9	19	54.8	ATCATCCCATTCCTCAATACA	219	20	55.2	211
EST	BQ593317	pentanucleotide	346	360	15	10	AATCA	TGTTGTTGTTCTGATGTTCC	307	21	55.3	TAATGAGCTGCTTTGTTGTT	487	21	55.1	181
EST	BQ593317	trinucleotide	280	291	12	9	TTA	TTTCTTATTTCTCTCTTGACC	58	22	52.5	TGTTGTTGTTGATTGATTGA	367	21	54.3	310
EST	BQ593319	trinucleotide	337	348	12	9	GAA	GACTGSGCTGCTGTAATGG	136	18	54.9	CCTTCTCTCTCATCAAGTTC	467	21	53.3	332
EST	BQ593338	trinucleotide	351	368	18	15	TAA	ATCAACTCTCTCCCAACTTC	40	21	54.9	ATGATAAGATTTCACACGCA	437	19	54.1	398
EST	BQ593342	trinucleotide	288	305	18	15	TAA	AGAGAAATGAAAGAAATGGTAA	219	22	54.8	CACCTGAAATACAAACACCC	362	20	55.4	144
EST	BQ593344	tetranucleotide	197	216	20	16	TCTT	TGTGTTTGTGTTTGTGTTGT	39	21	54.9	GAGATGACCGTGAAGATGATG	352	21	54.8	314
EST	BQ593366	dinucleotide	85	98	14	12	CT	ATCTTCACTCTCCCTCTCC	25	20	54.9	GTTACTCTTCACCTCCGCC	424	19	54.9	400
EST	BQ593369	dinucleotide	63	76	14	12	GA	GGTGATTGGCGTCTGAAA	13	18	58.1	TATGATGCTGCTGCTCTACTG	119	21	55.6	107
EST	BQ593374	trinucleotide	225	242	18	15	AAC	TGTTTGGTGGAGGAGAGAG	142	20	55.2	GATAAGCGGATTGATTCTT	319	21	55.2	178
EST	BQ593375	trinucleotide	103	114	12	9	GCA	TATTGAAAGGTGGCAGAG	36	19	53.9	GTGGTAGTGGCTCAGGTAG	344	20	54.9	309
EST	BQ593380	trinucleotide	197	208	12	9	ACA	AATGAAAGTGAAGCGATAA	137	20	55.1	ATTGGAAGCAAGTGAGTGAG	337	20	55.4	201
EST	BQ593391	trinucleotide	55	66	12	9	AGA	GCAGCTCTTCTCTCTCTTTC	11	21	55.2	ATCCACCTGTTCTCTCTTG	365	19	55.0	355
EST	BQ593392	trinucleotide	344	355	12	10	GA	CCTACATCAGCAGGTGTGA	224	19	55.4	TGTGTTACGAAATCTCCTCCT	414	22	54.9	191
EST	BQ593394	trinucleotide	357	371	15	12	CGC	TTCTCTCTCTCATCAACTCCA	254	21	55.0	GTCATGTTCCATCTCTCATC	425	20	55.4	172
EST	BQ593408	trinucleotide	192	212	21	18	CAC	TCCTCTCTCTCTCTCTACTG	56	21	55.3	GATGATGGTGGTGGTGATT	242	19	56.4	187
EST	BQ593408	trinucleotide	237	254	18	15	CAT	CACCAACAACAACAACAACA	206	20	56.3	TGAATAACAGGAGTATCACCA	426	22	54.9	221
EST	BQ593418	trinucleotide	213	224	12	9	AAC	TTGGATTGGTGGAGGTAGT	156	19	55.3	TCGTGGTATTGAGATGAAA	531	21	53.3	376
EST	BQ593423	trinucleotide	174	185	12	9	GAT	TTGGATTGAAGAGTATGATG	41	21	55.2	GGAGGTGAAAGAACCACTGT	237	20	56.6	197
EST	BQ593423	trinucleotide	253	267	15	12	CCG	CTCTCTCTCCCAACCGTAA	134	19	55.4	ACAAGCAGTAACCAACACT	532	21	54.9	399
EST	BQ593423	trinucleotide	440	454	15	12	TGA	CATCTTCTCTCTCTCTCCAAAC	267	21	55.6	ACAAGCAGTAACCAACACT	532	21	54.9	266
EST	BQ593423	dinucleotide	133	142	10	8	CT	GGAAGGTGAAGAAACATAGA	5	23	53.8	GTTTGGAGGAGAGAGAAGATG	287	21	55.6	283
EST	BQ593450	dinucleotide	111	120	10	8	AC	CTCTTCTCTCTCTCTCTCC	29	20	54.8	ATGAACAGGGTTTAGCTT	318	19	51.5	290
EST	BQ593455	trinucleotide	193	207	15	12	CCA	CTCCCTCAACTCTCTCTCT	148	20	55.2	AGTAGAACATCGTCGCCCT	519	19	51.5	372
EST	BQ593479	dinucleotide	55	90	36	27	AG	GACTATGCTTCTGTCTCTGA	20	21	54.7	TAAACCTCCCTCTCCACA	185	18	53.8	166
EST	BQ593484	trinucleotide	70	81	12	9	TGC	AAGATTATGACCCGTTTAGG	25	21	55.1	ACAGAGGAGGAGTATGAGAG	404	21	55.2	380
EST	BQ593490	trinucleotide	123	158	36	26	CAC	AAACAAGATGGCTCTCAC	62	19	55.2	ATCTCGCTTAGTTGTCGT	332	21	55.6	271
EST	BQ593490	trinucleotide	225	238	12	9	AAC	GTCTCCACTTCTCTCTCTCT	194	21	54.7	ATCTCGCTTAGTTGTCGT	332	21	55.6	139
EST	BQ593494	dinucleotide	162	175	14	12	GA	CCTTCTATCTCTCTCTCTCG	98	19	55.0	AGGATGTTGTTGATGATG	489	19	51.3	392

EST	BQ593498	trinucleotide	470	481	12	9	ATG	AAC	TACTGAACCCAAACACAGA	197	21	54.8	CTTCGCTCTATCACACCCAAAC	558	20	55.6	362
EST	BQ593509	dinucleotide	191	222	32	30	GA	TAC	ACTTCAGACACTGCTTGG	97	21	56.5	CTCTTTCTTTATCGGCACCTC	292	20	54.4	196
EST	BQ593512	trinucleotide	48	59	12	9	ACT	GG	ATTGTTGGCTCTGGTC	16	18	56.4	AAAGCGTGAGTGGGTGG	245	18	62.1	230
EST	BQ593520	dinucleotide	428	439	12	10	AT	TTG	CTGCCATAATCAGT	102	18	55.0	TAGTAACATAATCTCCAGCC	470	21	53.7	369
EST	BQ593535	dinucleotide	115	146	32	30	AG	TAT	CATCGTCTTCATCACTCC	49	21	55.1	CAAGTCTAAAGGTGTGCTGCT	228	20	55.0	180
EST	BQ593538	dinucleotide	283	310	28	26	GA	TTG	TTCCGCTTTCATGATGT	62	20	55.0	ACGATAGGGTGTGTGATGAG	341	20	55.9	280
EST	BQ593538	tetranucleotide	259	282	24	20	GTGA	TTG	TTCCGCTTTCATGATGT	62	20	55.0	ACGATAGGGTGTGTGATGAG	341	20	55.9	280
EST	BQ593552	dinucleotide	356	369	14	12	AT	GC	ATTCTCAGCTTCTCTCTT	261	20	54.7	GTCCCTTGTCTGCTTGATT	418	18	56.1	158
EST	BQ593553	trinucleotide	277	291	15	12	ATC	GC	ATTCTCAGCTTCTCTCTT	12	21	55.3	TAGCAGTCTCCCTCTCTCTCT	374	21	55.1	363
EST	BQ593566	trinucleotide	108	119	12	9	ACA	TC	AACAAACCTTAACTCAA	34	21	55.0	GAGCAGAGCAGAAGGTG	227	18	57.1	194
EST	BQ593579	trinucleotide	148	162	15	12	CAA	CTT	CTCTTTAGTTCAOCCCT	23	21	54.8	CTCTCTCTCTCTCTCTCTCGGT	211	21	55.1	189
EST	BQ593579	trinucleotide	195	206	12	9	GAA	ACA	CAACTCTTGAAGAGGACAA	155	21	54.9	GAAGTGAAGACAGAGGAGAAG	337	21	55.7	183
EST	BQ593583	dinucleotide	57	68	12	10	AG	CAT	CACCAAGAAATACCCAGA	25	20	56.0	ATTTCCACGAAGAGTTTCATT	318	21	55.5	294
EST	BQ593631	pentanucleotide	446	460	15	10	CTTTG	GAA	GTACAAAGATTTCAGCC	386	21	53.4	GGCATAGGTGAGAGAGAC	518	19	54.6	133
EST	BQ593659	dinucleotide	39	55	18	9	CT	CTA	CTACCCCTCCACCTT	7	19	53.3	ATTGTCTTCCAACTTCA	406	19	50.5	400
EST	BQ593666	trinucleotide	134	145	12	9	GCA	CAG	ACTTACGATAGTTGGACAG	61	22	54.3	AAAGATTAGGCAACCCAG	348	20	56.1	288
EST	BQ593678	trinucleotide	93	104	12	9	TAG	CA	TGAAGTGTGGTGAAGATA	41	21	50.4	GGCAGTGAAGAAAGGTCTC	259	19	54.8	219
EST	BQ593679	trinucleotide	195	213	18	9	CCA	TC	ACCATTAATCTCTCTCTT	79	22	54.7	GAGCGTAACATAAGAAATCAG	456	21	55.2	378
EST	BQ593693	trinucleotide	165	176	12	9	ACC	GAG	ACGGGAACACCCACAG	114	18	59.0	GACATAAGGAGGAGACATTGA	421	21	55.4	308
EST	BQ593698	trinucleotide	245	259	15	12	TCT	CTG	TTCTCTCTCTCTCTCTT	209	21	54.8	ATTTCTCAGTCTCTCTCGCT	399	21	55.9	191
EST	BQ593698	trinucleotide	224	235	12	9	TCT	GA	AGTAGAGAGATGGCTGTGA	68	21	54.6	GGATTGGAAGAAAGAAAGAA	266	21	55.2	199
EST	BQ593702	dinucleotide	241	250	10	8	CT	TC	TCTCCAACTCTGAATCTCC	147	21	56.0	CGAAGTGAACATAGCAAGAA	304	20	54.1	158
EST	BQ593703	trinucleotide	225	236	12	9	GAC	ATG	ATGCTCTTGGTGGTCT	12	19	55.5	CGTTACAGTCTTAGTGTCTT	318	21	53.9	307
EST	BQ593703	trinucleotide	285	296	12	9	GAC	AG	TACGCGAGAAGAACGCA	209	20	55.4	GTTGTTCCGACCACATACAG	362	19	53.8	134
EST	BQ593712	trinucleotide	222	242	21	18	CCA	CA	TCTTCACTCTCTCTCTTAC	161	22	53.2	GAAGTAGGTGCTTGGCT	298	18	55.4	138
EST	BQ593732	trinucleotide	84	95	12	9	GAT	AT	CCCACTTCTCTCTCTCTG	44	21	55.1	CACCATCTCTCTCTCTCTCT	158	21	55.0	115
EST	BQ593733	trinucleotide	425	439	15	12	GAA	CC	CTCAGAGTCTATTCAAG	222	20	55.1	TTCACTCTGAACGACATCCTC	514	21	55.2	293
EST	BQ593756	trinucleotide	32	43	12	9	CGC	CC	TCCACCACTACGCAAC	3	18	57.6	CTTCTTCACTTCCATTCATCTC	315	21	57.2	313
EST	BQ593761	trinucleotide	177	188	12	9	AGA	AG	CACTTCTTGTGGGTAA	118	20	54.9	ATTTGGGTAACACTCTTGGAC	465	20	54.0	348
EST	BQ593770	dinucleotide	179	188	10	8	CT	AA	ACCCATCTTCCCTAA	142	18	52.0	ACATACCCAAACTCATCCAC	536	20	54.7	395
EST	BQ593772	trinucleotide	293	313	21	18	ATC	TAC	TACGCGCAAGTTTCAATC	240	20	55.4	TACCATACCCCTCAATCTC	366	21	54.2	127
EST	BQ593772	trinucleotide	329	340	12	9	TGA	TAC	TACGCGCAAGTTTCAATC	240	20	55.4	ACTACTACATACACCTCTCAA	371	21	51.4	132
EST	BQ593781	trinucleotide	311	331	21	11	AGT	AA	CCACCAACAACTATTCAAG	257	21	54.3	TTCTATCAATACCATCATGAG	540	21	55.2	284
EST	BQ593788	trinucleotide	90	107	18	8	ACA	CG	TGAATACAAAGACCTAA	10	21	54.9	GCAATGGTTGGAGAAAGTAGA	241	20	55.4	232
EST	BQ593800	trinucleotide	206	217	12	9	CTC	CA	CACTATTACCAATTTCCACC	109	21	56.0	ATTTGAGAGCATGAGTGAAG	310	21	54.7	202
EST	BQ593809	dinucleotide	68	81	14	12	TC	CT	CACTCTCTCTCTCTCTCT	11	21	55.2	ATTTCCACTTCTCACACC	363	19	54.8	353
EST	BQ593832	dinucleotide	365	374	10	8	CG	AA	TGGAACGAATAGGAAGAG	243	21	55.2	CTGTCAAGGGAACTCAAGA	531	21	55.0	289
EST	BQ593848	dinucleotide	154	165	12	10	TC	AT	AAGAGCAAAAGACTGGAA	57	21	54.3	GTGAGAACAAAGAGGAGAACA	197	21	54.5	141
EST	BQ593858	trinucleotide	93	104	12	9	CAC	TT	CACTTCCCACTTTCTCTCT	1	21	55.6	GCTCAGTAACAAACAGCCA	390	19	54.9	390
EST	BQ593860	trinucleotide	470	481	12	9	ATG	AA	CTACTGAACCCAAACACAGA	197	21	54.8	CTCAACTGCTCCAACTCCT	532	19	55.4	336
EST	BQ593888	trinucleotide	102	116	15	12	TTC	TT	CTTCTTCTCTCTCTCTCT	38	19	54.7	TCCTCCACCTTCTACAAACA	370	21	55.0	333
EST	BQ593890	trinucleotide	98	109	12	9	CTT	GA	CTTCTCTCTCTCTCTCTCT	51	23	54.4	GCCTTAAACCTCGCAAAAC	225	19	57.6	175
EST	BQ593892	trinucleotide	277	291	15	12	ATC	GC	ATTCTCAGCTTCTCTCTT	12	21	55.3	TAGCAGTCTCTCTCTCTCTCT	374	21	55.1	363
EST	BQ593892	trinucleotide	423	434	12	9	GAA	TC	AGATAAGAGAGAGAGGAGA	347	22	55.0	GCAGGTTAGTCGGTCAG	575	18	54.1	229
EST	BQ593896	trinucleotide	30	44	15	12	TGG	CT	GTGAATCGGACAAAG	1	18	55.1	CAGCCACCCACTATCA	181	18	56.3	181
EST	BQ593896	trinucleotide	303	314	12	9	TGG	GA	ATCGGACAAAGAGACAGA	141	20	55.3	AGCCACCCACTATCAT	450	19	55.3	310
EST	BQ593909	trinucleotide	43	54	12	9	TAC	TT	CTCTTCTCTCTCTCTCTCT	10	21	54.6	TAAGTATAGTGGTGGTGGT	187	21	57.1	178
EST	BQ593909	trinucleotide	100	111	12	9	TAG	TT	CTCTCTCTCTCTCTCTCT	10	21	54.6	TAAGTATAGTGGTGGTGGT	187	21	57.1	178
EST	BQ593933	trinucleotide	158	169	12	9	ACC	TC	TCTGCGATCAACCCCTG	63	18	55.4	GAAACGAAGAAAGAAATTTGA	318	21	54.7	256
EST	BQ593939	trinucleotide	49	66	18	15	AAC	AA	ACACACAAACCAACCTAAA	16	21	54.8	GTGGAAGAAAGAAAGGAGA	156	21	55.3	141
EST	BQ593939	trinucleotide	105	122	18	15	AAC	AA	ACACACAAACCAACCTAAA	16	21	54.8	GTGGAAGAAAGAAAGGAGA	156	21	55.3	141
EST	BQ593939	trinucleotide	143	154	12	9	TTC	AA	ACACACAAACCAACCAAA	104	20	52.3	TGAAGAAGAGAGTTTGAGAGAG	205	23	54.9	102
EST	BQ593939	trinucleotide	167	178	12	9	TAC	TT	CTCTCTCTCTCTCTCTCT	134	21	54.6	TAAGTATAGTGGTGGTGGT	311	21	57.1	178
EST	BQ593939	trinucleotide	224	235	12	9	TAG	TT	CTCTCTCTCTCTCTCTCT	134	21	54.6	TAAGTATAGTGGTGGTGGT	311	21	57.1	178
EST	BQ593982	tetranucleotide	199	210	12	8	GCGA	GA	TTCTCTCTCTCTCTCTCTCT	55	21	56.2	ACACTGAAGCATCAACCACCT	301	20	55.7	247

EST	BQ593984	dinucleotide	73	82	10	8	AG	21	55.7	ACATCAACAACCCCTAACTGTG	299	21	55.1	277
EST	BQ593989	trinucleotide	247	258	12	9	CAA	21	54.9	ATTATCAGTATCACCAGCACC	333	21	54.2	272
EST	BQ593997	trinucleotide	143	157	15	12	GAC	19	55.4	GCACACCACTTCATCACTT	271	20	56.1	208
EST	BQ593998	trinucleotide	265	276	12	9	GAA	18	56.9	AAAGACGAAGATGAGGACAG	416	20	54.5	195
EST	BQ593999	trinucleotide	427	447	21	18	AAG	19	56.3	TATCATCAGGATTTCTTCATT	494	22	54.2	216
EST	BQ594011	trinucleotide	161	172	12	9	TAA	21	55.1	CCGATGAGATACACTGAAGA	226	21	55.4	181
EST	BQ594021	trinucleotide	187	198	12	9	GAT	18	53.1	TGTAATCGCTGTTTCCCTCT	269	20	55.2	147
EST	BQ594025	trinucleotide	345	356	12	9	ATG	21	53.9	ATCAGTTTCAGCATCACCA	408	19	54.9	173
EST	BQ594038	dinucleotide	202	213	12	10	GA	20	54.7	CAAGACGGAGAGATAGTCAA	248	21	54.8	170
EST	BQ594043	trinucleotide	74	85	12	9	GAA	21	55.3	CGTAAAGATGAGTAGG	212	22	54.9	175
EST	BQ594049	dinucleotide	204	213	10	8	CT	21	55.9	TACTTCAACATCCAAAGA	423	20	51.5	340
EST	BQ594053	trinucleotide	96	113	18	15	CTC	22	54.8	GTAGTCTCTGCCACCAC	248	19	55.6	226
EST	BQ594062	tetranucleotide	193	208	16	12	AAAG	22	54.6	GAGAGTTGGTGGCTTGTG	415	18	54.9	255
EST	BQ594062	dinucleotide	325	340	16	12	TTTC	21	55.2	GAGTTGGTGGCTTGTGATT	413	19	56.0	201
EST	BQ594062	trinucleotide	219	235	18	9	TC	21	55.2	AAACTCTGAAAGAAAGAAAGAA	346	23	53.8	163
EST	BQ594102	trinucleotide	299	313	15	12	GCT	21	54.7	ATCGGTTGGTGAATTCCTT	401	19	54.8	283
EST	BQ594118	tetranucleotide	81	92	12	8	TCTT	18	56.0	ATTCACTTCACTTCACTTGTCT	159	21	56.3	109
EST	BQ594138	trinucleotide	390	401	12	9	TGA	21	55.0	ATCACTCCGCGCCCTCT	443	21	54.5	359
EST	BQ594140	trinucleotide	49	63	15	12	AAC	21	55.2	CGCTCTTCTCCGATAA	391	18	58.9	319
EST	BQ594140	trinucleotide	195	206	12	9	TCC	21	54.8	TAAGTATCCGAAATCCCAATC	480	21	55.8	283
EST	BQ594143	trinucleotide	345	359	15	12	AAG	18	56.4	AAAGCTGGAGTGGGTGG	245	18	62.1	230
EST	BQ594145	trinucleotide	48	59	12	9	ACT	21	55.2	GATACCCATCTCCATCC	402	19	54.9	363
EST	BQ594149	trinucleotide	161	172	12	9	TCC	21	55.3	ACATCAACAACCCCTAACTGTG	298	21	55.1	273
EST	BQ594168	dinucleotide	72	81	10	8	AG	21	55.0	AATAATCCGATTCACCAAG	410	21	55.7	375
EST	BQ594169	dinucleotide	171	182	12	10	CT	21	54.9	CTCTTCTTCTCATCTTCA	317	21	55.0	127
EST	BQ594197	trinucleotide	257	268	12	9	GAT	21	54.9	CTTCTGCTATTAACAATCGG	416	21	54.5	363
EST	BQ594216	trinucleotide	240	251	12	9	TTC	22	55.0	GAAGTGGTAGTGGAAAGTGA	238	20	55.1	222
EST	BQ594240	trinucleotide	153	167	15	12	AAC	21	54.9	TGTTGTTGTTGTTGTTAGGT	168	22	54.9	157
EST	BQ594240	trinucleotide	103	114	12	9	AGT	21	54.1	TGTTGTTGTTGTTGTTGTT	345	21	54.9	303
EST	BQ594264	pentanucleotide	200	209	10	5	TTCAA	20	55.3	AACATGACCGAACGCAA	364	18	55.2	315
EST	BQ594276	trinucleotide	90	101	12	9	TCT	20	55.5	GCTTATAGGAACCACTTC	361	20	56.3	296
EST	BQ594289	trinucleotide	283	294	12	9	GAT	18	55.4	GAAACGAAGAAAGAAATGTGA	318	21	54.7	256
EST	BQ594293	trinucleotide	158	169	12	9	ACC	18	54.4	AGTTCTGTATGCTCTCTCA	393	21	55.2	142
EST	BQ594304	trinucleotide	345	356	12	9	ATG	18	55.8	TGTTGTTGTTGTTGTTGTT	127	21	54.2	128
EST	BQ594305	trinucleotide	53	70	18	15	AAC	21	54.2	GTGGAAGAAAGAAAGGAGA	160	21	55.3	109
EST	BQ594305	trinucleotide	109	126	18	15	AAC	20	52.3	TGAAGAAGAAAGTTTGAGAGAG	209	23	54.9	102
EST	BQ594305	trinucleotide	147	158	12	9	TTC	21	54.6	TAAGTATAGTGGTGGTGGT	315	21	57.1	178
EST	BQ594305	trinucleotide	171	182	12	9	TAC	21	54.6	TAAGTATAGTGGTGGTGGT	315	21	57.1	178
EST	BQ594305	trinucleotide	228	239	12	9	TAG	19	55.8	ATACTTGAATGCCCTCTCTTC	331	21	55.1	317
EST	BQ594310	trinucleotide	167	178	12	9	GAA	20	54.1	AAACCTCTCTCTCTCTCTCTC	127	22	55.1	100
EST	BQ594332	tetranucleotide	68	83	16	12	ATGC	21	55.1	CAGATTAGCAGCAGCATAAG	573	21	55.5	214
EST	BQ594335	trinucleotide	454	468	15	12	GGT	21	54.7	TGTCGCTCTCTTAATCATCTT	380	21	55.1	193
EST	BQ594335	trinucleotide	227	238	12	10	TC	19	56.3	TGTCGCTCTCTTAATCATCTT	380	21	55.1	336
EST	BQ594335	trinucleotide	86	97	12	9	CAA	18	55.7	AGTTGGAAGATAACGAAGGAG	141	21	55.2	124
EST	BQ594344	trinucleotide	84	95	12	9	TAC	21	54.9	TATCAACTCTCTCCACATACA	426	21	55.5	334
EST	BQ594365	pentanucleotide	127	136	10	5	CTCTC	19	53.8	CACACACACACACAGAGAGAG	244	21	55.1	173
EST	BQ594368	dinucleotide	160	175	14	12	TC	20	54.5	ATCCAAGAGGTTCTCCCA	619	18	55.3	392
EST	BQ594368	trinucleotide	144	157	14	12	TC	22	54.8	TAGGAATGCTGGTAGAAGA	289	21	55.1	172
EST	BQ594374	trinucleotide	507	521	15	12	GAT	21	55.1	AGTTTACCAATTCGACCA	444	19	55.7	392
EST	BQ594382	trinucleotide	215	226	12	9	ATC	21	55.3	TATGATCACCACCAACCACC	539	20	56.5	256
EST	BQ594383	trinucleotide	84	101	18	15	TCT	23	52.4	CAACTGGTGGAGACGATT	476	18	54.2	328
EST	BQ594384	trinucleotide	440	454	15	12	GGT	18	55.0	GTTGATGTTGTTCTTGGTGT	197	21	55.0	191
EST	BQ594393	trinucleotide	428	442	15	12	GCT	21	55.3	ATTTCGTTTCATCATCACTCC	433	20	54.9	169
EST	BQ594397	dinucleotide	45	54	10	8	AC	21						
EST	BQ594401	trinucleotide	351	362	12	9	GAT	21						

BQ594401	EST	trinucleotide	369	380	12	9	GAT	GTGGATTTCTCTGTCTCACAA	265	21	55.3	ATTTTCGGTTTCATCATCACTCC	433	20	54.9	169
BQ594409	EST	trinucleotide	150	161	12	9	GAT	ATTCTCTCTCTCTCTCTCTCT	94	21	55.3	TAGGGTATCTCTCAGCATCAA	476	21	55.1	383
BQ594414	EST	trinucleotide	351	362	12	9	ACC	TGTGCTCTTTCTTGTTGTTG	301	21	55.3	CGATGTCTGAAGCCATTAGA	405	20	56.5	105
BQ594431	EST	trinucleotide	262	273	12	9	GAT	TGAACATAGGAGGTTAGGA	208	20	54.7	TTAAACAGCTGTGAAGTTG	450	21	53.2	243
BQ594447	EST	dinucleotide	78	87	10	8	TC	TAACATCCCAGCTCTCTCTCC	46	21	55.9	TCTACACCTCATCATCTTCA	188	21	55.7	143
BQ594448	EST	trinucleotide	214	225	12	9	TGT	CGTCCAAAGATGTGAATGA	138	19	55.4	AAATAATAAAGCAAACCCA	318	19	50.2	181
BQ594471	EST	trinucleotide	207	218	12	9	TCG	CACCTCTGCCCATTTCTCT	147	18	56.8	ACTAAACCATACCCGCCAC	382	19	55.1	236
BQ594475	EST	trinucleotide	327	341	15	12	ACA	GATGGAGGACCAACTCTCTAA	145	21	55.9	CACCACCTGCTTTCATAATC	467	20	55.7	323
BQ594483	EST	dinucleotide	97	106	10	8	AC	GAGGCAGTGAGAGCAAGATG	61	20	54.1	CGCCATAGAAGTGGTAATG	378	19	54.2	318
BQ594496	EST	pentanucleotide	1022	1036	15	10	CACAT	GTAGTAGTGGGTGGATAACA	767	21	55.4	GGCGTTGTAGTGGCGGA	1082	18	63.2	316
BQ594496	EST	trinucleotide	831	842	12	9	TTC	GTAGTAGTGGGTGGATAACA	767	21	55.4	GTGTGGCGCTGAGGAGATT	901	19	63.2	135
BQ594503	EST	dinucleotide	42	51	10	8	TC	CCCACTTCTTTCTCTCTCTCT	0	22	56.1	ATTGCTCTCCAAATGA	236	18	53.9	237
BQ594507	EST	trinucleotide	69	80	12	9	TCT	CCAAACTCTCTTAACACCAA	29	21	54.6	CCAATAATCTCAATCCATCAA	301	21	55.1	273
BQ594515	EST	trinucleotide	355	366	12	9	ATG	TTCTCTCTCTCTCTCTCTCTC	48	21	54.5	CTTCAACAGAACTGATTC	412	20	55.7	365
BQ594518	EST	tetranucleotide	75	90	16	12	TAAC	GGGTGGGCAACATCAAA	17	18	61.6	CAACTCCATCAGCAACAGA	411	19	55.6	395
BQ594521	EST	trinucleotide	285	305	21	18	GCT	TTTGCTTGATGGCTCTCT	183	18	54.4	ATTCTCTCCGACTATGTTG	557	21	55.9	375
BQ594526	EST	trinucleotide	64	75	12	9	CAC	CCCTACCAACCAACACAAA	36	18	56.2	GAGACAAGGACAGAAAGA	304	19	55.1	269
BQ594556	EST	dinucleotide	93	104	12	10	CT	AATCATCTTCCCTTTCTCTC	31	20	54.9	TCGTTTTCTCTCTAAATCTCA	170	22	53.7	140
BQ594582	EST	trinucleotide	186	197	12	9	TCA	AGTGGTCTCCCTTCTCTTCC	48	19	55.7	CTTCGGGTGTAATAGTTGTG	428	21	55.0	381
BQ594697	EST	trinucleotide	223	242	20	18	GA	CAAGACCTCTTAGACACAAA	116	21	54.6	TAAACAATCGCCCAACTCATC	510	20	56.4	395
BQ594726	EST	trinucleotide	123	134	12	9	GAT	GGCTCTCTCTCTCTCTCTCT	10	21	54.2	TATCAATCCCGTGGTTACA	280	19	54.7	271
BQ594728	EST	dinucleotide	45	54	10	8	AC	CGTGGGTTCTACTCTTCTGT	6	19	55.3	GTTGATGTTGTTCTTGGTGT	197	21	55.0	192
BQ594736	EST	trinucleotide	135	152	18	15	CAA	TCACACAACAAACATCAACC	18	20	55.2	AGTCCCTCTCGCATCAACT	376	19	54.9	359
BQ594737	EST	trinucleotide	305	322	18	15	CAG	GCATACCAACCAATCAAGT	181	21	55.1	CGAGAAATACCAACAGGAG	485	19	54.4	305
BQ594746	EST	trinucleotide	96	107	12	9	CGA	AGAGAGAAACGGCATAAAC	31	21	55.4	ATGAATGACTGACGACTGACT	322	21	54.6	292
BQ594754	EST	trinucleotide	158	178	21	11	ACC	CAAGAGGAAGCAGCCGAG	2	18	59.8	ATGAGTGGTAGAGGACGATT	248	21	55.3	247
BQ594760	EST	trinucleotide	79	90	12	9	CTC	TCAACTCAACTTCTCAACTCC	44	21	54.5	TCTCTCTGATCGCATCTCT	305	20	55.2	262
BQ594761	EST	trinucleotide	329	343	15	12	GAT	AATCTCAACAAACAAATCAAC	125	21	54.9	TTCAATACTCCACCATCAAC	493	21	55.0	369
BQ594767	EST	trinucleotide	465	479	15	12	GAA	GGAACTACTAAAGCAAGAGCA	431	21	54.2	ATCAATCAAGACCAACCCAG	625	20	55.0	195
BQ594768	EST	trinucleotide	326	344	20	11	TC	TACAAGACCAACTCACAGTC	206	21	55.2	TCTCACCAAGAAAGACGATTAC	499	21	54.5	294
BQ594784	EST	dinucleotide	36	47	12	10	AG	CGTCCGCTCTCATACTCT	6	19	55.6	GATGTGATTTCTTCTGATT	284	20	51.6	279
BQ594804	EST	trinucleotide	188	199	12	9	AAG	AAGATGGCAAGATAAAGCC	145	20	56.1	CACTGAGACCTTAGCACCC	352	19	55.6	208
BQ594811	EST	trinucleotide	123	134	12	9	GAT	GCTCTCTCTCTCTCTCTCTCT	11	23	54.8	TTGAAATGAAGAATGCCAC	388	19	54.5	378
BQ594823	EST	trinucleotide	305	322	18	15	CAG	GCATACCAACCAATCAAGT	181	21	55.1	CGAGCAAAATCAACAGGAG	485	19	54.4	305
BQ594832	EST	trinucleotide	96	107	12	9	CGA	AGAGAGAAACGGCATAAAC	31	21	55.4	ATGAATGACTGACGACTGACT	322	21	54.6	292
BQ594835	EST	trinucleotide	359	379	21	18	ATC	GGTGAAGAAGCAACAAAGTAA	59	21	54.8	TGGAGATGAAGAAGAAAGAAA	457	21	54.3	399
BQ594835	EST	trinucleotide	532	543	12	9	TTC	CTCTCTTCTCTCTCTCTCAT	490	20	55.1	AGATAAGTGCCATCCAAAGT	600	21	55.5	111
BQ594838	EST	tetranucleotide	115	126	12	8	TTCT	TTCTCCAAAGTTTCTCTCTCT	40	21	54.9	TATTAGCCCTTAGCGTTGT	283	19	52.9	244
BQ594844	EST	dinucleotide	326	344	20	11	TC	TACAAGACCAACTCACAGTC	206	21	55.2	TCTCACCAAGAAAGACGATTAC	499	21	54.5	294
BQ594846	EST	trinucleotide	79	90	12	9	CTC	TCAACTCAACTTCTCAACTCC	44	21	54.5	TCTCTCTGATTCGCATTCT	305	20	55.2	262
BQ594853	EST	trinucleotide	465	479	15	12	GAA	GGAACCTACTAAGCAAGAGCA	431	21	54.2	ATCAATCAAGACCAACCCAG	625	20	55.0	195
BQ594860	EST	trinucleotide	60	71	12	9	CAC	CTCCACCCCAACACTCCAC	17	18	57.3	TCTCTCAGTAGAAACACAGTAA	386	22	51.2	370
BQ594869	EST	dinucleotide	36	47	12	10	AG	CGTCCGCTCTCATACTCT	6	19	55.6	GATGTGATTTCTTCTGATT	284	20	51.6	279
BQ594888	EST	trinucleotide	47	58	12	9	CAC	ATCATCTCTCAATCTCTTCC	0	20	55.5	ATTATGGCGTCTGTTGTT	188	18	54.4	189
BQ594892	EST	trinucleotide	188	199	12	9	AAG	AAGGTTAGATGGCAAGATAAA	140	22	55.0	GGAGGAATGAAGGACTCAAC	276	21	55.4	137
BQ594896	EST	trinucleotide	84	95	12	9	TGC	GTGTTTCTCTGGCTTCACT	18	19	55.3	GAGGCGTATCTTACACATAG	263	21	56.4	246
BQ594904	EST	dinucleotide	178	191	14	12	TC	TTCAATGGTGTGTTCAAGT	106	19	53.8	CACACACACACACAGAGAG	282	21	55.1	177
BQ594904	EST	dinucleotide	196	209	14	12	TG	TTCAATGGTGTGTTCAAGT	106	19	53.8	CACACACACACACAGAGAG	282	21	55.1	177
BQ594913	EST	trinucleotide	80	95	16	14	AC	ACTACTTGTCTTACTTCTCA	16	23	52.6	TTCTGTTATTATTGGGTTTCA	222	22	54.2	207
BQ594915	EST	trinucleotide	386	397	12	9	AAT	GGTTTGGTGTTCGATTGA	120	18	55.0	ACAGATTATTGAGCGGACA	481	20	53.0	362
BQ594945	EST	trinucleotide	132	143	12	9	AGG	AGGAACAGAAACACCCAC	89	19	54.9	ATAAGTTACACCCCATCACAG	239	21	55.0	151
BQ594965	EST	tetranucleotide	347	358	12	8	TTCT	CACACACACAGAGAAACCA	48	19	55.3	AATGAATCGTCTTAATGGAAG	411	21	55.8	364
BQ594976	EST	trinucleotide	341	355	15	12	ATG	AGTTCGGTGGATTCTGTGT	261	19	55.6	ATTATTCACGCCACCCACTT	539	20	56.2	279
BQ594991	EST	trinucleotide	394	405	12	9	TGA	ATCTCGTGTTCCTTCACTGG	160	20	55.3	AGTATCTATCGCTTGTGGATG	475	21	54.5	316
BQ594999	EST	trinucleotide	121	132	12	9	GAA	ATCTCTCTCTCTCTCTCTCT	47	19	55.3	CAAACCTACCCAGCCATAGTAA	273	21	55.5	227

EST	BQ594999	dinucleotide	110	119	10	8	GA	ATTCCTCCCTACCAACA	47	19	55.3	CAAACTACACAGCCATAGTAA	273	21	55.5	227
EST	BQ595005	dinucleotide	70	81	12	10	TC	TTCTCCCTCTCTACTTCC	31	21	54.4	CAGACATACCTCTCTCTTTC	269	21	54.3	239
EST	BQ595015	dinucleotide	175	190	16	14	TC	CCAAACCATCTCAATCTATT	70	22	55.8	TGCTAAACACACTCTCTCTC	267	21	55.7	198
EST	BQ595019	trinucleotide	190	201	12	8	TTC	AAGTTCTCTCTCTCTCCATT	44	21	56.1	GTTTCTCTCTCTGTGATGCC	428	21	54.1	385
EST	BQ595019	tetranucleotide	119	130	12	9	TGAG	AAGTTCTCTCTCTCTCCATT	44	21	56.1	GTTTCTCTCTCTGTGATGCC	428	21	54.1	385
EST	BQ595028	dinucleotide	193	206	14	12	AG	CTTCTTTGAGTGGGT	61	20	55.2	TACATTCCTCTCTCTCTTTC	355	21	55.1	295
EST	BQ595028	trinucleotide	395	415	21	11	TGA	ATACAATGATGACGACGAAGA	316	21	55.7	ATCCCTCTGACACCCAC	478	18	55.6	163
EST	BQ595033	trinucleotide	235	246	12	9	CGA	GTGAGAACGGCATAAACA	174	19	54.7	AATGACTGACGACTGACTGG	438	20	56.1	265
EST	BQ595039	tetranucleotide	147	166	20	16	TCTT	AATCCCTCAATGTTTCACT	58	21	55.3	ACCAATAATCTCATACAGG	435	21	54.2	378
EST	BQ595064	trinucleotide	334	351	18	15	GGA	CTAAGAACGAAACCCACGA	104	21	55.4	CTCCACAATCATCAAC	411	20	55.5	308
EST	BQ595077	trinucleotide	83	94	12	9	TCA	TCTCTCTCTCTCTCCATT	54	19	54.8	ATTCTCTACCACTACCGACT	453	21	55.3	400
EST	BQ595101	trinucleotide	68	91	24	21	CAC	CGACATCTCTCTCTCC	25	18	52.8	AAGTATCCGTGTGATTGCT	184	20	54.8	160
EST	BQ595108	dinucleotide	86	101	16	14	TC	CCTCAACCGCATACAA	31	18	55.5	CGTACTCTCTCTCTCTCTCT	334	22	54.3	304
EST	BQ595108	trinucleotide	314	328	15	12	AGA	AAATCTCTCTCTCTCTCTCT	83	23	54.0	TATTCATATCTCTCTCTCT	453	20	50.0	371
EST	BQ595108	trinucleotide	132	143	12	9	ATC	AAATCTCTCTCTCTCTCTCT	82	23	54.4	CGTACTCTCTCTCTCTCTCT	334	22	54.3	263
EST	BQ595124	trinucleotide	208	222	15	12	TCA	GGCTTCTCTCTCTCTCTCT	10	19	55.2	GACGCCATTATCAACCAAT	342	19	55.9	333
EST	BQ595124	trinucleotide	252	272	21	11	ATA	ATGGCGTCTCTCTCTCTCT	222	18	55.2	TCITTGAGTTGTGGATTCTG	565	21	55.4	344
EST	BQ595124	dinucleotide	86	95	10	8	TC	GGCTTCTCTCTCTCTCTCT	10	19	55.2	GACGCCATTATCAACCAAT	342	19	55.9	333
EST	BQ595127	trinucleotide	315	326	12	9	TGA	AAATGTGATCAATGGGTCTG	254	21	54.9	ATAGTGAATGCTTGGCTT	389	19	54.9	136
EST	BQ595129	trinucleotide	389	412	24	14	GTC	ATTATCTCTCTCTCTCTCTCT	323	21	54.8	CGGTGATGTATCTCTCTCT	517	22	54.3	195
EST	BQ595147	dinucleotide	168	179	12	10	TC	CAACTCTCTCTCTCTCTCTCT	137	21	56.4	CGGTCTCAAAAGTAATCC	380	19	55.4	244
EST	BQ595147	trinucleotide	154	165	12	9	TCT	CGCTCTCTCTCTCTCTCTCT	62	19	55.9	ATATTGTCTCTCTCTCTCTCT	214	21	56.4	153
EST	BQ595148	dinucleotide	44	59	16	14	TC	GCATTTCTCTCTCTCTCTCT	16	18	51.7	TCCTCTCTCTCTCTCTCTCT	357	22	54.4	342
EST	BQ595150	pentanucleotide	363	372	10	5	GTTTA	TACGAGTTTCAATCAGACGA	222	20	54.4	GAGTAAGACAACTTACCAAA	414	22	53.0	193
EST	BQ595154	dinucleotide	86	95	10	8	CTT	CACCGCATAAACTCTCTCTCT	10	20	55.1	ACTCAATCTCAACAAACACA	290	21	55.6	281
EST	BQ595157	dinucleotide	58	71	14	12	AG	GTGGTGTAGGTCTCTCTCT	7	18	56.3	ATGGATTTGAGGAGAGAGAAG	240	21	55.1	234
EST	BQ595163	trinucleotide	346	372	27	24	CAA	ATAATGGAAGGAAGTGGGT	246	20	55.1	ATGTTGTTGTGATGGTGT	443	21	55.3	198
EST	BQ595163	trinucleotide	328	342	15	12	CAA	ATAATGGAAGGAAGTGGGT	246	20	55.1	TGTTGTGTTGTGTTGTGT	373	21	54.9	128
EST	BQ595163	trinucleotide	233	244	12	9	TAC	TTTATTTCACTCTCTCTCTCT	110	23	54.9	GATTGTTGTGTTGTGTTGT	343	21	55.1	234
EST	BQ595201	trinucleotide	119	130	12	9	TCT	AAATGGCTGCTCTCTCTTATC	78	21	55.5	AAATCAAACTATCCGCC	336	18	55.0	259
EST	BQ595202	trinucleotide	118	129	12	9	TCT	AAATGGCTGCTCTCTCTTATC	77	21	55.5	AAATCAAACTATCCGCC	335	18	55.0	259
EST	BQ595203	pentanucleotide	178	187	10	5	TTTTG	TCTCTTTCTCTCTCTCTCTCT	15	22	54.2	TTGAGCAGTTTCATTAGGTT	391	20	55.0	377
EST	BQ595214	trinucleotide	372	386	15	12	ATG	AAGGAGAGATAAGGAGAGGTT	246	22	54.6	AATGTCCTCCACCACTAAGT	474	19	55.1	229
EST	BQ595227	trinucleotide	98	109	12	9	AGC	CAGCGTCTCAACTGACTTCT	2	20	54.8	CTTTGCCCGTCTCTAAATC	338	18	55.7	337
EST	BQ595236	dinucleotide	36	49	14	12	TC	CTCTCACTCTTCACTACACCA	4	22	54.7	ACAAGGTTTCTGAGGCGG	352	18	58.8	349
EST	BQ595243	trinucleotide	185	202	18	15	ATC	CTCTATCTCTCTTCTCTCCAC	37	21	54.7	AACCTAAATAACGCAACTTC	330	21	55.3	294
EST	BQ595254	dinucleotide	103	112	10	8	TC	GGAACTCTTCTCTCTCTCTCT	12	21	55.3	TTGTAGCATCAAAACCCAGT	285	21	54.9	274
EST	BQ595256	trinucleotide	87	104	18	15	GAA	AGAGAGTGAGGAGGAGGAAG	13	20	55.1	TTATGCTTACAACTATCC	346	20	52.9	334
EST	BQ595263	trinucleotide	226	243	18	15	GAA	CAGAAACTACTCTCTGGTCT	178	20	54.6	CTCATCTTCTCTCTCTCTCA	414	21	55.3	237
EST	BQ595270	dinucleotide	90	105	16	14	CT	CACATCGTCACTCTCTCTCT	36	21	54.9	CCAATCCGCTATCTCCATC	397	20	56.0	362
EST	BQ595273	trinucleotide	166	179	14	12	GA	CACCTCTCTCTCTCTCTCTCT	65	20	53.8	ACATAGTGAATGTTCCGCT	326	20	54.9	262
EST	BQ595273	trinucleotide	69	80	12	9	GTT	AAATAACTCCACTGCGACAC	24	20	55.2	ATTCTCTCTCTCCGACCT	148	20	55.4	125
EST	BQ595286	trinucleotide	295	318	24	21	CCC	AGGGTTTCTCAATCTACTCTC	137	22	53.5	TCATCATCTCTCTCTCTCTCA	370	21	52.4	234
EST	BQ595286	trinucleotide	319	333	15	12	GCT	AGGGTTTCTCAATCTACTCTC	137	22	53.5	TCATCATCTCTCTCTCTCTCA	370	21	52.4	234
EST	BQ595286	trinucleotide	288	279	12	9	AAG	AGGGTTTCTCAATCTACTCTC	137	22	53.5	TCATCATCTCTCTCTCTCTCA	370	21	52.4	234
EST	BQ595287	trinucleotide	74	85	12	9	TCT	AGTGAAGATAGCCATAAGTGA	22	23	55.0	GTGACCAACCCACATAGA	195	18	52.5	174
EST	BQ595291	trinucleotide	214	225	12	9	ACA	CACCAACACCAACAACAAG	77	19	55.8	GACACTACCATCAGCAAGAAC	401	21	54.9	325
EST	BQ595332	trinucleotide	216	230	15	12	CCA	TACACACCTAAACCTCCCAT	44	21	56.1	AGCATCTAACCCCTACAAGACC	397	21	55.1	354
EST	BQ595334	trinucleotide	343	354	12	9	AAG	ATTGGGTGAGGTGGTGACT	165	18	56.0	TTTGAATCTTGCTTTTCCC	425	19	52.6	261
EST	BQ595338	trinucleotide	165	176	12	9	CAA	ATTACTCCCAACCCAGAAC	51	20	55.6	AATCAACAGTGAACCGAACAC	301	21	55.2	251
EST	BQ595340	trinucleotide	236	250	15	12	ATA	ACCATCTTCTCTTACAGCAC	100	21	56.0	AAACTGCCCATTTATCCC	488	18	54.9	389
EST	BQ595350	trinucleotide	233	250	18	15	CAG	TGCTATGTATGGACAGATGA	117	20	52.3	ACTGAGATTATGAACTGGG	448	21	55.8	332
EST	BQ595350	trinucleotide	275	298	24	14	CAG	AGCAACAACAACAACAACAG	215	20	54.7	TGAATGGGTAGGATAGCA	436	20	55.9	222
EST	BQ595350	trinucleotide	218	232	15	12	CAA	TGCTATGTATGGACAGATGA	117	20	52.3	ACTGAGATTATGAACTGGG	448	21	55.8	332

EST	BQ595359	pentanucleotide	38	47	10	5	TTTTT	CTCACTCACAAAGACTCAACACT	0	22	54.5	387	21	54.7	388
EST	BQ595360	trinucleotide	335	346	12	9	CTG	TCTCTCTCTCTCTCTCTCTCT	292	20	55.0	423	18	55.5	132
EST	BQ595364	trinucleotide	72	83	12	9	CCA	TCTGTCTCTCTCTCTCTCTCT	1	23	51.8	172	19	55.4	172
EST	BQ595366	trinucleotide	345	359	15	12	AAG	TGGTCTCTCTCTCTCTCTCTCT	198	21	54.8	480	21	55.8	283
EST	BQ595383	trinucleotide	258	290	33	23	CAA	ACTCTCTCTCTCTCTCTCTCT	122	19	54.9	365	20	55.2	244
EST	BQ595383	trinucleotide	138	161	24	21	CCT	GGAGTGAAGGAGGAGGAGGAG	22	20	55.6	279	21	54.9	258
EST	BQ595383	trinucleotide	231	245	15	12	CAA	GGAGTGAAGGAGGAGGAGGAG	22	20	55.6	279	21	54.9	258
EST	BQ595383	trinucleotide	171	182	12	9	AAC	GGAGTGAAGGAGGAGGAGGAG	22	20	55.6	279	21	54.9	258
EST	BQ595391	trinucleotide	171	185	15	12	GCT	CTTGGCGAGTCTGAGAAA	143	18	56.1	365	18	55.5	223
EST	BQ595420	trinucleotide	391	402	12	9	ATC	TTCGATGCTCTTCCAACTATC	322	21	54.7	520	18	56.1	199
EST	BQ595462	trinucleotide	320	331	12	9	TCG	ACAGAGGACAAAGAGAGTTT	277	21	52.4	616	19	55.4	340
EST	BQ595487	trinucleotide	414	425	12	9	CAA	AAAGTAGAACTCAACTCAATC	175	23	51.6	510	21	54.9	336
EST	BQ595491	trinucleotide	252	263	12	9	GGT	TGGAGGTGGTTGATCTTG	136	18	55.2	449	20	53.3	314
EST	BQ595499	trinucleotide	452	478	27	24	CAA	CAAGAGGAGTATGAGGAGG	215	21	54.9	534	21	55.5	320
EST	BQ595538	dinucleotide	38	54	18	9	TC	CGCATCTCTCCGACAA	10	18	59.5	340	21	55.4	331
EST	BQ595539	trinucleotide	132	141	10	8	TG	TTCTCTCTCTCTCTCTCTCT	1	18	55.6	333	21	54.5	333
EST	BQ595564	trinucleotide	254	265	12	9	GAA	TTTACCCGCAATAATAACAA	204	21	55.1	380	21	55.3	177
EST	BQ595571	trinucleotide	43	59	18	9	CT	TCTCTCTCTCTCTCTCTCTCT	5	21	55.1	375	21	54.8	371
EST	BQ595571	trinucleotide	119	130	12	9	TCA	TCTCTCTCTCTCTCTCTCTCT	5	21	55.8	375	21	54.8	371
EST	BQ595593	trinucleotide	230	241	12	9	TTC	TCCTCTCTCTCTCTCTCTCT	3	21	54.1	395	22	54.6	393
EST	BQ595603	trinucleotide	274	285	12	9	GTT	CGAAGATGGAGGAGGAGAG	245	19	55.4	362	21	57.1	118
EST	BQ595621	trinucleotide	327	350	24	21	CAA	TCTTTGCTACTCTCTCTCTCT	207	21	55.1	491	18	55.0	285
EST	BQ595637	trinucleotide	242	253	12	9	TTC	AAGGTATTGGATAAGGATGG	45	21	54.8	345	20	51.3	301
EST	BQ595653	dinucleotide	67	78	12	10	TC	CTTCTCTCTCTCTCTCTCTCT	24	21	54.9	399	21	54.3	376
EST	BQ595663	trinucleotide	89	100	12	9	CTA	AAAGCATCCACCGCAAC	9	18	59.7	183	22	53.1	175
EST	BQ595663	tetranucleotide	169	180	12	8	TCT	CGCAACACGCGGTACT	20	18	59.9	401	19	54.2	382
EST	BQ595666	trinucleotide	242	251	10	8	CT	TCTCTCTCTCTCTCTCTCTCT	192	22	55.1	472	21	55.1	281
EST	BQ595666	trinucleotide	120	134	15	12	AAG	TTGTTCTCTCTCTCTCTCTCT	47	20	55.1	446	19	55.2	400
EST	BQ595685	trinucleotide	335	346	12	9	CTG	TCTCTCTCTCTCTCTCTCTCT	292	20	55.0	423	18	55.5	132
EST	BQ595722	trinucleotide	345	359	15	12	AAG	TGTTCTCTCTCTCTCTCTCTCT	198	21	54.8	480	21	55.8	283
EST	BQ595736	trinucleotide	154	168	15	10	ATCA	ATCCCAACCTCTCTCTCTCTCT	122	21	55.4	495	21	55.2	374
EST	BQ595754	pentanucleotide	287	298	12	9	AGA	CTCTTTCTCTCTCTCTCTCTCT	166	21	56.4	353	20	54.7	188
EST	BQ595756	trinucleotide	407	421	15	12	ACA	ACTAACCCACCAACCAACAA	156	21	55.0	460	21	54.5	305
EST	BQ595762	trinucleotide	147	170	24	21	ACA	CAACTCTCACTCTCTCTCTCTCT	68	20	55.6	459	21	54.8	392
EST	BQ595778	trinucleotide	82	93	12	9	CCA	TTCTCTCTCTCTCTCTCTCTCT	28	21	55.0	166	21	54.9	139
EST	BQ595778	trinucleotide	195	206	12	9	CTC	ACAACAACAACAACAACAACA	149	21	54.9	459	21	54.8	311
EST	BQ595785	dinucleotide	33	44	12	10	CT	TTTCTCTCTCTCTCTCTCTCT	1	22	55.2	150	19	57.1	150
EST	BQ595800	pentanucleotide	127	141	15	10	TTTTA	TCTTCTCTCTCTCTCTCTCTCT	82	21	54.8	217	21	55.0	136
EST	BQ595800	trinucleotide	343	354	12	9	GCT	TTTCAACCTCTCTCTCTCTCTCT	255	21	55.2	410	20	55.9	156
EST	BQ595836	dinucleotide	183	194	12	10	CT	TAGGAACCTTACAAACATCAA	142	21	50.3	359	21	55.3	218
EST	BQ595854	trinucleotide	465	476	12	9	GGA	GGGTACTCTCCAAAGCCAGT	282	18	55.0	574	21	54.5	293
EST	BQ595856	trinucleotide	454	465	12	9	CGC	CTTGGACTCTGGTTTACTTTG	295	21	54.2	504	20	55.1	210
EST	BU089549	trinucleotide	175	186	12	9	AAC	AAATCAAGCAACAACAACAAC	96	21	55.4	388	18	55.3	293
EST	BU089560	dinucleotide	329	338	10	8	CT	ATCCCATCTTCACTCTCTCTCT	248	21	54.9	495	21	55.5	248
EST	BU089562	dinucleotide	231	242	12	10	TC	GACGCTGTCTCTCTCTCTCTCT	175	20	55.2	442	19	56.0	268
EST	BU089564	trinucleotide	75	95	21	18	TCT	CTTCTCTCTCTCTCTCTCTCT	0	20	50.9	133	20	54.6	134
EST	BU089572	pentanucleotide	1906	1915	10	5	TTCTT	ATTCACTCTCTCTCTCTCTCTCT	1805	20	54.9	2151	22	54.6	347
EST	CB280906	trinucleotide	79	90	12	9	ACG	GAGGGTGTGGTGTGCTACT	15	18	53.3	137	19	54.1	123
EST	CF542669	trinucleotide	148	165	18	15	TTC	TAGATTTCCTCTCTCTCTCTCT	55	19	51.6	351	21	52.8	297
EST	CF542669	pentanucleotide	89	98	10	5	AGAAA	TAGATTTCCTCTCTCTCTCTCT	55	19	51.6	351	21	52.8	297
EST	CF542680	trinucleotide	255	266	12	8	TTTA	TACTCTCTCTCTCTCTCTCTCT	78	21	57.2	408	19	55.7	331
EST	CF542708	trinucleotide	309	320	12	9	TGC	AGCAACATCATTCATTACCC	89	20	55.0	447	18	54.9	359
EST	CF542728	pentanucleotide	431	450	20	15	TGGAA	GATAACTTCCAACTCCCATC	162	21	55.9	494	20	50.6	333
EST	CF542740	trinucleotide	94	105	12	9	TTC	AATCTTGAATGCTCTCTCTCT	26	21	55.3	320	21	55.3	295
EST	CF542740	trinucleotide	613	624	12	9	ACC	TACCAACAGACCAACAGAGA	299	21	53.8	695	21	55.8	397

EST	CF542767	trinucleotide	150	168	18	9	TCA	GCAATGCTCTACTATCTCTTCT	118	22	54.4	ATAATGGTGGTTGTGGTGA	282	19	54.4	165
EST	CF542771	trinucleotide	248	259	12	9	TGG	ACAACTCCAACCACTCTCTACT	215	21	55.3	ACCAATCTCTCATCTCTTTC	499	21	55.7	285
EST	CF542774	trinucleotide	448	459	12	9	TIA	TTGAGACTCAACATCTTCC	98	20	55.2	ACAATCCAGAAACCCATAAAC	492	21	55.6	395
EST	CF542850	trinucleotide	352	366	15	12	GAT	AGTAGCGGAAGAAGATGATGAA	288	21	54.4	ACTCGGAACCCAGACTCAAA	448	19	55.7	161
EST	CF542850	trinucleotide	399	410	12	9	TGA	AGTAGCGGAAGAAGATGATGAA	288	21	54.4	ACTCGGAACCCAGACTCAAA	448	19	55.7	161
EST	CF542851	trinucleotide	352	366	15	12	GAT	CTATGCGGTTTGTATGATG	225	19	55.1	ATCCGACTCTTCTGTATGTT	596	21	55.3	372
EST	CF542851	trinucleotide	399	410	12	9	TGA	CTATGCGGTTTGTATGATG	225	19	55.1	ATCCGACTCTTCTGTATGTT	596	21	55.3	372
EST	CF542859	trinucleotide	477	494	18	15	CAA	AAATCAACAACAACAACAACA	340	21	54.1	CAACTGTAATGAAGGAAGTAA	598	22	54.7	259
EST	CF542859	trinucleotide	345	359	15	12	CAA	CAGAAATAACAAGAAGCA	145	21	54.9	AAATGACAATCTAAGCCAGT	454	21	55.5	310
EST	CF542859	trinucleotide	292	303	12	9	CAA	CAGAAATAACAAGAAGCA	145	21	54.9	AAATGACAATCTAAGCCAGT	454	21	55.5	310
EST	CF542891	trinucleotide	95	106	12	9	TCC	CGTATCCCTCATATCGAGT	47	21	56.9	ATACCATCCATCATACCA	255	20	55.0	209
EST	CF542901	trinucleotide	396	446	51	27	CAA	TCCTTCTCTCTCTCTCTCTCT	162	23	55.1	GAATCCACATTAGTCGTTTGA	552	21	55.2	391
EST	CF542901	trinucleotide	109	123	15	12	TTT	GTCAACCCACTCCCACTCT	31	18	55.7	TTGATGTTGTTGCTGTGTT	418	20	55.1	388
EST	CF542922	dinucleotide	53	70	18	9	TC	GCCAACAACAATACTACACTCT	0	22	53.7	TCCTGAATAAAGACTCGTAA	366	21	54.6	367
EST	CF542925	trinucleotide	236	247	12	9	CCA	CCATAACCAATAACCAATAACA	108	21	54.9	GTGAGTAAAGTGAGTCCAGT	393	21	53.4	286
EST	CF542926	trinucleotide	236	247	12	9	CCA	CCATAACCAATAACCAATAACA	108	21	54.9	GAATCTACAGCATCCGTC	349	18	54.8	242
EST	CF542938	trinucleotide	236	247	12	9	CCA	CCATAACCAATAACCAATAACA	108	21	54.9	GAATCTACAGCATCCGTC	349	18	54.8	242
EST	CF542950	trinucleotide	236	247	12	9	CCA	CCATAACCAATAACCAATAACA	108	21	54.9	GAATCTACAGCATCCGTC	349	18	54.8	242
EST	CF542957	trinucleotide	554	565	12	9	GCT	AGTAGGTGGTTCAAAGGTT	201	20	55.2	CTGTTTCTGACTGCTGCTT	594	19	54.1	394
EST	CF542967	dinucleotide	133	142	10	8	TG	TCCTCTCTCTCTCTCTCTCT	49	21	54.5	ACTTCTCACCCCAACACTC	230	20	55.0	182
EST	CF543032	trinucleotide	416	433	18	15	ATG	GGCATTTCTCTCTGAG	269	18	54.0	CTCCAATCTTACGCCCTT	559	19	56.0	291
EST	CF543053	trinucleotide	171	182	12	9	ACG	GTGCTGTACTCCCTCTCTT	22	21	55.0	TAAATGCTCCAATCTCTC	228	18	50.9	207
EST	CF543054	trinucleotide	171	182	12	9	ACG	AAAGTCTGTTCTGGATTGA	69	21	54.1	CATTGCTCTACATCTGCTT	457	20	54.4	389
EST	CF543081	trinucleotide	314	325	12	9	GCA	ATGGCTCTACCAAGATTGA	244	20	55.7	TTCACTTGTATCTCGTCC	414	20	55.2	171
EST	CF543084	trinucleotide	171	182	12	9	ACG	AAAGTCTGTTCTGGATTGA	69	21	54.1	CATTGCTCTACATCTGCTT	457	20	54.4	389
EST	CF543104	trinucleotide	519	530	12	9	AGA	CTATTGACTTCCGTTGTCT	268	21	54.1	CTCTGCTCTCTCTCTGCTT	567	21	56.0	300
EST	CF543117	pentanucleotide	566	575	10	5	GAATA	AAGGTTGAATGATAAGCA	472	21	54.2	CCACTCATCCCATCTGT	623	18	56.6	152
EST	CF543133	dinucleotide	40	58	20	11	TC	TTCTGCCCTAAACTCTCTT	9	21	55.1	ATGAAGCAACACACTCTT	255	20	54.8	247
EST	CF543134	trinucleotide	98	112	15	12	CTT	GGTTTCATCTCATCTCTTCT	65	21	54.2	GCGGTTTGTGATTGGTTAG	214	19	56.6	150
EST	CF543136	trinucleotide	230	241	12	9	TCC	AACTCCATTGTATCACCAAC	35	21	54.8	GCACCTTGTCTCTGTAATCT	276	19	52.6	242
EST	CF543137	trinucleotide	230	241	12	9	TCC	TTCACTCTTCTCCACACAGT	86	21	54.9	CTCAATGCTCAGCAATCAG	473	19	55.1	388
EST	CF543165	trinucleotide	471	482	12	9	GAA	GTGTTCCATTTCAGACAACCTC	423	21	54.6	ATAATCTCTACCATTCCTCAA	529	20	54.5	107
EST	CF543185	trinucleotide	282	296	15	12	ATG	TTCACTACGTTTCACTTAGCA	231	20	54.8	ATGGATAAATAGCACCTTCA	379	21	56.3	149
EST	CF543200	trinucleotide	69	83	15	12	GAT	AGTAGCGAAGAAGATGATGAA	5	21	54.4	AACAGACTCAATGCCCT	158	18	55.5	154
EST	CF543200	trinucleotide	116	127	12	9	TGA	AGTAGCGAAGAAGATGATGAA	5	21	54.4	AACAGACTCAATGCCCT	158	18	55.5	154
EST	CF543209	trinucleotide	276	293	18	15	GAG	TTCTAATCTCTCTCTCTCTCT	78	19	53.3	CCATCTCTACCACTACCTCT	329	21	54.9	252
EST	CF543209	trinucleotide	188	199	12	9	GGT	TTCTAATCTCTCTCTCTCTCT	78	19	53.3	CCATCTCTACCACTACCTCT	329	21	54.9	252
EST	CF543209	trinucleotide	414	425	12	9	CTG	TTCTAATCTCTCTCTCTCTCT	78	19	53.3	CCATCTCTACCACTACCTCT	329	21	54.9	252
EST	CF543216	trinucleotide	206	217	12	9	CTT	AGACCATCTTCACTCTCTTCTA	160	21	53.9	GCCACATCAGACTTAGA	469	19	55.3	392
EST	CF543235	tetranucleotide	238	257	20	9	AATC	GCTGAAGACATTTGGTATGAAG	29	21	55.0	GCAGAGATTGAAAGCGGA	406	18	57.5	378
EST	CF543236	trinucleotide	536	550	15	12	TTC	AATCAATCAACAATCAATCAAC	237	21	54.1	TGAGAAGACGCAGAAAGAC	588	19	54.0	352
EST	CF543236	tetranucleotide	238	257	20	9	AATC	GCTGAAGACATTTGGTATGAAG	29	21	55.0	GCAGAGATTGAAAGCGGA	406	18	57.5	378
EST	CF543256	trinucleotide	448	459	12	9	TIA	TTCAAGCTCAACCAATCTTCC	98	20	55.2	ACAATCCAGAAACCCATAAAC	492	21	55.6	395
EST	CF543279	trinucleotide	181	195	15	12	GAT	AAACTCCCTCTCTCTCTCTCT	64	19	54.9	AACTCCATCAACCTTACTC	304	21	54.9	241
EST	CF543279	trinucleotide	150	161	12	9	CGC	AAACTCCCTCTCTCTCTCTCT	64	19	54.9	AACTCCATCAACCTTACTC	304	21	54.9	241
EST	CF543307	dinucleotide	44	53	10	8	CT	CTACACGAAACCCACAG	12	21	55.4	GCTACACGGCATAGAACAC	261	20	55.0	250
EST	CF543329	trinucleotide	295	306	12	9	CTG	CTACATCCAGACAATACAGG	146	21	55.8	AACCGAAGAGATTTCAGG	344	20	55.9	199
EST	CF543347	trinucleotide	295	306	12	9	CTG	CTACATCCAGACAATACAGG	146	21	55.8	AACCGAAGAGATTTCAGG	344	20	55.9	199
EST	CF543352	tetranucleotide	427	438	12	8	TAA	AACAATCAATAAAGTCAAAAT	262	22	50.3	ATCTCTCCCTCTTGGTAATC	581	21	54.1	320
EST	CF543353	tetranucleotide	427	438	12	8	TAA	AACAATCAATAAAGTCAAAAT	262	22	50.3	ATCTCTCCCTCTTGGTAATC	581	21	54.1	320
EST	CF543373	trinucleotide	277	288	12	9	ATG	TCACCATTTGTAACCAAAAC	168	19	54.7	ATCTCCCTCTTGGTAATC	330	18	54.7	163
EST	CF543380	trinucleotide	285	305	21	18	CAA	ATACTACCCCAAACTCAAA	150	20	54.6	TACAATGACGCTATCACTCT	537	21	55.0	388
EST	CF543406	dinucleotide	482	497	16	14	TA	GCAGTCCCGTTATGTTG	215	18	54.9	TTTGACACAGGGTAGAGAAGG	546	21	56.1	332
EST	CF543407	dinucleotide	482	497	16	14	TA	TTATTATCCCAACCCATTAG	295	21	53.6	CTGCCATCTCAACTTCATTAC	601	21	55.0	307
EST	CF543408	pentanucleotide	134	148	15	10	CTTTT	GTCAACAACCCACAAATCC	10	18	54.3	GCAACAACAGGAACAGAAAT	372	20	55.4	363

EST	CF543408	pentanucleotide	287	301	15	10	TTCA	AGTTCCCTACTTGATTGATT	205	22	53.9	CTTTCTTTATCTCTCTGCTT	572	21	54.6	368
EST	CF543408	trinucleotide	78	89	12	9	ACT	GTCAACACCCACAATCC	10	18	54.3	GCAACACAGGAACAGAAGT	372	20	55.4	363
EST	CF543408	tetranucleotide	164	175	12	8	TTTC	GTCAACACCCACAATCC	10	18	54.3	GCAACACAGGAACAGAAGT	372	20	55.4	363
EST	CF543413	trinucleotide	295	324	30	20	AAC	TGGAGAGATGAAGAATGTA	256	21	55.0	CAGAAGATGAAGAAAGCGAA	380	21	54.8	125
EST	CF543469	trinucleotide	118	135	18	8	TCC	AACCCCTCCTCTTTCTCT	16	21	55.4	CAGCCCTCTGTTTGTAAATA	353	21	55.0	338
EST	CF543470	trinucleotide	270	299	30	13	TAA	GTAAACAATGCTTCGGTGG	223	18	54.9	TATCGTCACTCTATTCCGT	592	21	57.4	370
EST	CF543470	tetranucleotide	502	513	12	8	CTAG	GTAAACAATGCTTCGGTGG	223	18	54.9	TATCGTCACTCTATTCCGT	592	21	57.4	370
EST	CF543498	trinucleotide	50	61	12	9	TGG	GAATCGTATCGTCGGTTG	3	22	52.1	GGACGGAGAAATCAGAACTATC	272	21	55.4	270
EST	CF543539	trinucleotide	235	246	12	9	CGG	GAATCGTATCGTCGGTTG	201	18	54.8	ATGAAGAGGAACTTTGGAGAC	459	21	55.0	259
EST	CF543545	tetranucleotide	351	362	12	8	CACAT	TGGTAGAGCAGAGGTATTGG	38	21	54.8	ATGAAGAAAGTTGGGCTTGG	409	20	55.1	372
EST	CF543564	tetranucleotide	286	297	12	8	TGTT	TCGTTCCAGGTTCTCTTT	43	19	54.9	AATCTCAITTTGCTCTCATTT	442	21	53.0	400
EST	CF543565	dinucleotide	156	171	16	14	TG	CCACCTGAAGTTTGATCTATT	100	22	55.1	GCCACCTACTGTTTCCG	446	18	56.7	347
EST	CF543566	trinucleotide	156	171	16	14	TG	CCACCTGAAGTTTGATCTATT	100	22	55.1	TTCTTTGATTGGCTGCTTT	413	19	56.1	314
EST	CF543569	trinucleotide	321	335	15	12	TGA	ATCGGAAGAAATACCTCAATC	230	21	54.9	ATGACCCGTTCCACCAGAG	470	19	55.0	241
EST	CF543577	dinucleotide	364	373	10	8	AG	GCTGTGTTGTTCTACAGATT	219	21	54.7	CGTAGTTTCTGCGTTGTG	516	19	55.5	298
EST	CF543596	pentanucleotide	259	273	15	10	TTTTTC	CGACCCCTTACTTATCATTACT	84	23	53.8	ATCTCACAAGCTCCCAA	405	18	56.6	322
EST	CF543600	dinucleotide	130	141	12	10	TC	ACCGACCTTCTCTCTTC	29	18	54.1	ATGTAATCATCTGGTTTGG	198	20	54.8	170
EST	CF543601	dinucleotide	131	142	12	10	TC	ACCGACCTTCTCTCTTC	29	18	54.1	ATGTAATCATCTGGTTTGG	199	20	54.8	171
EST	CF543608	trinucleotide	296	307	12	9	TTC	TTCCAGAAATAATCAGACAA	119	21	54.9	GAAGTAGAGAAACAAGATGG	447	21	54.0	329
EST	CF543618	trinucleotide	287	298	12	10	AG	AAAGGGAGGAACAGGAAA	257	18	54.6	CACCGCTCATAAAGCATC	545	18	55.2	289
EST	CF543629	dinucleotide	305	318	14	12	TA	ATGGAAGAAGAAAGATGGAAG	1	21	55.1	AACCTCAGGAAGAAACATCA	372	21	54.8	372
EST	CF543632	trinucleotide	69	80	12	9	ACC	TAATCACCTGGGAAGAAAG	4	19	52.7	TTGCTCGGTAGTAGTGGT	118	21	54.8	115
EST	CF543649	pentanucleotide	140	149	10	5	AAGC	ATTGTGAAGGAGGAAGGAAG	72	21	55.2	GAGTAGACCCAAAGCACTAAAC	204	22	54.9	133
EST	CF543656	pentanucleotide	50	59	10	5	TTTTTA	ATTTCACAAGCAAGAGGT	16	18	50.3	TTACATCACAGGATTACACA	415	20	54.8	400
EST	CF543659	dinucleotide	144	153	10	8	CT	GCACCTTCACTCTCTCTCA	115	19	53.7	GATGACCTTAACCAACCCATTC	331	21	56.0	217
EST	CF543665	trinucleotide	539	548	10	8	AT	AAGCGAGCACTATCGCC	214	18	61.5	CTTACACGACGAACCTCA	498	18	53.0	285
EST	CF543689	trinucleotide	256	267	12	9	GAT	CTTCTTCTTCCGCCATT	38	18	55.4	AGTCTTCCACTGCTTCCCTC	409	20	56.1	372
EST	CF543699	trinucleotide	82	93	12	9	TTC	TGTGAAGGGTAAATGCT	96	18	51.4	AGTAAAGAATGAGACACTCCAA	414	22	53.3	319
EST	CF543706	trinucleotide	294	305	12	9	TTC	TGTGAAGGGTAAATGCT	96	18	51.4	GAATGACACATACAAAGGCAC	408	21	54.9	313
EST	CF543707	trinucleotide	294	305	12	9	TTC	GAGTAGTGGCATCGTTTC	283	19	56.0	TATTATCTCTTTTGTGTTT	599	21	50.9	317
EST	CF543719	tetranucleotide	348	359	12	8	TGCA	CACCACAACCATCACAC	13	18	56.3	CCACCTCTCCTTCTCTCAC	174	18	55.4	162
EST	CF543778	trinucleotide	61	78	18	15	CCA	AACTATACACAACCTCTCAA	217	21	54.8	TAGTCTTCTTCCGCCACCAC	543	18	54.4	327
GSS	DX105750	tetranucleotide	319	334	16	16	AAAC	TCCATTAGCCTTCTTCTCTAC	175	21	54.6	CTCTCTCATTTCTTCTCCA	447	21	54.3	273
GSS	DX105781	pentanucleotide	302	326	25	25	AAGAG	GCACGCACTAAGCACTAAA	429	19	55.3	ACTATGTAGCCTCTTGCC	630	20	54.6	202
GSS	DX105901	dinucleotide	400	415	16	16	AC	TAAGATTGAGGTGCTGTAA	350	20	54.4	ACAAGATCCCTAACTGCCT	725	19	54.9	376
GSS	DX105905	tetranucleotide	445	464	20	20	AAAT	AGAGAAGAGGAGGAGACCAA	18	20	55.6	AAAGAACCAAGGAGAGGGTGT	279	20	55.4	262
GSS	DX105988	dinucleotide	63	110	48	48	AT	TTAGTTCAAGTGTAGTCTGTTTC	136	23	53.3	TTGGAATGAGGGAATGTG	312	18	55.1	177
GSS	DX106007	trinucleotide	180	203	24	24	AAT	TTTGAAGTTGATGATGTGAAA	289	21	54.2	GGATAGGTTAGGGTATGCTTG	685	22	54.8	397
GSS	DX106115	pentanucleotide	616	630	15	15	AATAT	GCAAGCTGTGTATTGGAAG	157	21	55.1	GTTTGTGGATGTGGGAG	553	18	57.1	397
GSS	DX106156	dinucleotide	514	533	20	20	AC	TTCATTGCTTACTTCTTCTTCA	315	23	53.9	CTATTATTAGGGAACGAGGT	607	21	54.2	293
GSS	DX106174	pentanucleotide	361	380	20	20	AAGAG	GCAAGCTGTGTATTGGAAG	157	21	55.1	GTTTGTGGATGTGGGAGG	552	18	59.7	396
GSS	DX106247	pentanucleotide	514	533	20	20	AC	TTCATTGCTTACTTCTTCTTCA	315	23	53.9	CTATTATTAGGGAACGAGGT	607	21	54.2	293
GSS	DX106285	trinucleotide	373	387	15	15	ACC	CTGTGATTGAGATTGCGAC	336	19	55.1	CGAAGTTTATGATGTTAG	642	21	54.2	307
GSS	DX106385	trinucleotide	611	628	18	18	AAC	CCCAATGAACAACTTAGCAC	336	21	57.2	ATAATGACCAACAACAAC	681	21	55.2	346
GSS	DX106388	trinucleotide	301	342	42	42	AT	GCTCCGAGACACTCTTTT	220	18	55.3	AGTTTGGAGTTGCTGTCT	479	19	54.8	260
GSS	DX106581	tetranucleotide	441	456	16	16	ACTC	GAGAAGTCGAGACATGTGAAAG	343	21	54.9	GTTAAAGGGCTAAACGCAAC	542	19	55.2	200
GSS	DX106615	dinucleotide	93	122	30	30	AT	AAGGTTGGAGTATTGAAC	14	19	53.9	CGATTGGCTCTTTAGCA	154	18	57.5	141
GSS	DX106679	dinucleotide	438	463	26	26	AC	TCCAGAACACAGCAGGAAA	122	19	53.8	GATAGGCACCTTTGTAATAG	487	21	53.1	366
GSS	DX106720	tetranucleotide	67	94	28	28	AAAG	GCTCCACAGACACAACA	39	18	56.4	GATGAACAATAAGATTGGATGA	155	23	55.1	117
GSS	DX106781	pentanucleotide	456	470	15	15	AAAAAC	AAACTCACCCGCTCAACT	248	18	56.7	CTTTCCCTTTCCCTCTTATT	581	20	54.3	334
GSS	DX106881	tetranucleotide	529	544	16	16	ACTC	ACAAACAAGAAGAAGACCC	223	21	55.1	ATAAATGAACCCCAACCCCT	583	20	55.1	361
GSS	DX106888	pentanucleotide	233	247	15	15	AAATC	CTAAACAACAATAATCACCAGA	161	21	55.3	CGAACAACAGGAAGAAGTAGA	507	21	54.8	347
GSS	DX106904	tetranucleotide	459	474	16	16	AAAT	TTTCCCACTTACTGTTCTAC	372	21	53.6	TCCCTTCTCTCTCTTACTTT	554	21	54.1	183
GSS	DX106975	dinucleotide	273	288	16	16	AT	AAAGTAGCACAAATCAGCATTT	196	21	54.3	TATTTGAAGGAGGTTGGGTAG	586	21	55.9	391

GSS	DX107024	dinucleotide	161	176	16	16	CG	TTCTCATCTTTGGTGGTT	3	20	55.5	CATTAGTGTGGTGGT	329	19	55.1	327
GSS	DX107076	trinucleotide	311	325	15	15	AAT	ATCACATCTGTGCTGTTT	250	21	54.5	TAACTCCGTTCAAATGCC	382	18	54.6	133
GSS	DX107085	dinucleotide	479	494	16	16	AT	CTGGGATTTCCGGAGTT	351	18	55.9	CCTAGATGATTTGACTGCCT	543	21	56.1	193
GSS	DX107086	dinucleotide	183	228	46	46	AT	ATGGTGGCTCCGGTAGA	56	18	59.3	GCTTAGATCTTTATGATCC	366	20	53.9	311
GSS	DX107096	pentanucleotide	138	152	15	15	AAAAG	GACTTTAGGTGGCTTCTCTT	15	21	54.6	CGATTGCTTGATGTGTTT	207	21	55.4	193
GSS	DX107179	dinucleotide	281	296	16	16	AC	GCACGCACTAAGCACTAA	310	19	55.3	ACTATGTGAGCCTCTTGCC	519	20	54.6	210
GSS	DX107221	pentanucleotide	245	259	15	15	ACTCG	ACATCCGACTCACCTCTATT	62	21	55.3	GACTCAACTCAAACTCAACTCA	294	22	54.6	233
GSS	DX107304	dinucleotide	262	277	16	16	AC	CATTAGTGTCTGGTGGT	231	19	55.1	TTCTTCTCATCTTTGGTGT	451	21	55.4	221
GSS	DX107378	tetranucleotide	419	438	20	20	AACT	TCACAGATAGAGAGAAAGAA	276	23	55.1	GGAGATCACTTACAGACAA	529	20	55.2	254
GSS	DX107391	dinucleotide	168	183	16	16	AC	ACTATGTGAGCCTCTTGCC	207	20	54.6	TAGCCGTATTTCCCACTAAA	591	20	55.1	385
GSS	DX107419	dinucleotide	407	430	24	24	AG	TTTCTCTCTCTCTCTCTCT	155	20	50.4	CTTTCTCTCTCTCTCTCTCT	476	21	55.0	322
GSS	DX107519	pentanucleotide	447	466	20	20	AAAAC	AATCAACCACTCAAAACCCA	385	19	55.3	ATAGACGAAGAAGAAAGGAG	583	21	54.5	199
GSS	DX107693	trinucleotide	284	301	18	18	AAT	AACCTCTCTACGCATCTAA	159	20	55.3	TAATGGAAGCCAAATCCT	363	19	54.8	205
GSS	DX107769	dinucleotide	148	167	20	20	AG	GACCTCACTTCTCAAGTAGCC	43	21	55.7	CAGCTTCTTCTTCTTCTT	242	21	55.6	200
GSS	DX107780	dinucleotide	36	51	16	16	AC	CATTAGTGTCTGGTGGT	5	19	55.1	TTCTTCTCATCTTTGGTGT	351	21	55.4	347
GSS	DX107859	trinucleotide	515	532	18	18	AAC	AGTCACACTTCTAGAGGAAGA	271	21	54.1	AATGCTCGTGGTAATAATGTT	582	21	56.2	312
GSS	DX107879	dinucleotide	150	165	16	16	AG	CACCTCTCTTCTCTCTCTCT	125	23	53.1	TTCTGTTGTTGGTTCACTTT	464	21	54.9	340
GSS	DX107918	pentanucleotide	186	200	15	15	AAATC	TTGGAAGTATGCTATGAGG	3	22	54.4	TTGATGCTTGTGTTCTTCT	235	21	55.2	233
GSS	DX108108	pentanucleotide	142	156	15	15	AAAAC	GGGTGTTTGTGCTGTTAGTG	1	21	54.8	TTAGTATTTGCGTTTCCCTG	297	21	55.0	297
GSS	DX108175	dinucleotide	484	483	20	20	CCCGG	AATCTGAACATCAAGGCTG	383	22	55.4	AATGCCCGCCAAAGCAAA	523	18	64.8	141
BES	DX579512	dinucleotide	524	541	18	18	AT	GTGACGAGAGAGAGAGATAG	119	22	54.9	ACAAAGGACATAGAAAGGAGG	508	21	55.1	390
BES	DX579515	pentanucleotide	260	279	20	20	AACTG	TGAACAAGTATGAACTCTAA	369	22	55.0	AAATAGGGAACACAAACCA	761	19	54.1	393
BES	DX579517	trinucleotide	500	517	18	18	AAC	ATCACCTACATTCACAAACGG	186	20	55.9	ATAAGGGTCTTCTCTTTGG	404	21	55.1	219
BES	DX579533	dinucleotide	448	495	48	48	AG	TTGAGTGAGTGTGTTATGTT	414	21	54.7	AGCGGTAGTCTTACTTGATT	665	21	54.9	252
BES	DX579663	pentanucleotide	725	739	15	15	AGCAT	TCAGTGTGCCAACATTT	210	18	55.8	CATTCACTCTTCTCCCTCTT	528	21	55.1	319
BES	DX579724	pentanucleotide	470	484	15	15	AAAAC	CATTGTTGTGAAGTATGATGA	499	21	54.6	GCATGACGTAGCATGATGAGT	818	21	55.1	320
BES	DX579799	dinucleotide	20	39	20	20	AG	AGAGATGCTTTATTTGACCT	248	20	50.8	ACACCAACACACACAAACAC	592	20	55.0	345
BES	DX579822	pentanucleotide	311	325	15	15	AGGGG	ATGGCAGGAGAGAGAGAGA	2	18	55.7	TGAAGGGAGTAGGATTTGAC	169	21	55.8	168
BES	DX579837	pentanucleotide	293	317	25	25	AATCC	CTCTCTCTACCACTTCTCT	224	20	55.0	TGAACAGAAATCAACACAGA	620	21	54.3	397
BES	DX579922	dinucleotide	540	603	64	64	AT	TCCTCTCAACATAAAGGG	142	19	55.1	AATCAAGCCGAACACAG	362	18	57.1	221
BES	DX579945	pentanucleotide	330	349	20	20	AACATG	AGAGGGAGCATCAAAAGATAG	368	21	55.3	TCAAGGAACAGTAAAGAAA	693	21	54.3	326
BES	DX579972	pentanucleotide	457	481	25	25	AACATG	AGATTACGACGATGATGATG	126	21	54.5	CTGAAGTGAACATGAACGTAAA	424	22	54.8	299
BES	DX580029	dinucleotide	136	153	18	18	AT	TGSCAAGTGATGTGTTCTTT	237	21	55.8	AAGTTCAGTTCAGATTAGTTGAG	514	23	52.3	278
BES	DX580039	trinucleotide	61	78	18	18	AAG	CTGTGTGATGACTTGTGACCT	109	21	52.3	TGAGCCAATAATCTTTCTG	213	19	53.4	105
BES	DX580049	pentanucleotide	202	216	15	15	AATTC	CTTTGTGTTCTCTGTTATGT	39	21	54.3	CAACTCCGTCATCAATGATGT	337	20	56.1	299
BES	DX580066	trinucleotide	291	305	15	15	ATC	ACAAACACCAAGAGAAATGAA	167	21	54.9	TGAACAGTCAGATTAGAGCA	518	22	55.4	352
BES	DX580097	dinucleotide	147	162	16	16	AT	TTGAGTAATGAACAAGTATGA	181	22	52.6	TTAGTGTAGTTGGGATTT	411	19	52.1	231
BES	DX580208	dinucleotide	105	182	78	78	AT	AAACTTACATTGAGGAGACAA	109	21	51.6	ATTTAGAGCTTTGGGATG	508	18	50.5	400
BES	DX580252	dinucleotide	93	114	22	22	AT	GGGTGGAGAGAGTGAAGTAG	54	20	55.2	GAGCAAGTGCATCAATAAGG	393	21	55.0	340
BES	DX580287	tetranucleotide	455	470	16	16	AAAT	AGATTGATTAATGTTGTTGGAG	43	23	52.9	AAGGTAGGTTTGGGATTT	416	21	53.0	374
BES	DX580290	dinucleotide	342	359	18	18	AC	GCCTTCGTCACTACTTTT	360	18	50.8	TGTTGGAGTCTTCTTGGG	552	19	56.2	193
BES	DX580299	dinucleotide	424	439	16	16	AT	TACCTTGCCCACTACTATT	181	21	53.4	GAGTTGAGGATTTGATGT	466	21	54.9	286
BES	DX580455	dinucleotide	321	338	18	18	AC	AAACCAATAAATGACAACCT	315	21	55.2	ACCTACACATCCATACCTTT	612	22	54.4	298
BES	DX580463	pentanucleotide	522	541	20	20	AGATC	ACTCATCCTTGCCCACTTAC	157	21	55.9	TGTTGTGATTTGGATTTG	404	19	55.2	248
BES	DX580514	dinucleotide	259	348	90	90	AT	GGCATGTCTCACTTCACTTT	454	20	54.3	GGGTGCTGTGATTTGTCCTA	750	19	54.2	297
BES	DX580560	dinucleotide	240	275	36	36	AG	CCTAATGCTCTTGTGCTAA	218	20	55.7	ATGACCTCTCTTGGGAAAC	477	21	57.1	260
BES	DX580560	trinucleotide	334	375	42	42	AAT	ACATCTTCTCTGCTCTTGT	117	20	51.1	TGGAGCCCTACTATCTTGT	388	20	51.7	272
BES	DX580617	pentanucleotide	258	272	15	15	AACATG	GAGAGTTGAGAGGACTGTTGT	25	22	55.2	TTATGTGATTTGTTTCCA	422	20	52.3	398
BES	DX580625	pentanucleotide	334	348	15	15	AACATG	TACAATCTCTTACCACTC	104	21	54.2	TCTAAACTGAACGGAACTGAA	333	21	55.2	230
BES	DX580646	pentanucleotide	311	325	15	15	ATCCG	CTTTGTTCTCTCTCTCTCTCT	257	21	55.4	ATATTCATCTGTTCACTTC	555	21	53.4	299
BES	DX580855	pentanucleotide	347	366	20	20	AACATG	CTCATCTCAAGGTCCTCCA	270	18	59.4	GGTGACGAGTCGGGTATT	643	19	55.2	374
BES	DX580963	pentanucleotide	649	663	15	15	ATCCG	TAGTCTCTCTCGGCTTATTT	300	20	53.5	CTCCCATTTGTTGCTCTATTG	614	21	54.8	315
BES	DX580992	pentanucleotide	780	809	30	30	AG	GTGTGCGGTTTGGATTAG	515	18	54.9	TTAGTACGTTGGGTGATTT	824	21	54.7	310
BES	DX581026	pentanucleotide	499	513	15	15	AAAAC	TCATCATCTCTGCTCTGT	658	18	52.0	GTGACGCCAATACATCCT	838	19	53.2	181
								TTCTTCTTAGATTTCTTCTTGT	263	22	54.7	CAATGTTTGAAGTATCTTTG	604	21	54.3	342

BES	DX581078	pentanucleotide	247	261	15	15	AATTC	CGCTTTATCTATCTTTACAC	121	22	53.7	CCATACATCAACAATCACAATCA	517	21	55.1	397
BES	DX581113	trinucleotide	663	686	24	24	AAG	GACCAACCCCTACACAGTAA	414	20	55.0	ATGCTCCTCATCACTCTGAAC	774	21	56.9	361
BES	DX581160	dinucleotide	509	528	20	20	AT	GAAGAACAAAGTGGCAAGA	361	19	56.3	ACAACAACCAATACATCTCC	717	21	54.1	357
BES	DX581173	tetranucleotide	294	309	16	16	AATT	TGAACAATGGAAGAGAAAGA	93	21	55.1	AGTGAAGTAGTGAGTAGTGGG	362	22	55.0	270
BES	DX581174	pentanucleotide	777	791	15	15	AAAAAG	TAGGGTAGAAGTAGGAGAG	475	20	54.7	AAAGAAGTTGAAGAGAGAA	820	21	50.4	346
BES	DX581224	pentanucleotide	405	419	15	15	AAAAAG	CGAGGTGTTCTCTCTGTT	168	20	54.6	TGGTGTGTTCTCTCTCTCA	527	21	55.2	360
BES	DX581228	tetranucleotide	625	640	16	16	AAAT	GCTTGAATCTTACTTCCCTATT	603	22	53.7	TGAATAGGCTTGATGGA	731	19	54.8	129
BES	DX581333	pentanucleotide	741	755	15	15	AAAAAG	CACACCATCTGCTTTCCAC	483	21	54.7	AATCCTACCAACCAATCAAA	880	21	54.6	398
BES	DX581340	trinucleotide	259	273	15	15	ACC	TTCTAATCATCTCTTACCAC	48	23	50.1	ACTGTGCTGCTATTGTT	311	20	50.4	264
BES	DX581364	pentanucleotide	261	275	15	15	AAATT	GTTCTTCAGATTTCGCTC	1	19	55.0	TAGTGGATTAGTGATGCTTT	313	21	54.1	313
BES	DX581376	trinucleotide	687	701	15	15	ACT	CTTTGATTCTCACCAATTTCT	446	20	54.3	TGTGCTCTTCTATTATTCCA	817	21	55.1	372
BES	DX581390	trinucleotide	288	308	21	21	ATC	TGCTAGATCTGCTGATTTCT	117	21	55.1	CGTGTGAAGATTATTACCAA	360	21	54.6	244
BES	DX581404	dinucleotide	191	284	94	94	AT	TGACTCTTTGCTGTGTGA	313	21	55.1	CGTGTGTGTGTCTCTCT	578	21	56.3	266
BES	DX581447	trinucleotide	348	362	15	15	ACC	TCCATTACCAACCAACACC	210	18	54.8	AGAGGAGAGAGAAAGAGAGTGT	394	23	54.8	185
BES	DX581469	pentanucleotide	325	339	15	15	AAACC	AAAGGTTGGCGTATTATGA	51	20	55.0	TGCTCTATGTGAAGTGTGGA	428	23	55.0	378
BES	DX810998	pentanucleotide	481	495	15	15	AAAAAG	TTCTGTGGATGAGGAGATG	457	20	55.1	TGAGTGAAGTGGTAGGGA	586	20	55.7	130
BES	DX811002	trinucleotide	722	739	18	18	AAG	TTCAAACCAACTTTACCCCTC	515	21	54.5	CATACCTTCACTCTCGCCAC	784	20	55.9	270
BES	DX811018	trinucleotide	120	173	54	54	AAT	GCACCAATTAATCTTTTCA	85	19	51.1	GAACAGTAGGTTCTCACGG	479	19	55.6	395
BES	DX811107	trinucleotide	473	487	15	15	AAT	CCAATAGTTGACCACTCTCA	174	21	55.3	ATTTCACTTTCAGCCCTCT	560	19	53.9	387
BES	DX811154	pentanucleotide	299	313	15	15	AATTC	TCATACCTTACCCCTAACCT	91	21	55.4	GCACCTACGCTTTTCACTT	446	19	55.3	356
BES	DX811176	trinucleotide	605	619	15	15	AAC	GTAAGATAACCCCAACCCCTG	492	21	55.4	CACATCCAGTCAATCAACCT	740	20	55.9	249
BES	DX811197	dinucleotide	426	461	36	36	AT	TTAGGTTCTCTTACCACTCC	247	21	55.0	TGCCCTTTCATCATCACTACTC	585	22	54.5	339
BES	DX811295	dinucleotide	712	731	20	20	AT	TTCAAGGAATAAGAATAGT	524	22	51.9	TGATAAAGTTGGAAGGAA	793	19	50.7	270
BES	DX811411	pentanucleotide	612	626	15	15	ACCCG	TGATGACTGAGGTGAAGTTGT	475	21	55.6	GGCTTTGGAGATTGATTTAG	716	21	55.7	242
BES	DX811534	trinucleotide	332	355	24	24	AAC	ACAAGCTATACCCATCATCAG	203	21	54.9	ACACAAATCCCAAGAAGA	580	21	55.6	378
BES	DX978293	pentanucleotide	203	222	20	20	AGATC	GGAAGGAGAGATAGTGTGAGG	465	21	55.5	ATCATTAGCGGACAAGTTTC	666	20	56.8	202
BES	DX978676	pentanucleotide	156	170	15	15	ACCCC	GAGACGAATCAACAAGAACCC	99	20	54.7	AGATAGTTGGGAGAGGAACAC	455	21	54.9	357
BES	DX978752	trinucleotide	402	419	18	18	AG	ATACCGCTGGAAGGGGCAAA	6	21	65.9	ATCGGGTGGTGTATTGGG	282	18	59.0	277
BES	DX978845	pentanucleotide	649	668	20	20	AGAGG	TCAACCTACCCCAACAATAAGA	319	21	54.8	TGAGGAGAAACAGGAAATAAA	654	21	54.2	336
BES	DX978874	trinucleotide	386	400	15	15	ACT	AATAGCCAACACTTCTCCTTC	593	21	55.2	ATCTCGCTCACTTCTCTCTC	696	21	55.5	104
BES	DX978885	dinucleotide	147	164	18	18	AG	TCAGACACACAATGCTAACCC	264	20	54.5	CCTAAGACTCCAAACAACA	434	21	55.4	171
BES	DX978937	tetranucleotide	129	144	16	16	AAAT	GCAGGTTAGAAGGAATGTTT	114	21	52.2	CATTAGGATTAGGGTTGGA	308	20	54.3	195
BES	DX978954	pentanucleotide	251	265	15	15	AACTG	GGAATACCCCAACATAAAT	32	19	53.3	AATAACTGCGCAACCAA	363	18	54.9	332
BES	DX978980	trinucleotide	559	573	15	15	AGC	TTTAGGGCTGTTCTCCCTC	224	18	55.3	GCTTGGTCCGCTATCC	478	18	60.6	255
BES	DX979003	pentanucleotide	284	298	15	15	AAAAT	GTGTTCACTGTGTTCCTCAATC	378	21	55.4	CCTTACCTCTTCTCTCTCTG	624	21	54.9	247
BES	DX979032	dinucleotide	243	258	16	16	AC	TAATCGCCCTCCTCTATCGT	58	20	58.8	CAAATAACAACAACCCCACT	352	21	55.1	295
BES	DX979035	dinucleotide	354	369	16	16	AG	ATGAGAGAGAAGAGTTTGGT	102	20	50.3	TTTCCATTCCATTACACT	346	19	50.4	245
BES	DX979090	pentanucleotide	472	486	15	15	AGGGG	GAAGAACCAACGACCTCTAA	297	21	56.1	TATCTCAAGGGAACCTCCTG	524	20	54.4	228
BES	DX979113	pentanucleotide	650	669	20	20	AAAAG	ATACTATTCCACACAAGCAA	344	21	55.8	TAACTTCTCCATCACTCCCGT	710	21	58.7	367
BES	DX979115	trinucleotide	92	118	27	27	AAT	GGAATAAATGGTGTGATGAAG	433	21	54.6	TGAAGACCTATGGAGAGTAG	737	21	51.3	305
BES	DX979150	trinucleotide	282	320	39	39	AAT	TATCGTAATAAGCAGCAAAACC	60	21	54.9	ACAACCTTCCAAAGAACACAA	286	21	54.9	227
BES	DX979202	pentanucleotide	391	405	15	15	ACCCC	CCGAGAGAGAAGATAGAGAATG	46	22	55.1	AAATAAGGTTGGTAGATGTA	435	22	50.3	390
BES	DX979236	pentanucleotide	265	279	15	15	AATTC	GTTTCAACCTTTCTCCTCTC	320	18	54.4	TTCCTTTCTTTATGATTTCCC	698	21	55.1	379
BES	DX979239	pentanucleotide	270	284	15	15	AGCCG	TCATACCTTACCCCTAACCCCT	52	21	55.4	GGACTCACGCTTTCATCTCT	414	19	55.3	363
BES	DX979278	trinucleotide	553	570	18	18	AAC	GAATAGCACTGGTGTTCGG	228	18	56.6	TGATAATGGAGCTTGACAA	593	18	50.3	366
BES	DX979315	pentanucleotide	202	216	15	15	AAAAAG	TTGAGGTGGAGTGTGATGTT	495	21	54.7	CGTTGTTGATACCTTTATGG	713	20	50.9	219
BES	DX979363	dinucleotide	562	579	18	18	AC	ATTATTGAAAGTTGGTCAAT	164	21	50.7	AAAGGAACACTCTCTCA	530	18	52.9	367
BES	DX979470	pentanucleotide	208	222	15	15	ATATC	CACAGACACAGACACAGACAG	419	21	55.1	TTATCAAAAGCCCAATAAGA	682	21	55.1	264
BES	DX979483	trinucleotide	50	64	15	15	AGG	CTATGTCAGTCCACCTTATT	103	22	55.0	GGTCTTTGTTGATTGTCTCA	353	21	55.3	251
BES	DX979508	pentanucleotide	386	400	15	15	AAAAT	ACCTCATCTCCAGGCTTCT	12	20	55.6	TATGCTTGTCTCTGTTGTT	188	21	55.1	177
BES	DX979691	pentanucleotide	536	550	15	15	ACTGG	CTCGTTCGTCGGTGTCT	178	18	59.8	AAACTCACCACTTCTCAAAA	425	22	54.0	248
BES	DX979870	tetranucleotide	590	609	20	20	ACAT	ATTGCGAGACGGGCTACT	373	18	58.4	TCCAAGAGAGGAGAGTCAA	659	20	55.0	287
BES	DX980014	pentanucleotide	302	325	24	24	AAAT	GTAAGTTGTGTGGCGGTATT	310	21	56.7	GTCGTGGTGTATTCTGTTG	671	19	54.9	362
BES	DX980108	dinucleotide	747	762	16	16	AG	AGCTTCCGCTGCTAAGTAA	125	20	54.6	CGTCTATCACTACACTCA	389	20	54.5	265
								GTCCTCTCTCTCAAAACCCCTC	719	21	54.7	TAACTTGTGGGCAACTCTG	915	19	54.7	197

BES	DX980117	dinucleotide	605	666	62	62	AT	AAATCACTCACTTCCCATTC	445	20	54.0	CCCAACAAGGTTGCTCTAA	781	18	54.3	337
BES	DX980165	dinucleotide	287	302	16	16	AG	CCGAAGGAGGTACTATG	259	19	54.7	GTATGTTGTTGGATGCTCTGT	492	21	55.2	234
BES	DX980294	trinucleotide	139	156	18	18	AAG	TAATCCAAGCATACAGTTGA	68	21	55.8	TGAGGAACAGGAACATCAAT	217	20	55.5	150
BES	DX980375	pentanucleotide	57	71	15	15	ACCAT	ATTAGTTGAGATCTGTGAA	13	21	54.1	TATGACTGATGGTGGTTGA	200	19	52.8	188
BES	DX980440	trinucleotide	57	71	15	15	AAT	TTGTATGTGACTTCTCCCA	20	21	55.1	CATCATGCTTGGTTCCT	223	18	54.3	204
BES	DX980558	pentanucleotide	431	450	20	20	AGATG	ATCCGACCTATTGTCACTTT	306	21	55.3	ACCTCACACATTTTCATTCA	703	21	55.6	398
BES	DX980722	tetranucleotide	695	710	16	16	AAAG	GTCCATCCTTTGCCAGTAG	395	19	55.7	CTCGGTTTGGTTTGAAGTAA	794	21	54.7	400
BES	DX980725	dinucleotide	26	71	46	46	AC	CTATCAACACACACACACC	5	21	57.2	CCCAACATTTCTCACTTTG	261	19	54.0	257
BES	DX980983	pentanucleotide	704	723	20	20	AACTG	TACTATCTGAATGTGGGCTT	398	20	52.4	GACCTGAATGAACACTGACTGA	788	21	55.3	391
BES	DX981086	trinucleotide	87	101	15	15	ACC	CTTTATTATTCTGCCACCA	66	20	55.4	GTAGAGACATCACGCCCA	363	18	55.4	298
BES	DX981098	dinucleotide	489	602	114	114	AT	AAGAGGTGGAGTTATGTCT	313	20	51.5	TCTACGGTCTATTGGG	689	18	54.3	377
BES	DX981165	dinucleotide	352	371	20	20	AG	CITTCACCAACCCCAACAA	250	19	54.6	AGAGCAACATCCAGTAAGACA	543	21	55.0	294
BES	DX981168	pentanucleotide	355	369	15	15	ACCAG	TGTGCTGTAACTAAGGGTGTG	322	22	55.4	CGTTGTATTATTCGGAG	588	18	50.2	267
BES	DX981228	dinucleotide	311	366	56	56	AT	TCAATCTTCCCTATTGTTG	166	20	50.4	TTTGTGCTGTTGTGTAA	475	19	54.3	310
BES	DX981367	pentanucleotide	256	270	15	15	AATTC	AGACGGAATGAATGAATAAA	225	21	54.0	TTTGAGCGAGAAGGTTAG	539	19	55.5	315
BES	DX981389	tetranucleotide	712	727	16	16	AAAC	TAGCAGAACTTACCCATCAAG	492	21	54.8	GCAACAAACACAAAGAATCA	753	21	56.4	262
BES	DX981429	pentanucleotide	190	214	25	25	AGATC	AGGCTATGTTCAAGTTCACCT	147	21	55.6	GGTCTTTGTTGATTCGTC	350	19	55.4	204
BES	DX981452	trinucleotide	272	286	15	15	AAC	ATTCTGATAGGAGTGTGACC	146	21	53.2	AGCCATGAGGGATTTCG	433	19	54.3	288
BES	DX981456	trinucleotide	624	638	15	15	AAT	TTTGAGTTGTGGAATTGATTT	551	22	54.1	GACCGACTTGACTTCCTAAT	706	21	55.1	156
BES	DX981566	pentanucleotide	577	591	15	15	AAAAAC	CAOCTCGGAATGTGAGTTT	522	19	56.0	GTCCTTGTAGGATGGGAGTT	655	21	55.0	134
BES	DX981579	tetranucleotide	727	742	16	16	AATT	TCTCTTCTCTTCTCTGCTT	407	22	54.6	GTAAGTAGTGGAATGATGGGT	794	22	54.9	388
BES	DX981604	trinucleotide	492	506	15	15	AAT	TTATTCCCGAATCCAAA	376	18	54.0	AACCGAACTGAACCTGAGA	603	18	51.1	228
BES	DX981678	pentanucleotide	304	323	20	20	AATTC	TTATGCCGAAGAGAACA	458	18	52.6	GGACAGTGGAGGATTCGAAG	656	19	55.4	199
BES	DX981722	pentanucleotide	434	453	20	20	ATCOG	AAATGAAAGCAAAATCAATCA	204	22	51.4	GGAGTTGGACCGAATAAGT	603	19	54.1	400
BES	DX981731	dinucleotide	277	294	18	18	AC	TACCTTGCCCACTTACTATT	116	21	53.4	GAGTTGAGGTGTTGATGT	401	21	54.9	286
BES	DX981735	tetranucleotide	212	227	16	16	AAAG	TTTGTGTGAGTTGAGTTGTT	114	22	55.0	GGTGTGAGGTAGATTGATGA	470	21	54.2	357
BES	DX981819	dinucleotide	32	61	30	30	AG	TTTGATTTCCCTTCACT	3	18	52.9	CACGCATACACACACCTATC	355	20	54.9	353
BES	DX981883	dinucleotide	658	743	86	86	AT	TTGTGTATCCTTTGCTTGCT	517	20	56.1	TCTCTTACCTATCTCTCCAC	827	22	54.3	311
BES	DX981891	tetranucleotide	460	475	16	16	AAAG	AAATCCCAAGTAACTCAAA	289	20	54.6	CTTCTCAAACACACACACAC	668	21	55.7	380
BES	DX981953	pentanucleotide	524	538	15	15	AGAGG	GAAGAAGAGGGGAGAGTGT	211	21	54.3	ACAAAGGAGAGAGAGGGAG	558	20	55.2	348
BES	DX981975	trinucleotide	434	457	24	24	AAC	CATTTGACCTAAACACACTT	265	21	52.1	ACCCAAGCAACACACTACTAC	487	21	54.2	223
BES	DX981993	pentanucleotide	138	157	20	20	ACCCC	TGGAAGCAGTCAGTGTA	48	18	50.4	TGTGCCATATAAAGATGT	374	19	51.0	327
BES	DX982016	pentanucleotide	161	175	15	15	AACTG	TTTCAGTTCAAGTTCTGTTCC	137	20	55.4	ACTTCATTCGTTTCCATTTT	342	21	55.9	206
BES	DX982037	dinucleotide	485	500	16	16	AC	AAATGATGTGTTGTTGTTGTT	188	21	55.2	GGTCTTATATGTTTGTGAGT	540	22	54.8	353
BES	DX982089	trinucleotide	447	464	18	18	ATC	TATTTCTGTCTCTATGCGG	188	21	55.6	GATGGGACTCTATGCTTG	525	20	55.7	338
BES	DX982119	trinucleotide	689	703	15	15	AAC	ATTACTCTCCACTCTCATCA	472	21	53.8	GTCGCTGTTGCTGTTCTC	761	18	54.9	290
BES	DX982137	trinucleotide	77	94	18	18	ATC	TCTTGATGTTGATGTTGTTG	251	21	54.6	ACTACTCTGGCAATCGTG	470	21	54.7	220
BES	DX982231	pentanucleotide	501	515	15	15	ACGGC	CTGTCACTTCTCTTTGTTT	373	20	54.4	ATTTGATGGGACATCTTGA	631	21	54.9	259
BES	DX982261	trinucleotide	377	391	15	15	AAG	GTCCCGTTTCACTCC	51	18	58.9	TCCTCTAACCTCCATCTCTC	435	21	55.1	385
BES	DX982493	trinucleotide	187	228	42	42	AT	TTTGAACGAAGAAGGTGT	10	18	51.3	TAGCCAACAACCAACCAA	347	18	55.9	338
BES	DX982503	trinucleotide	328	354	27	27	AAC	GTAAACCTCGAACCACTCTT	235	20	56.0	TACAGAGAATGACAGCC	403	18	52.9	169
BES	DX982546	tetranucleotide	712	727	16	16	AAAG	GGTGGGATGATGTTTAGGA	469	21	54.2	TTTGTGTGAGTTGAGTTGTT	825	22	55.0	357
BES	DX982575	trinucleotide	121	135	15	15	ACC	CGCTGTGCTGTTATGATG	51	18	59.1	GCACACTCTCAACCAA	159	18	52.6	109
BES	DX982617	dinucleotide	647	662	16	16	AG	CTATCCTTCATCTCTCTCAAC	331	21	55.4	CTTCCCTCTTCTCAATCTGT	683	21	55.2	353
BES	DX982669	pentanucleotide	594	608	15	15	AAATG	TTAGGACCACTCTGAAATGA	646	21	54.9	ACATAGGAGACATGAGTGA	802	21	54.6	157
BES	DX982688	tetranucleotide	545	560	16	16	AAAT	GCCACGAATCCACACTAA	308	18	55.4	TTCATAAACAACCAAGCA	677	19	52.7	370
BES	DX982704	pentanucleotide	449	463	15	15	AAAAAT	TTGTTCAAGCGTAAAGTAGGAA	367	21	55.4	TAACCAAAAGTCACGAAATAA	624	21	55.0	258
BES	DX982707	pentanucleotide	611	625	15	15	AAAAAG	TCCACAAGAGATAAGGAGAA	437	21	54.2	AGTCTAGTGCCAAAGATGA	807	21	55.0	371
BES	DX982710	pentanucleotide	324	338	15	15	AAACT	AGGGTGGCTCGTAACTGT	25	18	56.2	CGTTGCTCATCTCATGGTT	409	20	56.0	385
BES	DX982713	pentanucleotide	209	228	20	20	AATCC	CAAAAGAGTTAGAGTAGGG	162	21	51.1	TGCTATGTGTTATGGGCTT	456	19	54.2	295
BES	DX982715	pentanucleotide	204	218	15	15	AATTC	AGTCTTGTGTCTCTCTTGA	136	20	54.8	TTTAGGGTATGTTCTCTCGG	373	21	56.1	238
BES	DX982783	pentanucleotide	152	166	15	15	ACTGG	CTCAAGCATCTCAACAACCT	88	20	53.0	AGTCCAATCCAGTCCCAATAA	207	20	54.5	120
BES	DX982792	dinucleotide	165	220	56	56	AT	CTTGATGGCAGAGATTCAATC	57	21	54.9	GAGTTCTGAGTGAGAGAGTG	421	21	55.0	365
BES	DX982794	pentanucleotide	175	194	20	20	AACTG	GTGTAGAGATGAAGGGTGTG	138	22	55.0	AAGTGGGTTTATTTGCTTT	510	21	55.6	373
BES	DX982816	trinucleotide	464	478	15	15	AAAG	AGAAACCCCAACTTTCATTCCT	197	20	55.3	TTTGCTCTCCACCATCTTT	540	19	55.5	344

BES	DX982852	pentanucleotide	506	520	15	15	ACATC	TGTGGTGAATGAAGATAGAGA	419	22	55.0	GAACAAAGAGAGCAAAACAAAC	636	21	54.3	218
BES	DX982854	dinucleotide	495	528	34	34	AC	AAAGCAAAACACTGCCTC	237	19	55.3	GGAGATGAAGATTATTGAAGGT	615	22	54.1	379
BES	DX982875	dinucleotide	236	261	26	26	AC	ATAGAGGTGGGTGGGAGTT	154	19	55.9	TATGTAAAGTTTGTGGGTG	485	21	54.9	312
BES	DX983008	dinucleotide	528	549	22	22	AT	GTTTACAAGAGAGAGGGAGGA	378	22	54.5	GCTACATACAGACGCTATT	642	20	52.2	265
BES	DX983014	dinucleotide	572	589	18	18	AT	AAATAGAGGGCGTGGAGG	411	18	55.3	AAGGAACAGACAGTCAATAAG	768	22	52.2	358
BES	DX983096	pentanucleotide	487	506	20	20	AATCC	CGATAATGGCTTGGATAA	426	18	52.0	GAAATGCTATGTATTGGGT	734	21	54.2	309
BES	DX983102	pentanucleotide	210	229	20	20	AACTG	TTGAGTTCAGTTTCGGCTC	187	18	54.7	AAGTGGTTTATTGTGCTTT	499	21	55.6	313
BES	DX983124	trinucleotide	157	171	15	15	ATC	ATCTATCTCCAAACACAA	96	21	54.6	CTTGCTGACACAGATAACA	484	21	54.9	369
BES	DX983126	dinucleotide	621	636	16	16	AT	TCTCATCTACAAGTTTCTCCT	482	22	54.8	TATCATCTGTCCCATCTCTG	837	21	55.1	356
BES	DX983168	dinucleotide	390	407	18	18	AT	TGAGGGTTGTAAGTAGTCTT	111	21	54.0	GTGATTGTTCCTGCTCTGT	507	20	54.9	397
BES	DX983172	dinucleotide	572	589	18	18	AC	TTTCTGCCCTCTGATCTCT	280	21	55.9	GTGTGAGTGTGTGTCTGTCTG	617	21	54.7	338
BES	DX983199	tetranucleotide	339	354	16	16	AATT	TCCCATCTATTACCAACCA	182	21	54.8	GTTGTGCGACGAGCGAAG	571	18	61.8	390
BES	DX983293	dinucleotide	443	482	20	20	AT	AGTGTGTTCTCTGTTCTCT	354	21	53.1	ACTTGACTGTGTTCTCTGCT	629	20	54.9	276
BES	DX983371	pentanucleotide	190	204	15	15	AAAAG	CGGTAAACAGTCAAGAAA	70	18	52.3	ACTCAACAAGAGGCAATCA	346	20	55.9	277
BES	DX983380	dinucleotide	455	472	18	18	AT	ATCCGAATAAGATGCGATAA	369	21	56.5	ATGAATGAAGAGATGGAGGA	646	20	54.5	278
BES	DX983457	trinucleotide	216	347	132	132	AAT	CGTTTCTCCAAATCAGCT	126	19	55.2	TATGAACCTCTTAGCCAC	415	20	54.5	290
BES	DX983486	trinucleotide	605	674	70	70	AT	CTATTGCTGATTTCCTAGGT	530	21	54.1	CAACTCTGTCTATACGCCCTC	875	20	55.9	346
BES	DX983565	trinucleotide	73	90	18	18	ACT	CAGTAGAAGAGCAACAGGA	45	21	54.9	AAGGAGATCAGATACCCAA	284	21	55.4	240
BES	DX983590	tetranucleotide	695	710	16	16	AAAG	GGTGTGATGATAGTTTAGGA	452	21	54.2	TTGTGTGAGTTGAGTGTTTGA	803	21	55.2	352
BES	DX983709	dinucleotide	363	422	60	60	AT	TGTTAGCTTGTGCTGCTG	327	21	54.2	CTCTGCTATCTGGCTATCTTT	485	22	54.9	159
BES	ED018926	trinucleotide	324	338	15	15	AAT	TATCGGAGCTCATCTG	110	18	55.5	TATCAACACACACAAACAAA	388	21	52.6	279
BES	ED018936	dinucleotide	463	484	22	22	AG	ATGAAGAAGCAAGTGGGTG	271	21	56.8	TATTTCCATCTACGGTCGG	612	19	56.0	342
BES	ED018996	pentanucleotide	320	334	15	15	AATTC	CGAAGAAGTTATGCTCGTTT	14	20	54.9	GAACAAGACGGAAGAATG	372	20	54.9	359
BES	ED019022	pentanucleotide	395	409	15	15	AACAG	ACTCTTTACCTTTGCTTTGG	312	21	55.5	TACCATCTTATGCTTCAGT	495	21	54.1	184
BES	ED019033	trinucleotide	139	153	15	15	AAG	CGCTTTCTCCAAATCTCA	77	18	55.7	ACCCCAATACATCTCTCTCT	208	21	54.7	132
BES	ED019054	trinucleotide	211	225	15	15	ATC	ATGGATTGTGGAAATAAAT	107	21	55.1	TCGAACATAGTAACATCGTGA	467	23	55.1	361
BES	ED019059	pentanucleotide	164	183	20	20	AATGT	AAGGTAGCCGTTGGTAAA	89	18	53.3	TATTTGGTAATGAGGGCAAG	419	20	55.4	351
BES	ED019111	dinucleotide	463	526	64	64	AT	GAACATACTCAGGGTCATTCA	163	21	55.0	CAATAAATCAATCTCACCT	562	21	51.2	400
BES	ED019168	dinucleotide	254	275	22	22	AC	ACACATACTCGAAGGAAGAA	233	20	55.1	CTGGAGTTTGACTGAATGAAC	337	21	54.8	105
BES	ED019176	pentanucleotide	444	458	15	15	ACTGG	GGGAGGAAGTAGAGAGACTGA	108	21	55.2	TTGGAGCTGGATTGGACT	498	19	55.5	391
BES	ED019185	trinucleotide	578	592	15	15	ATC	GAGAGGAAGAGTAGCAGAGG	465	21	55.1	ATGAACGACGAAGAGAGAA	816	20	55.2	352
BES	ED019342	tetranucleotide	133	148	16	16	AATC	CTATTCCTTGGGATTTCAT	34	20	54.6	TCTGTATTGTTCTTGGCAT	210	21	55.2	177
BES	ED019356	trinucleotide	74	143	70	70	AT	AACCTATCAACAATCTCAA	5	20	54.5	GCTAGTCTTGATGCGGG	391	18	54.0	387
BES	ED019413	tetranucleotide	555	574	20	20	AGGG	TGGAGTAGAGATAATTAGGG	469	21	54.2	GGGACCAATACTAAAGGG	807	20	55.3	339
BES	ED019459	tetranucleotide	209	224	16	16	AAAG	TTTGTGTGATTTGAGTTGTT	112	22	55.0	AGGTTGGATGATGTTTAGG	469	22	55.0	358
BES	ED019492	pentanucleotide	414	433	20	20	AATTC	GCTCAGTTTGGTTCAGTTCA	358	20	56.4	TCAGTTTCAAGTTTGTTCAGTTCA	488	23	54.5	131
BES	ED019554	dinucleotide	698	715	18	18	AT	CGTATTGATTGAAGAGGATGA	477	21	55.3	AGTGAATGACACATAAGCAA	747	21	55.8	271
BES	ED019569	pentanucleotide	115	129	15	15	AAAAT	TGATTATTGTGCTCCTCTTT	8	21	54.2	TTTGGCTGGATTATTGTTAG	380	21	54.7	373
BES	ED019696	trinucleotide	499	513	15	15	AAT	TACCAAGCAAGGAGATGG	279	19	56.3	GCTAATGACACCTTACACAA	662	21	55.3	384
BES	ED019856	trinucleotide	335	352	18	18	AGC	CGAGACAGCAGAAATCTCAC	292	21	55.2	GAAGAGACTGAAGAGGAGAAGA	394	22	54.6	103
BES	ED019865	pentanucleotide	184	203	20	20	AATCC	TAAGTCTGAAGCGGTAGATTG	54	21	54.9	GTTTGGGCTATGGAGTAGGT	421	21	54.9	368
BES	ED019886	tetranucleotide	243	258	16	16	ACCC	CACAGTAGTAGTCCGGAACA	140	21	55.4	ATTTGGAGCGTAGAACACCC	520	20	56.8	381
BES	ED019915	trinucleotide	324	338	15	15	AAT	TATCGCAGGTCATCTGG	110	18	55.5	TAATCAACACACACAAACAAA	388	21	52.6	279
BES	ED019925	dinucleotide	72	95	24	24	AT	TCACAACTGGTGGCTTT	46	18	57.5	AACACACTCTCCTCCTCTCTC	210	21	55.1	165
BES	ED019929	trinucleotide	196	213	18	18	AAC	ACTACCAAGGGAATAAACCC	90	21	54.8	AACTCAACGCTAAATGACTAA	267	21	54.2	178
BES	ED019981	tetranucleotide	255	270	16	16	AAAG	TTTGTGTGATTTGAGTTGTT	157	22	55.0	GGTGTGGATGATGTTTAGGA	513	21	54.2	357
BES	ED020040	dinucleotide	501	520	20	20	AT	TACATACCTCGTTCTGTTCTG	458	21	55.5	GTTCCCTGTTGGTAGTGA	750	19	55.8	293
BES	ED020223	pentanucleotide	331	345	15	15	AGCCC	CACGAGCCGAGCCCTAAC	238	18	59.5	GACCCGTTGTAAGAAGAA	537	19	55.2	300
BES	ED020224	dinucleotide	100	151	52	52	AT	CTAACCGCCGAACCCAAAT	56	21	62.6	AGCGGAAGGAATCATAGAA	257	19	54.9	202
BES	ED020231	pentanucleotide	356	370	15	15	AGATC	TAAGGCTATGTTTGTTCACC	313	21	51.5	TAAGGCTATGTTTGTTCACC	635	21	51.5	323
BES	ED020251	pentanucleotide	464	478	15	15	ACCC	AGTTCAAGAGGTTGACTTGG	244	21	56.0	CTACTAAGATGGGAGTGGTTT	621	22	54.4	378
BES	ED020305	pentanucleotide	757	776	20	20	AACTG	CTGTTTCACTTTTCACTCCGT	495	20	55.3	ATTGAGTCAGTTTCACTTCA	819	20	50.4	325
BES	ED020318	dinucleotide	402	433	32	32	AG	CCTCAGCGAATAGACTTACT	193	21	55.4	GTTCCAGTTGCCAATACA	502	20	55.9	310
BES	ED020325	trinucleotide	229	249	21	21	ATC	CCCATCTCCCATCAACT	157	18	55.7	ATTGACTTCCCTTTCTCAGG	415	19	55.4	259
BES	ED020501	pentanucleotide	162	176	15	15	AACTG	AGTTTCAAGTTTGGTTTCGTTCT	141	20	54.6	ATTTCACTTTCATTGTTTCTCC	347	21	55.7	207

BES	ED020504	trinucleotide	706	720	15	15	ATC	TCCCTTACACAGTCTCTTCA	580	21	55.0	CGTCTTCAACCAATTGCTC	794	18	55.1	215
BES	ED020544	tetranucleotide	460	479	20	20	AAAT	ATTCCCTATTATACCCTCTCA	364	21	54.6	ATCACCCCTTGTTCCAC	682	18	55.6	319
BES	ED020611	pentanucleotide	43	57	15	15	AATCC	GGGTGAAGTTACGAATAAA	17	20	52.1	GAAGGATTGAAGTGCTATGTG	290	21	55.0	274
BES	ED020673	trinucleotide	362	376	15	15	AATTC	GAGGAGAAGGGTTAGGT	98	18	54.2	CAAAACACCAAGAGAAATGAA	413	21	54.9	316
BES	ED020743	trinucleotide	122	136	15	15	AAC	ACCAGCAATAACCCCTAATC	101	20	55.7	TACCTACAGTCTTACCA	228	20	55.6	128
BES	ED020847	pentanucleotide	437	456	20	20	AAAAG	CTACACGCAGTTGACCCA	311	18	56.6	CTTCTCTCTTCTCATCCTC	601	21	54.8	291
BES	ED020897	pentanucleotide	549	563	15	15	AAC TG	GCATAACCCCAAGCTTAATAC	478	21	55.6	ACTGGTCTGAAGTGAAGTGA	604	21	54.9	127
BES	ED020920	trinucleotide	207	224	18	18	AG	CAAGAAACCAATCAACAAC	91	21	55.6	CGAGGAGAGAGAGAAAGACA	388	21	56.4	298
BES	ED020993	dinucleotide	278	297	20	20	AC	TACCTGCCCACTTACTATT	119	21	55.5	TTGTGAGGTGATTCGG	411	18	55.3	293
BES	ED021039	pentanucleotide	484	498	15	15	AAACC	AAATACTGGGAATGGAATAG	407	21	52.7	CAAAGGGTGAGAAGTTAGT	602	21	55.2	196
BES	ED021072	trinucleotide	223	261	39	39	AAT	AGTTAGGCTTGTTGTTCTTT	75	21	52.8	TATCTTCGGTCTTTTACCA	422	20	56.1	348
BES	ED021073	trinucleotide	192	207	16	16	AAAT	AGTGCTGCTGCGCCATT	7	18	61.9	GCACTAACAACTAACACAACA	400	22	53.3	394
BES	ED021095	trinucleotide	388	405	18	18	AAG	AAGGTAGAGTGAGGTGAAG	122	21	55.1	AAGAGCAATTAAGGCTG	466	18	54.6	345
BES	ED021220	pentanucleotide	267	281	15	15	ATATC	GAAGCAATGTAATGAAGTTG	232	21	55.0	AGAGGCTGAAGAAGAAAGAG	523	21	54.8	292
BES	ED021243	dinucleotide	859	876	18	18	AT	GCATTAAGACATTAAGGCAC	731	21	55.2	TACGAGCAGTTTCGGTT	921	18	54.4	191
BES	ED021266	pentanucleotide	285	309	25	25	AAC TG	GTATGTGATTATTGAGGCAC	241	22	54.4	AGTTCGGTGTTCAGTTT	378	20	55.4	138
BES	ED021342	dinucleotide	254	271	18	18	AT	ACACACACATACACACAC	226	22	55.0	ATGAGAAACGAGAAATGGA	419	18	51.0	194
BES	ED021349	trinucleotide	720	737	18	18	AT	TACTTAGCGGAATGGTATG	459	19	51.3	AGCGTTCATCATCAATAAA	858	21	55.1	400
BES	ED021355	trinucleotide	157	174	18	18	AAT	AGTTCGGAGAGATTCCATT	85	20	55.4	AGCAGCAATGGTGATGTT	762	20	55.5	294
BES	ED021366	trinucleotide	714	731	18	18	AGC	GAGCTATTACGAGGACACT	469	21	55.3	AGCAGCAATGGTGATGTT	762	20	55.5	294
BES	ED021393	pentanucleotide	686	700	15	15	AAC TT	TGTGGCTTCATACACTTC	549	19	54.4	TATCAACGGAGAACCTG	903	18	54.3	355
BES	ED021445	tetranucleotide	854	877	24	24	ACTG	TGACTGATGACTGACTGACTG	882	21	54.6	GTTGATCTCGTGCTT	993	18	54.6	112
BES	ED021451	pentanucleotide	592	606	15	15	AAAAG	AATAACTGCTTCTCTCAATC	262	21	50.3	GCAGCCACTACTCCTGTT	659	19	55.9	398
BES	ED021474	trinucleotide	304	318	15	15	AAG	AGAAGGTGAGAGAGAGAGAA	247	21	54.9	ACTCACAAACCAATGAAA	349	21	55.6	103
BES	ED021502	trinucleotide	566	631	66	66	AAT	ATTGTTATTGTTATTGTTATCGT	413	23	50.4	TATCAGTTGGGATGGA	747	18	54.5	335
BES	ED021667	pentanucleotide	580	599	20	20	AGAGG	GAAGAGGAAATGGCGTG	492	18	56.7	CCTAAGACCTAACTAAACCAG	651	23	53.6	160
BES	ED021669	trinucleotide	396	515	120	120	AT	CACACCTCAACGATGACTAC	316	22	54.9	CACATAGAGACCCACACA	556	20	55.2	241
BES	ED021730	trinucleotide	531	608	78	78	AAT	TTGTTATCTTTGGATGACC	354	21	54.4	ATCGTTGTTCAGCTGCTCC	650	20	57.0	297
BES	ED021746	tetranucleotide	618	633	16	16	AATC	GGCTTCTACACGAGTAACCTC	449	21	55.6	ATCCATACCAACACACAG	758	21	55.0	310
BES	ED021762	dinucleotide	135	172	38	38	AT	AGCGGAATGAAGTGAA	42	18	55.1	GTAACAGCAGCCTAACACAG	389	21	55.3	348
BES	ED021798	pentanucleotide	516	530	15	15	AATCT	CACATAGAGGAGGTGTTCTCA	571	21	55.3	CAGGCGAGTGATCTTTCT	738	21	55.4	168
BES	ED021825	trinucleotide	620	637	18	18	AAT	CTCAACTAATCAACCGACA	507	21	55.5	AACTCCAGTGTTAATGCC	799	21	55.1	293
BES	ED021853	pentanucleotide	624	638	15	15	AAAAT	GCTTGAATCTACTTGCCTAT	602	22	54.7	TTGAATGGTCTTGATGGA	730	19	54.8	129
BES	ED021882	tetranucleotide	529	544	16	16	ACAT	CACTATCTCTTTATTCAACC	448	23	51.9	CCATTGTTGGCATTTCT	728	20	55.2	281
BES	ED021949	dinucleotide	287	314	28	28	AG	TAGTAAAGGAGGAGGAGGTT	252	21	54.0	ACAGTAAGATGTGGTGAAGA	376	21	54.7	125
BES	ED021964	trinucleotide	54	109	56	56	AT	AGCAGATGTTGAACAAGAA	463	20	55.9	TCCACTTTAGGCGAGTCC	765	18	56.3	303
BES	ED021966	pentanucleotide	602	616	15	15	AAAAG	AGAAGGTAATGGGATTTGTT	341	20	55.1	AGTAAGGAGGCGCGCAA	703	18	58.5	363
BES	ED021993	pentanucleotide	689	703	15	15	AAAAG	CCTCTCTTTGTTATTGCTTT	618	22	54.8	GCTAATCTGGGATGGTTTC	820	21	55.2	203
BES	ED022107	tetranucleotide	279	298	20	20	AAAT	GTAGTTTGTCTTTGTTGGG	73	20	55.0	GTAAGGACAGACAGATGA	332	20	55.0	260
BES	ED022116	trinucleotide	126	140	15	15	AAG	TAGCTTTATTCGGCCATC	93	20	56.8	ATCATCTCATTTCCAGAGTT	248	21	55.3	166
BES	ED022150	trinucleotide	296	337	42	42	AAT	GCCTTATTCGGCTGGAT	168	18	55.2	TTACATTTGGTATGCTTT	532	20	50.3	365
BES	ED022268	trinucleotide	134	151	18	18	ACC	GATAAATCAAACTACTCCAAA	4	23	52.4	CTTCACTTCATTTCTTAACC	257	21	55.5	254
BES	ED022269	trinucleotide	135	152	18	18	ACC	ACTGCGACCAACAGCAAC	83	18	58.3	CCCTTCTCTTCTTCACTCC	269	21	54.9	187
BES	ED022478	pentanucleotide	161	175	15	15	AGAGG	CATCTACCAATCAATACACCA	270	21	53.6	GAGAAGAAAGAAAGAGGAGAA	637	22	54.0	368
BES	ED022561	dinucleotide	540	559	20	20	AT	ATAAATGGGATTTGTTCTGA	468	20	55.6	TAAGTAGGGGAAGATGGTGA	424	18	55.0	321
BES	ED022613	tetranucleotide	236	251	16	16	AAAT	ACAGTGCTTGTCACTCAA	189	19	55.1	CTAAGGCGAACCATACA	366	18	54.6	178
BES	ED022641	trinucleotide	840	857	18	18	ATC	GATTACACACCTCATCAAC	702	20	55.3	TATCAAGCACCGTTCCAC	1012	18	55.4	311
BES	ED022744	pentanucleotide	274	288	15	15	AATTC	TCATACCTTACCCCTAACCT	63	21	55.4	GGACTCAGCTTTCACTCT	424	19	55.3	362
BES	ED022766	pentanucleotide	394	408	15	15	AGCCG	AGAAAGCAAGTAATAAGGGA	165	22	54.3	GAACGAGCCGCAACATAC	536	19	55.5	372
BES	ED022822	trinucleotide	304	360	57	57	AAC	CCCTTATGTACCTGCTGCTGA	94	20	55.4	CCTGTGTTACTGGACTCTGT	407	21	54.3	314
BES	ED022929	trinucleotide	459	473	15	15	AAG	CCGATTGAGAAGAAAGATG	294	20	55.0	CGTTTGTGTTGAGAGAGATT	609	21	54.5	316
BES	ED023022	dinucleotide	623	644	22	22	AT	CGTTTCTGGTTTACGCAC	538	18	55.2	GGTAGTTACTTCTCATTTT	703	23	53.8	166
BES	ED023072	trinucleotide	217	231	15	15	ACC	ACCATCTCTCACCTTACCC	144	19	54.7	GCTCACTTACTCGTTACAGG	475	21	54.4	332
BES	ED023088	tetranucleotide	330	345	16	16	AATT	ATCAAGCCCAACAAACAGAA	257	20	55.9	CTCTCTCTCTCTCTCTCTC	642	20	54.7	386

BES	ED023152	tetranucleotide	563	16	16	AAAT	GATTCCTACAAATAACCTTGA	534	22	55.0	AGAAACTCCTTGCTCTCCC	750	19	56.0	217
BES	ED023328	trinucleotide	1	21	21	AAC	TTCAGGTGTTCTAAATGATG	71	21	52.9	ATCTCCTTACTTTCTCTCTCT	449	22	50.2	379
BES	ED023332	pentanucleotide	437	456	20	AGATC	GTGGATGGATAAGGAAGTGA	315	20	54.9	GAGACGAATCAAAACAAGACC	566	20	54.7	252
BES	ED023339	dinucleotide	216	231	16	AG	CAGAGACCACAAGTGAAGTCA	73	21	54.8	ATGAGGATGATTTGGGAATAG	396	21	55.6	324
BES	ED023392	dinucleotide	363	378	16	AG	AACACCTTCAACAGCACTCT	130	20	54.7	TAAACTCTCTCTCCCTCTCT	458	21	54.4	329
BES	ED023504	trinucleotide	558	572	15	AAC	AGATACATTCACTCTCTGGAC	348	22	54.9	GTTACCTCAACAATCTTACC	686	21	55.2	319
BES	ED023545	pentanucleotide	164	178	15	AGATC	TAAGGCTATGTTAGTTTCAAC	121	21	51.5	AGGATTTGGGTAGTTCAATTC	469	21	54.8	349
BES	ED023559	dinucleotide	254	287	34	AT	CCTAAGGCCTCTTGTCGTA	213	20	55.7	GGCGAAATCTAAAGTCCTAAA	574	21	55.5	362
BES	ED023593	dinucleotide	692	763	72	AT	TGAGAAGGAAATAGTTTGTG	566	21	54.9	ACATACCTCTCACACACACATCA	790	22	53.8	225
BES	ED023599	pentanucleotide	259	273	15	AACTG	TACCTTGCCACCTTACTATT	236	22	55.2	TTAGTGGATGAGTTTGTAAAG	511	21	52.1	276
BES	ED023619	dinucleotide	308	325	18	AC	TAACCTAAACAGATGGTGAA	147	21	53.4	GAGTTGATGGAGTTGTGATGT	433	21	54.9	287
BES	ED023642	dinucleotide	597	628	32	AT	CTTTGGGTTTGAGTCTTTC	368	21	54.8	GTTCAATAAGTCCAGTCCAA	654	20	55.0	287
BES	ED023663	pentanucleotide	372	391	20	AGCGG	GCTTGGGTTTGAGTCTTTC	280	19	54.9	CGTTCAGTATTTATTTGCTGT	576	23	53.8	297
BES	ED023681	dinucleotide	549	566	18	AG	CACGCCAAGAAAGGATTGA	240	18	58.3	GGGAGGAAGAAAGGATAGG	591	20	56.9	352
BES	ED023709	tetranucleotide	684	699	16	AAAT	ATTAGACCAAGGAGAAATCCAG	438	21	55.0	TTGAGGACAAGGTGAAAGT	799	19	53.0	362
BES	ED023767	trinucleotide	475	489	15	AT	GGTCAGCGTTTGAGGTAA	320	18	54.6	GTTCTTTGTGATGAAGGGTC	716	20	54.5	397
BES	ED023772	trinucleotide	151	216	66	AT	CATCTGACGAACATACATCCAC	42	21	55.6	TATCCTCCACCCCTCCCTC	253	18	57.3	212
BES	ED023802	dinucleotide	239	254	16	AG	GACTAAGCAACAGCAGCAC	77	19	54.6	GTCATATATCTCCCATCTCC	400	21	55.1	324
BES	ED023806	tetranucleotide	213	228	16	AAAG	TTTGTTGTTGATGTTGTTT	115	22	55.0	GGTGGATGATAGTTTAGGA	471	21	54.2	357
BES	ED023864	dinucleotide	153	168	16	AT	TTCCAGGCTCTTCTTGCC	12	18	58.7	TTACTTATTTCCCGTATTCC	237	21	55.3	226
BES	ED023901	pentanucleotide	307	321	15	AACTT	AACCACATCTCACATAACAG	233	21	55.0	TCCTAAAGTCTACCCGCATT	430	20	56.5	198
BES	ED023928	trinucleotide	471	485	15	AAT	GGATCTCGGTGGATGTGT	284	18	56.5	TCAAATGGTAAATGGTAAATGGT	636	21	54.5	353
BES	ED023947	trinucleotide	410	436	27	ACC	AGAACCAACTCTCAGTCTCC	382	21	55.1	AGAAACCTGCTGCTGCTGT	631	19	56.0	250
BES	ED023954	pentanucleotide	170	184	15	AGATC	AGGCTATGTTCACTTCACTT	127	21	55.6	GGGCTCTGTTTGTATTCGTC	320	19	55.4	194
BES	ED024102	trinucleotide	386	400	15	ACT	TCGACACACAATGCTAAAC	264	20	54.5	CCTAAGTCTCAAAACAACAACA	434	21	55.4	171
BES	ED024148	trinucleotide	558	572	15	AAC	AGATACATCACTCTCTGGAC	348	22	54.9	GTTACCTCAACAATCTTACC	686	21	55.2	319
BES	ED024209	dinucleotide	155	182	28	AC	AAATGTGGTGTGCTAAATGA	48	20	54.1	TGACCTCTGCTGGGATT	369	18	56.6	322
BES	ED024210	pentanucleotide	541	555	15	AAAT	CGTCAATCTCTGTTGGTATT	503	20	52.7	ATGAGGCGGGTTTCTACTTAC	793	21	57.4	291
BES	ED024232	tetranucleotide	364	437	74	AT	TTCTCTTTTCCACAATAAGA	169	21	52.0	CCACATCTCTCTCTCTACAC	568	21	54.8	400
BES	ED024234	pentanucleotide	627	642	16	ACAT	AGTGTGTTTCTGTTGGAAGT	540	20	56.0	ACGATGTTATGTTGTTTCAG	741	21	53.6	202
BES	ED024250	pentanucleotide	154	183	30	AACAC	AGCCTTGAGTAAGAGGGTTC	79	20	55.2	TAACTCGTCTGAGTAACA	208	20	51.5	130
BES	ED024310	trinucleotide	147	161	15	ACC	ACCATCAATACGCAACAC	116	18	55.4	GAGGAGAGAGAAAGTGAGAGG	231	21	54.9	116
BES	ED024457	tetranucleotide	178	193	16	AAAC	TCTTCTCTCATCTCTCTTGA	51	21	55.0	AGTTGGCACTGTTCAATTAC	352	20	55.1	302
BES	ED024483	dinucleotide	447	462	16	AG	AGAAAAGATGTCGTGTAGAA	426	21	54.2	TGATAAAGACGAAAGCGG	604	18	55.1	179
BES	ED024512	dinucleotide	216	281	66	AT	TCACACAAGACAACGACAAC	63	20	55.5	TATTGCTGCGTATGGGTAAA	429	20	56.9	367
BES	ED024590	trinucleotide	480	494	15	AAT	TAATGATGTAAACGAACGG	642	18	50.1	CCATAGATAGAGAAAGCATAAAGT	944	23	51.7	303
BES	ED024596	pentanucleotide	243	257	15	AAGAG	AGACTGTGTCGTGGTAGGAG	83	20	55.2	CCATTATTTGCTGTCCATT	354	20	55.2	272
BES	ED024608	trinucleotide	541	561	21	AAC	TTCCTTCTCTCTCTTTGTC	289	20	56.0	TTGTGTAATGTATGTTGTTT	635	21	51.8	347
BES	ED024609	dinucleotide	811	828	18	AG	CGGGCAGGCTTTCTGGG	486	18	68.5	GTCGCGTGGAGGATGTT	882	18	60.6	397
BES	ED024749	pentanucleotide	683	702	20	AGAGG	AGTCTTACCTCTCTCGTTTCC	524	21	54.4	GATGTTGGTCAATTAGGCTGT	897	20	55.1	374
BES	ED024772	dinucleotide	555	576	22	AC	TCTGATGAAGACCACTCAAA	324	21	54.1	GTTAGAACCTGCTGATGAAG	693	21	55.0	370
BES	ED024881	pentanucleotide	610	624	15	AGGGG	CTAATGTAACCTGCTGCTTGT	551	21	55.2	TAATGCCGTTCTTGTC	879	18	57.0	329
BES	ED024887	dinucleotide	64	119	56	AG	CATCTTCTTCTGCTTCTCT	45	19	54.7	GTTTGATACCTTTGTTTCCC	228	19	51.9	184
BES	ED024914	tetranucleotide	475	506	32	AAAG	AATCGCAGAGGAGAGAGAC	184	19	54.5	CTCAACAACCCCTTTTACTTT	557	21	53.7	374
BES	ED024926	trinucleotide	531	551	21	ATC	ACCTTCTGTTAGGGACATT	484	20	55.2	TATTACTACTGCTAGCGCA	825	20	54.7	342
BES	ED024929	trinucleotide	8	28	21	AAC	ACAACAACAACAACAACAAC	41	21	54.3	GTCGATGTCGGGCAAA	245	18	66.6	205
BES	ED024955	pentanucleotide	334	348	15	AAATT	AGTCAATCACATAAATTTGCC	294	21	54.4	TAACTTCCCTACTTGTCTCCA	557	21	56.7	264
BES	ED024994	pentanucleotide	318	332	15	AATTC	AGGCAGAAGGTTAGGTG	55	18	55.2	CAAGAACAAGACGGAATAAA	373	21	54.7	319
BES	ED025021	dinucleotide	256	321	66	AT	GGTGAGATTGAGATGATAAGA	147	22	53.6	TAAATAAAGTTGCCCTTG	491	21	51.9	345
BES	ED025086	dinucleotide	473	490	18	AT	TCTTAGCAACCCCAACACTAC	379	21	54.7	TGTCCTACACCTCTACATAA	547	21	55.5	169
BES	ED025122	pentanucleotide	148	172	25	AGATC	TAAGGCTATGTTCACTTCAAC	103	21	54.6	GGGCTCTGTTTGTATCGTC	308	19	55.4	206
BES	ED025178	tetranucleotide	288	303	16	AGAT	ACTCTCTATGGAAGCGTCA	229	21	56.7	TCATTGTCGTTAGTTATGGA	547	22	55.0	319
BES	ED025237	trinucleotide	770	787	18	AAG	GTATGTTTCAGCGTCAACCA	412	19	55.5	GCTAACTTTCTTCTGCTCT	809	20	50.9	398
BES	ED025259	pentanucleotide	265	279	15	AAC	GAAGCGAAACTCCAATCT	166	18	54.5	TTGCTACTGAACCTGAACCTGA	443	20	51.9	278
BES	ED025269	tetranucleotide	510	525	16	AGCT	TTTGTCAGAGGGTGGATG	489	19	55.2	AAGGAGTAGTAAGTAATGGTAGTG	683	22	52.1	195

BES	ED025322	pentanucleotide	117	131	15	15	AACTG	TTCAATTCAGACAGTTCAGT	147	21	54.9	ACAGGAGCAACAGCAATAA	544	19	54.4	398
BES	ED025389	dinucleotide	50	67	18	18	AG	TTGGATGGTATTCAGGATTT	2	21	53.8	ACAACAGTCATTTAGACACA	158	21	54.0	157
BES	ED025430	dinucleotide	418	439	22	22	AT	TTGTAATCTAATCCAATCGTG	340	22	54.6	TTATTCGGTGTGCTTCTC	865	20	55.5	326
BES	ED025455	dinucleotide	621	635	15	15	ATC	TAACCTTTGATTCAGAGGCT	531	19	55.8	GATGATCTTTCTTGTTCT	749	21	52.7	219
BES	ED025486	dinucleotide	419	436	18	18	AT	TGCCATAGTTCCTTCATAC	366	19	50.9	TCAGATAGAGCGTAAGTGAT	587	21	51.9	202
BES	ED025575	pentanucleotide	674	688	15	15	AAACT	TTACAGATGGTGTCAGGAATAA	503	22	54.9	GCTTTATTCGGAGAGTG	846	19	55.2	346
BES	ED025625	dinucleotide	261	276	16	16	AT	ATTGAAGGTAACTATCGGT	208	21	52.8	CAACAAGAAACAAACAAGG	419	21	55.1	212
BES	ED025639	trinucleotide	158	172	15	15	AAG	GTTTGGAGTGTGATGGG	44	18	55.8	TTAGTGGCTCTTCTTCTC	419	21	54.2	376
BES	ED025643	trinucleotide	329	344	16	16	AAAT	GTATTTTCATCTCCAAAGGG	155	20	53.8	GCATCATCTCAAAACCTG	489	18	54.8	335
BES	ED025673	trinucleotide	158	235	78	78	AAT	TCTACATCACTGTTTGCCTCT	134	21	55.0	TGTATCGGCTCAATCACTAC	525	21	55.4	392
BES	ED025762	trinucleotide	377	433	57	57	AAC	GCTGCTATTGATGTGTTGTT	442	21	55.5	AATGATCTGAGAGAGGA	808	20	55.0	367
BES	ED025785	dinucleotide	530	545	16	16	AG	GTATGCCAATCTGTGTCATT	484	21	54.0	CTTTCAGTAGTTCGTTAGCA	879	21	55.0	396
BES	ED025795	trinucleotide	180	194	15	15	CCG	ATATCAAAATCAACGCTAAA	33	21	50.9	CGACAACAACAACAATAACA	337	21	54.7	305
BES	ED025852	dinucleotide	400	415	16	16	AC	GATGCTAAGTCTCGCTTGT	121	20	55.3	GTGGAGGGTGTGTGTGT	438	18	57.5	316
BES	ED025880	pentanucleotide	552	571	20	20	AGATC	AGACGAATCAACAGAGACC	464	19	55.2	CATACGCAGAAATACCCAGT	803	20	55.3	340
BES	ED025915	dinucleotide	535	566	32	32	AC	GGATGTTGTTGTGAAGGAAA	431	21	54.4	GTCTTTGGTGAGAGTGAA	721	20	55.2	291
BES	ED026093	pentanucleotide	247	271	25	25	AAGAT	ATGTTCTAATCTCATCCACAC	173	21	51.5	ATAACGGTCTCTCCATCTT	534	21	54.6	362
BES	ED026150	pentanucleotide	444	458	15	15	AACTG	CACCATTCATTCAGTTTCAGT	375	21	55.1	ACTTAGGATTTCTCTCTCGG	490	21	55.2	116
BES	ED026176	trinucleotide	180	197	18	18	AAT	TGTGTTGATTATGTCGTGTA	57	21	52.3	ATTATTGCGTGTGCCCTT	458	18	56.6	400
BES	ED026180	trinucleotide	584	601	18	18	ACC	AGAAGTTGATGAGAAAGATGG	461	21	53.6	TGTGAGAGAGATGAGAGT	625	21	53.9	185
BES	ED026242	pentanucleotide	50	64	15	15	AACTG	ACTTGGTTCAGTTAGTTTCTCT	66	21	52.3	TGAGGTGAGAAATAGAGTTCA	222	21	54.9	157
BES	ED026250	pentanucleotide	316	332	15	15	AATTC	AGGCAAGAGGGTTAGGTG	55	18	55.2	CAAGAAACAAAGACGGAATAA	373	21	54.7	319
BES	ED026317	pentanucleotide	184	198	15	15	AAAAAG	GTGCGAGCCTACCTCTCTCT	29	18	55.5	GGTGAACGCATAGATTGA	366	20	55.2	338
BES	ED026421	trinucleotide	489	508	110	110	AT	TTCCAAAGTAGTAAGTGA	465	21	51.8	ATTGCTGCTGTGTGTGTAG	686	21	57.1	222
BES	ED026591	trinucleotide	575	589	15	15	ATC	ATACCCGATTAACCTTC	459	18	54.9	TTATCTTCATCTTTCATCCA	617	22	51.7	159
BES	ED026621	dinucleotide	152	171	20	20	AC	AGTGGAGGCGAGGTAAATC	35	19	55.0	TGAACCCGTAATCTCATTT	432	20	54.7	398
BES	ED026639	dinucleotide	505	526	22	22	AG	CTCCTTCACACGCCATTC	486	18	57.6	AAAGAAATCAACCAACAAGAG	725	21	53.7	240
BES	ED026699	dinucleotide	549	586	38	38	AG	TACACATCAACCAACCCGA	481	20	55.1	AGCAACAGCTAGAACCGAGA	710	20	55.2	250
BES	ED026787	dinucleotide	686	711	24	24	AT	CAGATTGAGTGGTCACTCTAA	588	21	55.2	GCAGAAAGCTAGAAACATACC	766	23	54.2	179
BES	ED026801	dinucleotide	477	504	28	28	AC	ACACTCACGCACACACAC	458	18	54.4	TTAGATGTTTATCACCCCTTCA	568	21	52.5	111
BES	ED026814	dinucleotide	210	225	16	16	AT	TGTTAGTCTTTGGATTGT	3	21	54.7	ATACCTCAGTCTTGGGATGT	298	21	55.2	286
BES	ED026820	trinucleotide	210	225	16	16	AG	ATTGTTCTGCTCGTCACT	1	20	55.8	ATCATCTCAGTATCTCACCC	280	21	55.5	280
BES	ED026820	trinucleotide	616	633	18	18	AAT	ACAGAGGAGAGACACACGAA	377	20	54.9	TTTATTTGAGTTGGAGTATGAA	760	22	52.0	364
BES	ED026924	dinucleotide	646	677	32	32	AT	GTGAAGATAAGTGGGCAAG	498	20	55.0	CCGAACCAACATCATAATAC	740	21	54.6	243
BES	ED026936	dinucleotide	402	433	32	32	AT	TCAAGCAGTCTCTCAAGTTC	194	21	54.9	GAAGGAAAGGTTATTTGTG	500	22	54.7	307
BES	ED026957	pentanucleotide	432	446	15	15	AACTG	GGACTTGTCTTATTCGGCA	383	19	56.3	GCAATCAGTTCACTTCAGTTC	554	21	55.0	172
BES	ED027028	pentanucleotide	706	725	20	20	AACTG	AGAAAGGAAAGAAAGAGATG	568	21	54.5	TCTGAACCTGAACTGAACGTAA	750	22	55.2	183
BES	ED027119	trinucleotide	665	679	15	15	ACC	ATTGGATTGTCTGAAGTGA	434	20	53.0	CAGGTGGTGTGTGGTG	708	18	59.3	276
BES	ED027151	pentanucleotide	351	365	15	15	ACACG	GGACACATTACTTGGATACTT	366	22	52.6	ACTATGATTGAAGGCTGTT	711	21	53.3	346
BES	ED027238	dinucleotide	155	176	22	22	AG	ACGGTGAAGAAACAGAGGA	98	20	54.9	AAATAATGCAAGAAAGTGACAAA	368	23	53.0	273
BES	ED027256	tetranucleotide	249	264	16	16	AATC	CTCTCGCTCCCTCACAC	9	18	56.9	GGTTCCAGTCAACAACACTAC	371	21	54.6	363
BES	ED027293	dinucleotide	625	672	48	48	AG	TGTTATCTTCTCTCTCTG	423	21	54.9	CCACTCAGTCTCACTCTCT	801	21	54.4	379
BES	ED027320	trinucleotide	94	189	96	96	AAT	CTAAACTGAACCGAACTGAAC	290	21	54.2	TGATGTTGGGTAATAGGATTT	641	22	55.2	352
BES	ED027395	trinucleotide	442	456	15	15	ACC	ACTGTGTTGCTGTTATTGTT	406	20	50.4	TTCTAATCATCTTCTTACCAC	669	23	50.1	264
BES	ED027401	trinucleotide	390	404	15	15	ACT	CCCTCTTTATCTAGGCGTT	223	20	55.3	CAATGGCTTGGCTATTGG	607	19	55.2	385
BES	ED027478	pentanucleotide	262	281	20	20	AATTC	AAAGACGGAACTGAAGATAA	229	22	54.9	CCCGCACCTCTGTTTGG	509	18	62.1	281
BES	ED027509	tetranucleotide	60	75	16	16	AAAT	GCGGTGGAATACAGCATC	12	16	57.5	CAGCAAGAAATAGGAAGGAG	203	21	55.9	192
BES	ED027536	dinucleotide	213	228	16	16	AT	ACACAAGAACCCACATACAA	143	21	55.5	TGTTGCTGAAATGGAGAAG	541	19	54.6	399
BES	ED027546	trinucleotide	247	261	15	15	AAC	GTAATAGGAGGGTGAAGGAGA	180	21	55.0	CATCAACATAACAAATGGAAGA	317	22	55.3	158
BES	ED027585	trinucleotide	592	606	15	15	AAC	TCTGGACACATCATCGTAA	429	20	54.9	GTTGTTGCCCTCTCTTTAG	720	20	55.0	292
BES	ED027610	pentanucleotide	686	700	15	15	AATTC	AAACAACGCCCAACATAC	645	19	55.6	GGTGTGAAATCAGGAACGG	752	20	56.2	106
BES	ED027612	pentanucleotide	540	554	15	15	AACTG	GAACTGAACCTGAATGAATGA	483	22	54.8	ATGTGCTGTGCTATGATGA	775	20	55.1	293
BES	ED027666	trinucleotide	490	504	15	15	AAT	CGTAGAACAACCACTCAGT	431	19	52.7	AAGCCGACAAATAACACC	671	19	56.0	241
BES	ED027649	dinucleotide	631	646	16	16	AG	GAGGAAAGAAATAGAGGGAC	456	22	55.4	GTGCTGTTGTGAATAACCC	758	20	55.4	301
BES	ED027851	trinucleotide	278	296	18	18	AAC	ACACACAACCAACAACAACA	255	21	55.8	AACTCTCTCTCCCTCTCTGTC	641	20	55.1	387

BES	ED031524	pentanucleotide	412	426	15	15	AAATC	TGAAGAACTCACAATGAATAAA	360	22	52.7	TTGAAACGGAGGAAGTAA	618	18	51.6	259
BES	ED031564	tetranucleotide	339	358	20	20	AAGG	ATTACCAACCAACCCAGAAC	158	19	54.7	AAGGAGGAGAAAGACAGAG	462	20	55.2	305
BES	ED031602	pentanucleotide	91	105	15	15	AAGTG	TACCAAAATCAGATCAAGGTG	15	21	55.2	CCCATCAATCCAGTTTCA	137	18	54.8	123
BES	ED031643	trinucleotide	332	346	15	15	ATC	TGCCAAACCTATCACTAAGAC	263	18	54.6	TACTTCTCAAACTCTGCC	601	21	53.9	339
BES	ED031725	dinucleotide	217	294	78	78	AT	GGTATTTCTTGGCTGGCT	180	18	55.3	GATTATTGATGCGTGATTT	523	21	54.5	364
BES	ED031783	tetranucleotide	597	612	16	16	AAAT	TTAGCAACAATGACAAATACA	328	21	55.2	ATTCACAAATCACAACTTT	865	20	52.1	338
BES	ED031879	tetranucleotide	782	777	16	16	ACTG	AGTAAGGCTGTTCTCCAC	657	19	54.5	TGACAAATGATAAAGGATGAG	798	21	52.8	142
BES	ED031899	pentanucleotide	541	555	15	15	AACTG	GTCTGTTCTCTTCGGGATAAA	455	21	57.1	ATTTCTTCTCTTCGGG	742	18	56.7	288
BES	ED031993	dinucleotide	518	533	16	16	CG	ACTATGTGTAGCTCTTGCC	573	20	54.8	GACTATGCGATTGGTGATG	931	19	54.9	359
BES	ED031994	dinucleotide	162	179	18	18	AG	AGATTGAAGGAGGAGCAAA	108	19	56.1	TACAGACACACACAGGATAA	381	21	54.8	274
BES	ED032035	dinucleotide	140	173	34	34	AT	TTGGAGAACATGAGTAAATGA	59	22	55.0	TTCAAGTAGAGATGACAGGTTT	338	23	54.8	280
BES	ED032111	tetranucleotide	551	566	16	16	AAAC	GCACCTACATCACTAAGGACA	514	21	55.3	CTATTACGACTCAATTCATCA	856	22	54.5	343
BES	ED032228	pentanucleotide	363	377	15	15	AACTG	GTTTGTGCGAGATTGGA	52	18	58.4	TTGAACAGAACTGAAATGAATAG	434	23	54.0	383
BES	ED032315	pentanucleotide	805	819	15	15	AGATC	TTATGTTCTTGTACAACTCAAACTC	739	23	53.7	ATCAACCACTCCAAATACCT	920	19	51.7	182
BES	ED032383	trinucleotide	281	295	15	15	AAC	CACCTCTTGTACCTTTGTC	126	21	54.9	AACCTTCATCCTCATCATCTT	377	21	52.9	252
BES	ED032394	dinucleotide	148	219	72	72	AT	TAAAGGAACTGAAGCAAA	37	18	51.7	TCATTAGAAACATACCATACCAA	275	23	54.1	239
BES	ED032421	pentanucleotide	525	539	15	15	ATCCG	ATTCCTCTGTCTCCCTTTC	195	20	54.9	ATCAGTAGCGGTGTTCAATGT	588	21	57.2	374
BES	ED032468	tetranucleotide	647	682	16	18	AAAG	TCITGGTGATTATGTCGG	336	18	52.5	GGAGGAGAGGATAGAAAAGGA	709	20	55.0	374
BES	ED032499	trinucleotide	587	604	18	18	ACC	AAGTGGGAGGAAGGAGAG	468	18	55.5	TCTATCACCAGAACACCATC	784	21	55.0	317
BES	ED032544	tetranucleotide	394	409	16	16	AATT	GAAGGAATGATGGAACCTGACT	183	21	55.7	ACTGTTTGTGGAGTAATGGG	581	20	55.0	399
BES	ED032598	tetranucleotide	576	591	16	16	AATT	GCAATCACCAAGAGGAAGT	385	19	55.2	TGAACTGAAGAGTAAGGAGTGT	650	23	55.0	266
BES	ED032698	pentanucleotide	282	276	15	15	AAATT	GATTTGCTCAAAACCTT	12	18	55.3	GTGATTAGTGGATGCTTTAC	312	21	53.9	301
BES	ED032766	dinucleotide	188	211	24	24	AC	ACACACACACGCAAAAG	122	18	54.7	TCAAGTCTCATCCCAATAA	327	20	55.6	206
BES	ED032774	trinucleotide	296	391	96	96	AT	ATTTGGGTTTGGGAGAGA	15	18	55.4	TCAATCAGTAGCATACATACATA	414	23	53.8	400
BES	ED032791	trinucleotide	156	173	18	18	AAC	CACAACAAGTAGACAAATCCA	31	21	53.7	GTAAGTGAGGTCGGTGCT	263	19	55.3	233
BES	ED032805	dinucleotide	66	113	48	48	AAT	GCACCAATTATCTCTTTCA	30	19	51.1	AGCAAGTCATACACTCATACCA	252	22	54.9	223
BES	ED032858	dinucleotide	377	396	20	20	AG	ATGTGTCAAACTGCTCTGCT	314	20	56.0	ATTCATCTCCCTTTTCATTAC	582	21	54.8	269
BES	ED032881	pentanucleotide	561	585	25	25	AAAGG	TCCTTCTTACTTCCAATGA	314	21	54.2	ATTTCTCCACCTCAAA	671	18	52.9	358
BES	ED032913	pentanucleotide	392	406	15	15	AAAC	GCATAAAGCTGTAATCTGCT	339	21	53.9	GTAAGGAATACTAAACTTTGGG	633	21	50.2	295
BES	ED032931	pentanucleotide	304	318	15	15	AAAAG	ATTGTTGGTGGTGTGAA	261	19	54.6	CGCTCCTCTCTCTTACC	363	18	55.0	103
BES	ED033042	trinucleotide	781	810	30	30	AT	GCTTTGCTGAAGAGTTCC	528	18	53.4	AAATGAATGCGGTAGTTC	846	19	52.8	319
BES	ED033048	dinucleotide	278	295	18	18	AAC	CAACCAACAATACAACTCTC	231	21	55.1	TAACCTGTTCTGCCTCTCTT	493	21	55.1	263
BES	ED033087	dinucleotide	222	309	88	88	AT	TTTGTGGTAGGTCACTTTCA	185	21	55.7	TCTCTTCTCTCTCCATTATTC	550	23	53.8	366
BES	ED033276	pentanucleotide	245	259	15	15	AGATC	GGTCTGTTTGAATTGTCTCA	116	21	55.3	AGCAATGTTTCACTTCCCTT	303	21	55.6	188
BES	ED033297	pentanucleotide	157	171	15	15	AAGAT	CTAAGGGCTAAACTTAAACTC	110	22	52.4	ACAAGTGAAGAGTGCAAACTCA	397	21	54.8	298
BES	ED033300	pentanucleotide	674	703	30	30	AACTG	TCATTTCAAGTTCAGTTTCACTC	646	22	54.6	CTCAGCTATCTCCCTT	818	18	55.3	173
BES	ED033321	trinucleotide	627	662	36	36	AAT	TGGACAGAAATCAAAATCAAGT	501	21	54.8	GGTTCGTGCTACTATTGGG	747	19	55.7	247

**SUGARBEET RESEARCH
USDA-ARS MOLECULAR PLANT PATHOLOGY LABORATORY
BELTSVILLE, MARYLAND**

2006 REPORT

SECTION E

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***This research was supported in part by funds provided through the Beet Sugar
Development Foundation (Projects 811 and 831)***

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GENE STACKING FOR DURABLE PEST RESISTANCE IN SUGAR BEET ROOTS (Project 811)

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Cloning of sugar beet resistance genes

We are exploring novel approaches for managing sugar beet root pests. Our goal is to gain new knowledge of root defense response mechanisms that could be more broadly applied for control of plant pests and pathogens. Using the sugar beet root maggot (SBRM, *Tetanops myopaeformis*) and sugar beet as a root model system, we recently identified sugar beet root ESTs that are modulated by SBRM feeding in both a moderately resistant (F1016) and a susceptible parental (F1010) line (Puthoff and Smigocki, 2007). The EST libraries we generated are enriched for genes important in the initial responses of sugar beet roots to insect herbivory. Our experimental system utilized tissues from a feeding bioassay capable of screening for SBRM resistance and thus reflects field-like conditions (Smigocki et al., 2006).

While not definitive, the degree of sequence similarity of the ESTs at the amino acid level can aid in the identification of protein function and give a starting point for determination of a gene's role in plant cells. Functional annotation of the sugar beet ESTs in our libraries grouped the unique clones into many different categories. However, the largest number of clones fell into the defense-related class reported to be regulated by other pathogens including insect pests. The remaining ESTs included genes involved in secondary metabolism and signal transduction. Using macroarrays, gene expression profiles of the cloned genes were also obtained following mechanical wounding and treatment of roots with defense elicitors methyl jasmonate, salicylic acid and ethylene. The greatest number of the examined root ESTs were regulated by methyl jasmonate and salicylic acid suggesting these signaling pathways may be involved in sugar beet root defense responses to SBRM (Puthoff and Smigocki, 2007).

Cloning of proteinase inhibitor genes

A gene of particular interest to our work on SBRM resistance was found to encode a protein with a conserved motif denoting it a member of the Kunitz trypsin (serine) proteinase inhibitor (PI) family. This gene, *BvSTI*, is specifically up-regulated in the moderately resistant F1016 germplasm by SBRM infestations. It shares sequence similarity with a tomato gene that is primarily expressed in the root, secreted to the rhizosphere and induced by nematodes (Jofuku and Goldberg, 1989; Brenner et al. 1998). Since we showed that serine and aspartyl proteases comprise the major digestive enzymes in root maggot midguts (Wilhite et al. 2001), our findings suggest that the PI encoded by the *BvSTI* gene may form a zone of protection surrounding the moderately resistant roots and act as a first line of defense in the peripheral cell layers.

PIs occur naturally in a number of plant species and in some cases have been shown to enhance insect resistance in experimental trials. Higher levels of more than one PI have been found in insect resistant plants as compared to susceptible plants, and incorporation of PIs into artificial feeding diets had a deleterious effect on insect development. Some insects have been shown to avoid toxicity induced by PI ingestion by secreting "inhibitor-insensitive" enzymes and by the proteolysis of PIs by non-target digestive proteases. To overcome this

problem, the use of a combination of PIs proved more toxic at levels where individual inhibitors were not as effective.

Gene stacking strategies are being used to address the limitations encountered with cultivation of genetically engineered plants. Buildup of resistance in pests or pathogens targeted by the newly introduced resistance gene is a serious concern that has led to the development of strategies that employ stacking of multiple transgenes in the same transgenic plant among other tactics like the use of recombinant hybrid toxins (Mehlo et al., 2005). Simultaneous over-expression of two classes of PI genes has been shown to induce durable levels of insect resistance in tomato (Abdeen et al., 2005).

To functionally characterize *BvSTI* and determine its potential role in mediating resistance to SBRM, we cloned its full length coding sequence using 5' and 3' RACE and fused it with the constitutive CaMV 35S promoter in a plant transformation vector. Similarly, utilizing PCR and gene specific primers, we isolated a squash aspartyl PI gene and a *Nicotiana* gene that encodes five individual PIs, one chymotrypsin and four trypsin inhibitors. In addition, we cloned the *BvSTI* gene promoter and fused it the *GUS* reporter gene for analysis of temporal and tissue specific expression patterns of the *BvSTI* gene *in planta*.

Expression of PI genes in sugar beet

A number of independently transformed sugar beet hairy root lines carrying either the reconstructed *BvSTI*, aspartyl, *N. alata*, a combination of the PI genes (stacked) or the *BvSTI* promoter-GUS construct were regenerated from both SBRM-susceptible F1010 and moderately resistant F1016 genotypes. Hairy roots transformed with *BvSTI* exhibited a variable pattern of root growth, which ranged from relatively slow to fast. Preliminary analyses indicated that the rate of hairy root growth was not directly related to the level of *BvSTI* gene expression, i.e. slow growth, high levels of *BvSTI* gene expression.

Fusion of the *BvSTI* promoter to the GUS gene was used to determine *BvSTI* gene expression patterns in sugar beet roots. Using histochemical methods, varying levels of GUS gene expression were observed in both F1010 and F1016 independently derived hairy root lines. Expression levels ranged from constitutive as with the 35S promoter to relatively low levels of expression.

PI activity in the *BvSTI* transformed hairy roots was analyzed using a radial diffusion assay. Preliminary results indicate that a number of the independently derived F1010 transformants had higher levels of PI activity than the controls. Using soybean trypsin inhibitor (TI) as a positive control, PI activity in the *BvSTI* transformants ranged from about 0.04 to almost 0.07 µg TI equivalent/µg protein as compared to 0.02 in the control.

Transformed F1010 hairy root lines that showed highest levels of expression of the *BvSTI* gene were subjected to further analysis using native protein polyacrylamide gels. In comparison to the control roots, new PI activity was detected in the *BvSTI* transformed roots. To confirm that the new PI activity corresponds to the *BvSTI* protein, we are in the process of analyzing the transformants by Western blots with *BvSTI*-specific antibody.

BvSTI transformed hairy root lines showing high levels of proteinase inhibitor activity will be used in an *in vitro* SBRM bioassay (Smigocki et al., 2006) to determine the effect of *BvSTI* gene expression on larval feeding. Bioassays are also being developed to test the effect of *BvSTI* on other pests of sugar beet.

Sugar beet hairy root cultures transformed with the cloned squash aspartyl, *Nicotiana* serinase or a combination of the three cloned PI genes were also generated. These transformants are in various stages of analysis to determine their role in insect and disease resistance in sugar beet.

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**IDENTIFICATION OF CFP GENE-CARRYING PROGENY
FROM GENETIC CROSSES OF ELITE GERMPLASM
WITH A TRANSGENIC SUGAR BEET**
(Project 831)

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Cercospora-induced leafspot disease (CLS) can limit the profitability of sugar beet production in most of the U.S. growing regions. Since conventional plant breeding has produced only moderate CLS resistance with low heritability, a new biotechnological approach was needed. *CFP*, the cercosporin toxin export gene from *Cercospora kikuchii* was successfully introduced into *Beta vulgaris* L. clone REL-1. The transgene was stably inherited. Expression of both RNA and protein products was monitored using RT-(reverse transcriptase) PCR and Western blots. Production of viable seeds by the transgenic genotype was successful and, in 2004, a number of seeds of the *CFP* transgenic genotype were sent to the Sugar Beet Research Unit at Fort Collins, CO where crosses were performed, in 2004 and 2005, using lines C842 and 9933 from the program of R.T. Lewellen, USDA-ARS, Salinas, CA. In 2006, the identification of *CFP*-carrying progeny resulting from two such crosses with the 9933 line out of Salinas was successful although only a low proportion overall of the available progeny evidently carry the transgene.

Justification for Research:

The phytopathogenic fungal species *Cercospora beticola* Sacc. is the causal agent responsible for inducing CLS, the most serious widespread disease of sugar beet in most production areas. CLS destroys mature, highly photosynthetic leaves, which are then replaced by the growth of new leaves at the expense of carbohydrate stored in the root, thereby reducing root yield, percent sucrose, and purity. *Cercospora* leafspot currently is controlled using moderately disease resistant germplasm and timely foliar spraying with expensive commercial fungicides. The use of biotechnology to improve *Cercospora* leafspot resistance in sugar beet would be a sustainable solution. Especially since *Cercospora* can become tolerant to fungicides as a result of direct *in situ* selection, genetic resistance to this serious pathogen is needed.

Summary of Literature Review:

Cercospora leafspot has long been a serious disease problem in the sugar beet growing areas of the United States where the summers are often hot and humid (Red River Valley, Michigan, Ohio, and, less often, Great Plains growing areas and California). It has been estimated that severe epidemics cause as much as a 40% loss of

sugar yield (Smith and Martin, 1978; Smith and Ruppel, 1973) and a corresponding, equal loss in farm revenue (Shane and Teng, 1992).

Tolerance to CLS is defined as a plant genotype performing well despite the presence of symptoms of the disease (Fehr, 1987). Generally the *Cercospora*-resistant germplasm in use today was originally derived from outcrosses with *B. vulgaris* spp *maritima* to import resistance genes; this early plant breeding had been done by Munerati in Italy (Lewellen, 1992). With this genetic source, an estimated 4 or 5 genes are thought to be involved in conferring moderate CLS resistance (Smith and Gaskill, 1970). Broad-sense heritability estimates range from 12 to 71% (Bilgen *et al.*, 1969), narrow-sense heritability is 24% comparing well with realized heritability, and about 50% of the variation is environmental (Smith and Ruppel, 1974). This high degree of environmental variation makes the development of resistance through mass selection difficult. Incorporation of CLS resistance into varieties with superior agronomic performance is also difficult (Smith and Campbell, 1996) and, therefore, commercial resistant varieties have required some fungicide application to provide adequate levels of protection against *Cercospora* (Miller *et al.*, 1994).

A major problem in the development of *Cercospora* leafspot resistant sugar beet is the loss of vigor due to the continual inbreeding (Coons, 1955 and McFarlane, 1971). The use of hybrid varieties has lessened this problem to an extent, but seed production on the highly inbred O-type males and CMS females continues to be a problem. This creates an urgent need to continue the development of a broader genetic base of CLS -resistant germplasm. As commercial hybrid parents become more inbred, there must be sufficient diversity in the germplasm base for maximum gain through heterosis. In addition to broadening the genetic base of the commercial sugar beet germplasm, novel genes for resistance to CLS resistance might lead to transgression of tolerance to CLS (de Vicente & Tanksley, 1993).

The non-host specific phytotoxic polyketide cercosporin is a lipid-soluble perylenequinone that, upon light activation, catalyzes the production of highly reactive oxygen species, principally singlet oxygen (Daub, 1982). Singlet oxygen-catalyzed peroxidation of membrane lipids results in loss of membrane integrity, cytoplasmic leakage and cell death (Daub & Ehrenshaft, 2000). *Cercospora* hyphae enter the host plant passively through open stomata and grow intercellularly. Toxin-mediated disruption of the cellular membranes of host cells provides the pathogen with nutrients for *in situ* growth and sporulation.

Recent studies have focused on identifying genes for resistance to cercosporin in *Cercospora* fungi themselves (Daub & Ehrenshaft, 2000). One such resistance mechanism apparently involves the export action of the Major Facilitator (MF)-like protein gene, *CFP*, which was isolated from *C. kikuchii* (Callahan *et al.*, 1999). Targeted disruption of the *CFP* gene resulted in mutants that lacked virulence on soybean and were inhibited by cercosporin. Cercosporin export was substantially elevated in *CFP* multi-copy strains of *C. kikuchii* that over-expressed CFP protein (Upchurch *et al.*, 2001). Moreover, transgenic expression of *CFP* in the cercosporin sensitive fungus *Cochliobolus heterostrophus* resulted in significantly increased cellular resistance to the toxin (Upchurch *et al.*, 2002). Cercosporin-deficient mutants of *C. kikuchii* do not produce lesions on soybean, indicating that cercosporin is an essential virulence factor (Upchurch *et al.*, 1991).

Kanamycin-resistant clones were regenerated *in vitro* following conjugal mating of wounded REL-1 leaf pieces with *Rhizobium radiobacter* carrying pCFP. Transgenic plants were confirmed by PCR of leaf DNA using CFP-specific primers (Kuykendall *et al*, 2003). Moreover, vegetatively propagated kanamycin-resistant plants and seed-grown transgenic REL-1 plants stably maintained the ability to produce a DNA product of the approximate size predicted for PCR using the CFP-specific primers. Expression of the transgene in sugar beet was reported in 2004 (Kuykendall and Upchurch).

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Objectives:

1. The evaluation of *Cercospora* leafspot resistance in transgenic sugar beet genotypes, relative to parental germplasm tolerance--- is *CFP* useful in enhancing leafspot resistance in sugar beet?
2. The identification *CFP* positive progeny from crosses of the T7#12 transgenic sugar beet with the high quality genotypes 9933 developed by Bob Lewellen in Salinas, CA.

Materials and Methods:

We plan to use seeds obtained from progeny of crosses with the transgenic genotype PT7#12 to develop plants for CLS evaluation. Controlled environmental conditions in a growth chamber will be used. Seeds from greenhouse-grown T7#12 seed were sent to Lee Panella in Fort Collins, CO, to cross. Transgenic plants were crossed in Ft. Collins with sugar beet genotypes 'C842' and '9933' both out of Salinas, CA (See Table below). Seed from the crosses of *CFP* transgenic T7#12 with these sugar beet genotypes were received in Beltsville. About 100 progeny from the male sterile parent of three such crosses were grown out in the greenhouse for the nondestructive evaluation of *CFP* based on DNA PCR analyses.

Genotype C842 is released from Salinas – It is rhizomania resistant (RhzmR), monogerm (*mm*), self-fertile (S^f), Curly top resistant (CTR), segregating for genetic male sterility (*A-:aa*), and green hypocotyl color (*R-:rr*), - it is a facilitated random mated population with variable reaction to bolting, *Erwinia* and powdery mildew.

Genotype 9933 comes from 8933, which consists of - #s *aa* x *A*. It is rhizomania resistant (RhzmR), multigerm (*MM*), self-fertile (S^f), Curly top resistant (CTR), Virus yellows resistant (VYR), Powdery mildew resistant (PMR), *Erwinia* resistant, bolting resistant, segregating for genetic male sterility (*A-:aa*), root aphid resistance, and green hypocotyl color (*R-:rr*) w/ normal cytoplasm.

T7#12, a transgenic sugar beet (*Beta vulgaris* L.), was derived from clone Rel-1 by so-called "agrotransformation" with the cercosporin toxin export gene *CFP* from *Cercospora kikuchii*.

Time Line of Anticipated Accomplishments:

Analysis of an expected pattern of segregating genetic traits in the F_2 generation of crosses between the high quality genotype 9933 which is elite germplasm and the Rel-1 biotechnology clone-derived *CFP* transgenic sugar beet, relative to that of the respective parental germplasm, is planned. This research is needed in order to evaluate the concept that the *CFP* gene can enhance CLS resistance in sugar beet. The identification of *CFP* positive progeny from crosses of the T7#12 transgenic with the high quality genotype 9933 was an important step and next the goal is to obtain seeds from these plants. Seeds obtained from multiple *CFP* positive progeny will be grown out in the greenhouse to permit the evaluation of the genetic traits including *Cercospora* leafspot resistance segregating in the F_2 generation of crosses between elite germplasm and the *CFP* transgenic sugar. Varying degrees of relative robustness of growth and *Cercospora*

tolerance are expected. Identification of vigorous progeny with tolerance to CLS is being sought.

Thus, gradual, stepwise progress continues to be made toward the evaluation of whether *CFP* expression in transgenic sugar beets enhances CLS resistance.

Research Progress 2006 and plans for 2007:

We now have identified progeny *CFP*⁺ progeny resulting from crosses of T7#12 with genotype 9933. These plants have been confirmed by PCR and seed will hopefully be obtained in 2007. The *CFP* positive progeny identified in 2006 from two crosses are indicated in the table showing the crosses done at Ft. Collins in 2004 and 2005.

Greenhouse crosses from January, 2005 through January, 2006.

orange	2004A001,	PT7#12	transgenic	Kuykendall
blue	2004A002	C842	biennial	Lewellen
yellow	2004A013	9933	biennial	Lewellen
Color Stake	Hypocotyl color	PF or MS	Plant #	Assigned number
Orange	Pink	PF	#1	20041021H-01s
Blue	Pink	MS	#1	20041021H2-01
Orange	Pink	PF	#2	20041021H-02s
Blue	Pink	MS	#2	20041021H2-02
Orange	Pink	PF	#3	20041021H-03s
Blue	Pink	MS	#3	20041021H2-03
Orange	Pink	PF	#4	20041021H-04s
Yellow	Pink	MS	#4 CFP+ progeny	20041021H3-04
Orange	Green	PF	#5	20041021H-05s
Yellow	Pink	PF	#5	20041021H3-05
Orange	Pink	PF	#6	20041021H-06s
Blue	Pink	MS	#6	20041021H2-06
Orange	Pink	PF	#7	20041021H-07s
Blue	Pink	MS	#7A	20041021H2-07A
Blue	Green	PF	#7B -- after 7A died	20041021H2-07B
Orange	Pink	PF	#9	20041021H-09s
Yellow	Green	MS	#9	20041021H3-09
Orange	Pink	PF	#10	20041021H-10s
Yellow	Pink	MS	#10 CFP+ progeny	20041021H3-10
Orange	Pink	PF	#12	20041021H-12s
Blue	Green	PF	#12	20041021H2-12
Orange	Pink	PF	#13	20041021H-13s
Blue	Pink	MS	#13	20041021H2-13
Orange	Pink	PF	#14	20041021-14s
Blue	Pink	MS	#14	20041021H2-14
Orange	Pink	PF	#15	20041021H-15s
Blue	Green	MS	#15	20041021H2-15
Orange	Pink	PF	#16	20041021H-16s
Blue	Green	MS	#16	20041021H2-16
Orange	Pink	PF	#18	20041021H-18s
Blue	Green	PF	#18	20041021H2-18
Orange	Green	PF	#19	20041021H-19s
Blue	Pink	PF	#19	20041021H2-19
Orange	Pink	PF	#20	20041021H-20s
Yellow	Green	PF	#20	20041021H3-20

Greenhouse crosses from January, 2005 through January, 2006.

orange	2004A001,	PT7#12	transgenic	Kuykendall
blue	2004A002	C842	biennial	Lewellen
yellow	2004A013	9933	biennial	Lewellen
Color Stake	Hypocotyl color	PF or MS	Plant #	Assigned number
Orange	Pink	PF	#23	20041021H-23s
Blue	Pink	MS	#23	20041021H2-23
Orange	Green	PF	#25	20041021H-25s
Blue	Pink	MS	#25	20041021H2-25
Orange	Green	PF	#27	20041021H-27s
Blue	Pink	MS	#27	20041021H2-27
Orange	Pink	PF	#30	20041021H-30s
Blue	Pink	MS	#30A	20041021H2-30A
Blue	Green	PF	#30B – after 30A died	20041021H2-30B
Orange	Pink	PF	#33	20041021H-33s
Blue	Pink	MS	#33B	20041021H2-33A
Blue	Pink	MS	#33B	20041021H2-33B
Orange	Pink	PF	#34	20041021H-33s
Blue	Pink	MS	#34	20041021H2-34
Orange	Pink	PF	#41	20041021H-41s
Blue	Pink	MS	#41	20041021H2-41
Orange	Pink	PF	#42	20041021H-42s
Blue	Pink	MS	#42	20041021H2-42
Orange	Green	PF	#43	20041021H-43s
Pink	Blue	MS	#43	20041021H2-43
Orange	Green	PF	#44	20041021H-44s
Blue	Pink	MS	#44	20041021H2-44
Orange	Pink	PF	#45	20041021H-45s
yellow	green	PF	#45	20041021H3-45
Orange	Green	PF	#46	20041021H-46s
Blue	Pink	MS	#46	20041021H2-46s
Orange	Pink	PF	#55	20041021H-55s
Blue	Pink	MS	#55	20041021H2-55
Orange	Pink	PF	#56	20041022H-56s
Blue	Green	PF	#56	20041021H2-56

**SUGARBEET RESEARCH
TEXAS AGRICULTURAL EXPERIMENT STATION
BUSHLAND, TEXAS**

2006 REPORT

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This research was supported in part by funds provided through the Beet Sugar Development Foundation (*Project 508*)

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ETIOLOGY OF RHIZOMANIA IN FIELDS PLANTED TO RESISTANT CULTIVARS

(Project 508)

Charlie M. Rush, Rodolfo Acosta-Leal and David C. Jones
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The incidence of rhizomania in fields planted to resistant cultivars in Minnesota and North Dakota has steadily increased during the last 2 - 3 years. In 2006, we continued to investigate factors that were involved, or not involved, with development of rhizomania. Numerous ideas as to the cause of rhizomania in resistant cultivars have been put forth and the most commonly suggested include 1) problems with seed quality during production of hybrid seed, 2) soil physical or chemical factors, 3) inoculum density of the pathogen, and 4) emergence of new resistance-breaking strains of BNYVV. Research on all four of these was conducted and some were eliminated as factors involved with break down of resistance.

METHODS

Seed Purity. Studies were conducted to determine whether rhizomania in fields planted to resistant cultivars could be associated with seed purity issues. Our two basic questions were whether the plants exhibiting severe rhizomania symptoms possessed the *Rz1* resistance gene, and secondly, whether the observed distribution of rhizomania in the field was consistent with what one would expect if a portion of the seed did not have the *Rz1* resistance gene.

Blinker *Rz1* Study. Plants for this study were collected from individual grower's fields located near Crookston, Moorhead, and Renville, MN. Plants exhibiting the typical fluorescent yellow foliage that is associated with rhizomania, and asymptomatic plants, were collected from each field. Multiple locations in each field were sampled, and 10 to 20 beets were collected from each location. The sampled plants were individually rated for rhizomania severity on 0 – 4 scale with 0 = no symptoms and 4 = extremely severe root stunting, constriction, and bearding. Foliage from each plant was collected and scanned using a hyperspectral radiometer to quantify the degree of leaf chlorosis, and root and rhizosphere soil was collected so *Beet necrotic yellow vein virus* (BNYVV) could be baited from individual plants if deemed necessary. After roots were rated and rhizosphere soil collected, symptomatic and asymptomatic plants were separated and those in each group were bulked for sucrose determination. Subsamples of root tissue from each plant were tested for BNYVV by the enzyme-linked immunosorbent assay (ELISA) test and leaf tissue was sent to the various cooperating seed companies to test for the presence of the *Rz* gene. Collected data was subjected to a variety of statistical tests to determine whether the *Rz1* gene was actually present in severely diseased plants, and, if it was present, whether it had a significant effect on disease severity and percent sucrose. Over 500 individual beets were included in this study.

Spatial Analysis Study. Four fields were selected to test whether the incidence and distribution of rhizomania in fields planted to resistant varieties was random, and possibly a result of planting a percentage of seed that did not possess the *Rz* gene. Within each field, four areas were sampled. Each sampling area was fifty feet x 20 rows. The number of symptomatic

plants and the total number of plants in each sampling area was determined. Approximately 15 symptomatic plants and 15 asymptomatic sugar beets were collected to determine root yield and sugar differences between healthy and diseased plants, within the sampled area. The sugar beets were rated for rhizomania severity on a scale from 0-4, and the diseased and healthy plants were bulked separately at each location. This gave a total of four paired samples for each field. Each sample was processed for sucrose content and yield. BNYVV was assayed by ELISA on feeder root tissue of the taproot.

A white tarp measuring approximately 3ft by 10ft was placed at each sample location so that it could be identified in aerial photography (Fig. 1A). Immediately after the fields were sampled on the ground, digital images were acquired at an altitude of approximately 1700 ft mean sea level (800 ft above ground) using fixed wing aircraft. The images were acquired with an Olympus 765 UZ digital camera. The nominal field of view of the camera was 43° by 38°. This resulted in an area of about 8 acres with 1.05 ft resolution. Images were processed using ENVI version 4.3 (RSI, Boulder, CO) (Fig. 1B). The actual sampling area was selected in each field image resulting in four images per field. Within each image, pixels were classified using unsupervised classification with three classes. The classes represent healthy beets, diseased beets and background (soil). An area and percent of each class was calculated for each image. Statistical analysis was done on each classified image to determine the spatial distribution of diseased plants in the sampled area.

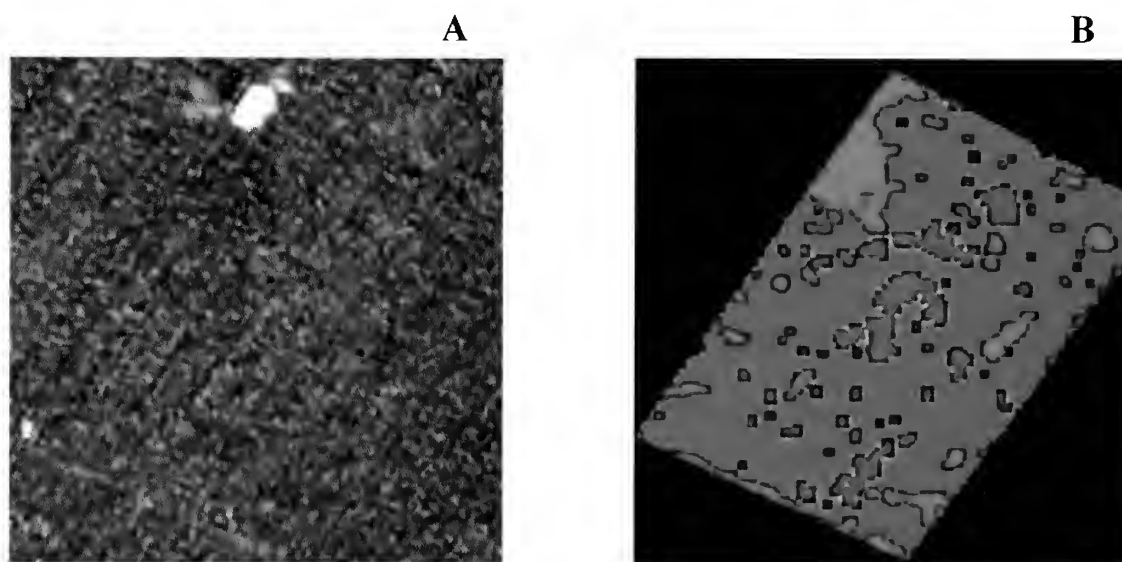


Figure 1. Aerial image of sugar beet sampling area. Image on left is original image and image on right is classification where light areas = healthy beets, and dark areas = blinkers. The blinkers developed in an aggregated pattern.

Soil Characteristics. Fields with discrete patches of diseased sugar beets were selected for this study. At each sampling location in each field, four soil samples were taken inside and four outside of the disease patch. Each individual sample was a composite of four, 1" diameter cores taken to a depth of 1'. Soil cores were dried, ground, and sent to Servi-Tech Laboratories for a complete chemical and physical analysis. Paired t-test analysis was conducted to determine if any of the measured variables from samples taken inside and outside of disease patches were significantly different.

Soil Inoculum Density. Currently, the only way to quantify inoculum density of BNYVV in the soil is to conduct the most probably number assay, which is a very time consuming and inaccurate procedure. For this reason, we attempted to develop a molecular technique that would detect and quantify BNYVV directly from the soil. A soil dilution series with varying amounts of BNYVV-infested rhizosphere soil was made and used in these studies. Rhizosphere soil is essentially the same as tare soil, i.e., that which remains attached to the collected sugar beet roots. The rhizosphere soil we used came from severely infected sugar beets that possessed extremely “hairy” roots and therefore, it contained a very high proportion of decayed infected root material and sporosori of *Polymyxa betae*, the soil fungus that vectors BNYVV. Initially, only the undiluted rhizosphere soil was used. Rhizosphere soil was pulverized using a bead beater and total RNA was extracted using an RNA extraction kit and following manufacturer’s instructions. The total RNA was then used in a real time quantitative PCR assay to test for the presence and quantity of viral RNA using primers and probes specific for BNYVV RNA2.

Emergence of New Resistance-Breaking Strains of BNYVV. This study was a continuation from 2005 and the same methods were used. Symptomatic and asymptomatic plants were taken to the TAES plant pathology lab in Amarillo and total RNA was extracted from all plants. Extracted RNA was used to generate cDNA, which in turn was used as template for PCR amplification. Specific primers for RNA 3, the RNA species which has been associated with symptom expression and disease severity, were used to amplify the entire P25 ORF on RNA 3. DNA bands of the expected size were generated. The DNA bands were excised from the electrophoresis gel and these were gel purified and sent off for sequencing. Sequence data was analyzed using a variety of DNA analysis software programs, to determine whether differences between wild type and resistance breaking isolates could be identified.

RESULTS AND DISCUSSION

Seed Purity. Results of the blinker and spatial analysis studies were similar to those from previous years and supported our conclusion that incidence and severity of rhizomania in fields planted to resistant cultivars is not a result of seed purity or seed production issues. In the blinker study, healthy, asymptomatic plants had a significantly greater percentage of plants that possessed the *Rz* gene than those in the blinker group. Healthy plants also had significantly higher root weight and percent sucrose and a lower disease rating than the blinkers (Table 1). More importantly however, when only the blinkers were analyzed, 81% tested positive for the *Rz* gene. Furthermore, there was no difference in disease rating, the number of blinkers that tested positive by ELISA for BNYVV, or the average BNYVV value (virus concentration in infected plant tissue) between blinkers that possessed the *Rz* gene and those that didn’t (Table 2). This means that without question the *Rz* gene was overcome by BNYVV.

Table 1. Disease rating and yield data from all samples^x

Symptom	Percent <i>Rz</i>	Disease Rating ^y	Mean Root Wt.(lbs)	Sucrose (%)
Healthy	98*	0.5*	2.04*	15.84*
Blinker ^z	81	2.5	0.96	14.47

^x Healthy means followed by an asterisk are significantly different from blinker means.

^y Blinker is the term used to describe an individual sugar beet infected by BNYVV, which exhibits the fluorescent yellow foliage typically associated with rhizomania, surrounded by healthy beets with dark green foliage.

^z Severity of rhizomania was based on a 0 – 4 scale, where 0 = healthy disease free roots and 4 = severe stunting, root constriction, and massive root proliferation.

Table 2. Results for Blankers only^a

Rz Category	Percent in Category^b	Disease Rating^c	BNYVV Positive	BNYVV Value
Rz Positive	81	2.5 NS	94NS	1.0NS
Rz Negative	19	2.8	97	1.1

^a Blinker is the term used to describe an individual sugar beet infected by BNYVV, which exhibits the fluorescent yellow foliage typically associated with rhizomania, surrounded by healthy beets with dark green foliage.

^b Means in the top row followed by an asterisk are significantly different from those in the second row.

^c Severity of rhizomania was based on a 0 – 4 scale, where 0 = healthy disease free roots and 4 = severe stunting, root constriction, and massive root proliferation.

An interesting aspect of the blinker study (data not shown) became apparent when data from the American Crystal area was compared to results from the Southern Minn area. In healthy beets, sucrose was higher in those from the Crystal area but this could have been due to the fact that fields in the Crystal area were sampled two weeks later in the season than those in the Southern Minn area. However, when only the blinkers were evaluated, the mean disease rating was higher in beets from the American Crystal area and mean sugars were not significantly different. This result suggests that disease was more severe in the American Crystal area and losses were greater.

A second interesting result of the blinker study was observed when a subset of data from a single field in Southern Minnesota planted to Beta 4811 was analyzed. Beta 4811 has displayed exceptionally strong resistance to rhizomania and is widely planted in the southern production area. Although no discrete spots of rhizomania existed in this field, one end of the field exhibited an exceptionally large number of blinkers. These were sampled and it was quickly realized that some of the blinkers had large, perfectly formed roots with no symptoms of rhizomania while others were severely infected and displayed typical symptoms of rhizomania. When only the blinkers were analyzed, those possessing the *Rz* gene had significantly lower disease ratings than those without the *Rz* gene. Furthermore, when the total blinkers were divided between those with severe root symptoms and those without, there were several interesting differences between the two groups of plants. Those blinkers without root symptoms had a significantly higher incidence of the *Rz* gene, significantly lower disease severity and significantly higher sucrose content and root weight. These results suggest that the virus population in this field is in the midst of an evolutionary shift. The genetics of 4811 are such that resistance is still active against most BNYVV in the field but some isolates may be beginning to develop the ability to break that resistance. The isolates of BNYVV obtained from the blinkers with the *Rz* gene, both those with and without severe root symptoms, will be highly valuable for future study and further molecular analysis.

A third interesting aspect of the Blinker study had to do with the impact of nitrate nitrogen on disease and sucrose content. In every sample that was tested, except two, healthy, asymptomatic beets always had higher sucrose content than blinkers in paired tests. However, in the two exceptions where the healthy beet sample had a lower sucrose content, the ppm of nitrate in the samples exceeded 130 ppm in one and 200 ppm in the other. In one of these, the disease rating of the blinker sample was 2.8 and the sucrose content 14.4, while in the paired healthy sample the disease rating was 0.5 but the sucrose content was only 11.8. The exact same trend was observed in the other sample. These results demonstrate the extreme importance of nitrogen management, even in fields with high disease pressure. In most cases, ppm nitrate was significantly higher in healthy than in blinker samples and this may partially explain the fluorescent yellow coloration of BNYVV infected plants. However, despite higher ppm of nitrate in the healthy plants, proper nitrogen management allowed high root yields and high

sucrose contents. It was only when excessive nitrogen was present that sucrose content was severely reduced and nitrogen caused a greater loss in sucrose than disease.

In the spatial distribution study, the spatial patterns of the pixels were statistically determined to ascertain whether they follow a random or aggregated pattern. In all fields, the distribution of the pixels followed an aggregated pattern (Fig. 1B), with spatial autocorrelations ranging between 0.54 and 0.81 on the scale where 0 represents a random distribution and 1 represents a strongly aggregated distribution. Plant disease, resulting from a mixture of susceptible and resistant seeds, or plants with and without the *Rz* gene would display a uniform or random pattern in the field, and would not be distributed in aggregated patterns. Aggregated stress patterns usually arise from soil inhabiting infectious agents such as fungi, bacteria or viruses and are restricted in movement or due to localized soil chemical constituents. The results of this study verified statistically what is visually obvious even from ground level, i.e., disease is occurring in clusters and this spatial pattern could not reasonably occur from planting mixed seed or seed that lacked the *Rz* gene due to problems during hybrid seed production. The results from these two studies support the hypothesis that resistance breaking isolates of BNYVV have emerged and are causing rhizomania in Minnesota.

Soil Characteristics. Analysis of soil chemical and physical characteristics from inside and outside discrete patches of plants exhibiting severe symptoms of rhizomania revealed no significant differences. In this study, samples were taken only to the depth of one foot and it is possible that differences may have been found in the lower soil horizons. However, result of this study do not support the idea that rhizomania in fields planted to rhizomania resistant cultivars is due to variability in the soil.

Soil Inoculum Density. Our attempts to develop a molecular test to directly detect and quantify BNYVV directly from the soil were unsuccessful. Rhizosphere soil for this study was obtained in late September and to date we have only conducted a single round of experiments. It is recognized that soils often have properties that interfere with extraction of RNA, especially soils with high organic matter. Although initial tests were unsuccessful, we believe the technology exists to successfully extract and quantify BNYVV RNA from the soil but it will take further experimentation to identify the factors that interfere with the extraction and amplification process.

Emergence of New Resistance-Breaking Strains of BNYVV. In this study, isolates of BNYVV were obtained from fields in both Minnesota and California. In resistance breaking isolates from California we were able to detect a specific unique amino acid motif, VLE, that distinguished these isolates from wild type isolates. Isolates of wild type BNYVV that were unable to cause rhizomania in infected resistant plants did not possess the VLE motif but rather displayed an ALD or ACD motif. Using a specific application of real time PCR termed allelic discrimination, we were able to use the amino acid motif as a marker to identify resistance breaking isolates of BNYVV without the time and expense of full length sequencing. Unfortunately, resistance breaking isolates from Minnesota did not possess this marker and we are still unable to distinguish those using molecular tests.

Virus isolates baited from soil samples collected from rhizomania patches and surrounding asymptomatic areas in the field were genotyped using real-time allelic

discrimination assays. Most of the isolates (11 out of 13) baited from the diseased areas carried the resistant breaking VLE motif. By contrast, just two out of 22 isolates collected from the surrounding green areas were resistance breaking isolates and the rest were wild type strains. The near exclusive presence of resistance breaking isolates of BNYVV in rhizosphere soil from rhizomania patches suggests that they have gained a fitness advantage over wild type isolates, under the specific host-environment (*Rz1* cultivars) to which they had been exposed in the field. Also, the occurrence of mixed infections (resistance breaking and wild type) revealed that sometimes, during development of rhizomania in the field, wild type and resistance breaking isolates can coexist in the same *Rz1*-plant. However, this condition is apparently very unstable.

The almost complete exclusion of wild type isolates of BNYVV from the rhizomania patches suggests that over time resistance breaking isolates likely will become the dominant strain in the field. Therefore, new sources of resistance to BNYVV, other than *Rz1*, need to be incorporated into regionally adapted cultivars in order to maintain a viable sugar beet industry. However, in order to insure long term effectiveness of any genetic resistance, it is imperative to elucidate the mechanisms involved in resistance breakdown because incorporation of new dominant resistance genes will be exposed to the same selection pressures as was *Rz1*. The fact that we have identified on numerous occasions, severely diseased plants in fields planted to a cultivar with the *Rz2* resistance gene supports this contention.

**SUGARBEET RESEARCH
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2006 REPORT

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*This research was supported in part by funds provided through the Beet Sugar
Development Foundation (Project 840)*

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NEW STRATEGIES FOR MODIFYING SUCROSE DISTRIBUTION IN SUGARBEET

(Project 840)

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JUSTIFICATION OF RESEARCH:

Sucrose accumulated in the sugar beet tap root is synthesized in the leaf and then transported to the root in the phloem cells of the plant's vascular system. The proton-coupled sucrose transport protein mediates the key step in the long-distance transport of newly synthesized sucrose from the leaf to the taproot because it is responsible for sucrose accumulation into the leaf phloem cells and that activity drives sucrose flux to the tap root. We recently discovered a control pathway that regulates the activity of the sucrose transporter and, because of the transporter's role in loading the phloem, this regulatory system appears to control sucrose export from the leaf (Chiou and Bush 1998, Bush 1999). This was a very significant finding because loading the vascular system for sucrose export from the leaf determines how much sucrose is delivered to the tap root. Defining the biochemical and molecular steps involved in controlling sucrose delivery to the beet will allow us to develop new strategies for manipulating productivity.

RECENT PROGRESS:

Research this year focused on two areas: 1) experiments aimed at defining the key steps in sucrose-sensing regulatory pathway described above and 2) a biotech approach to express a hyperactive form of the sucrose transporter in the leaf phloem with the goal of increasing the amount of sucrose transported to the storage beet. We have developed a novel method to determine all the genes expressed in the plant's vascular cells. We are currently looking at those genes for candidates that play a role in sucrose sensing and will test them this coming year using plants in which those genes products are no longer produced. For objective two, we are collaborating with Marc Lefebvre (SES Vanderhave) to make transgenic plants expressing the hyperactive transporter in the leaf phloem cells. We have constructed the expression vector and sent it to Marc for beet transformation. The first plants are just starting to grow and we'll analyze their growth and yield this year.

**SUGARBEET RESEARCH
USDA-ARS
KIMBERLY, IDAHO**

2006 REPORT

SECTION H

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**Dr. Carl A. Strausbaugh
Research Plant Pathologist**

***This research was supported in part by funds provided through the Beet Sugar
Development Foundation (Projects 311 and 320)***

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List of Publications and Abstracts for the Kimberly Sugarbeet Group

Publications:

- Strausbaugh, C. A., and Gillen, A. M. 2007. Bacteria and yeast associated with sugar beet root rot at harvest in the Intermountain West. *Plant Dis.* 91:(submitted).
- Strausbaugh, C. A., Gillen, A. M., Camp, S., Shock, C. C., Eldredge, E. P., and Gallian, J. J., 2007. Relationship of beet curly top foliar ratings to sugar beet yield. *Plant Dis.* 91:(submitted).
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- Strausbaugh, C.A., and Camp, S. 2007. Verticillium wilt in commercial sugar beet cultivars in Cassia County, ID, 2006. *Plant Disease Management Reports* 1: V112.
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- Strausbaugh, C.A., Gallian, J.J., Camp, S., Foote, P., and Gillen, A. M. 2005. Managing curly top in southern Idaho. Proceedings of the University of Idaho Winter Commodity Schools 2005. (Published as a CD).

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- Strausbaugh, C.A., Rearick, E., Camp, S., Gallian, J.J., and Dyer, A.T. 2007. Sugar beet storability and the influence of *Beet necrotic yellow vein virus*. (Abstr.) *Phytopathology* 97 (submitted).
- Strausbaugh, C.A. and Gillen, A. M. 2007. Sugarbeet root rot in the Intermountain West. (Abstr.) *J. Sugar Beet Res.* (submitted).

- Strausbaugh, C.A., Gillen, A.M., Gallian, J.J., Tindall, K., Camp, S., and Strander, J.R. 2007. Influence of host resistance and insecticide seed treatments on curly top in sugarbeets. (Abstr.) *J. Sugar Beet Res.* (submitted)
- Lewellen, R.T., Liu, H.-Y., Gillen, A.M., and Strausbaugh, C.A. 2007. Performance of rhizomania resistant sugarbeet under normal and resistance-breaking strains of *Beet necrotic yellow vein virus*. (Abstr.) *J. Sugar Beet Res.* (submitted).
- Strausbaugh, C. A. and Gillen, A. M. 2007. Bacteria and yeast associated with sugar beet root rot at harvest in the Intermountain West. (Abstr.) *Phytopathology* 97 (submitted).
- Strausbaugh, C. A., Gillen, A. M., Gallian, J. J., Camp, S., and Stander, J. R. 2006. Influence of host resistance and insecticide seed treatments on curly top in sugar beets. Abstract for American Phytopathological Society Annual Meeting. Quebec City, Quebec, Canada. July 29 – August 2, 2006. *Phytopathology* 96: S111.
- Gillen, A. M. and Strausbaugh, C. A. 2006. The new USDA-ARS Sugarbeet Germplasm Development Program at Kimberly, Idaho. Workshop presentation. Plant and Animal Genome XIV Conference. San Diego, CA. January 14-18, 2006. Paper W179.
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SUGARBEET ROOT ROT IN THE INTERMOUNTAIN WEST (Project 311)

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Root rots in sugarbeet are widespread and problematic in all growing regions. A number of the primary causal agents include: *Rhizoctonia solani*, *Aphanomyces cochlioides*, *Fusarium oxysporum* f. sp. *betae*, *Rhizopus stolonifer*, *Pythium aphanidermatum*, and *Phytophthora drechsleri* (Schneider and Whitney 1986). *Rhizoctonia solani* is considered one of the most economically important diseases of sugarbeet worldwide (Büttner et al. 2004, Kiewnick et al. 2001). In fields severely infested with *R. solani*, root yield and sugar content can be reduced by 50% or more (Büttner et al. 2004). Researchers have worked with *Rhizoctonia* isolates from the central U.S. and Red River Valley growing area but not the IMW. Recent research from Europe (Ithurrart et al. 2004) indicates that *R. solani* 2-2 IIIB can utilize corn as a host which will further limit crop rotation options. The most economical means of control for root rots is the use of resistant varieties. Currently, only two varieties resistant to *Rhizoctonia* are approved for production during the 2005 growing season in the IMW. In the past some varieties considered resistant to *Rhizoctonia* have not performed well in commercial fields with root rot problems. Therefore we wish to make a collection of *Rhizoctonia* isolates from the IMW and characterize them for AG group, pathogenicity, and genetic diversity. This research will also establish the distribution and pathogenicity of other potentially important pathogens such as *Fusarium* spp. and *Erwinia* which some in the industry indicate are becoming more prevalent. Thus by isolating from root rot lesions in sugarbeets from the IMW, we can establish a baseline to track pathogen population changes for this area to aid in the development of resistant germplasm and improve management options.

Recently harvested sugarbeets were harvested both years throughout southern Idaho and eastern Oregon to identify the fungi and bacteria associated with root rot. Isolations were made from 533 and 287 roots for fungi and bacteria, respectively. A total of 362 potential pathogenic fungal isolates (Table 1) were obtained: *Fusarium oxysporum* (29% of isolates), *Rhizoctonia solani* (18%), *Fusarium acuminatum* (18%), *Rhizopus* spp. (16%), *Phoma betae* (7%), oomycetes (6%), *Fusarium culmorum* (3%), and *Fusarium equiseti* (3%). A 197 fungal isolates (68 isolates were *Geotrichum candidum*) were considered saprophytes. From the bacterial isolations, a total of 396 bacterial and yeast isolates (Table 2) were obtained: lactic acid bacteria (41% of isolates), acetic acid bacteria (29%), enteric bacteria (17%), and yeast (13%). The lactic acid bacterial group contained *Leuconostoc mesenteroides* subsp. *dextranicum* (80%) and *Lactobacillus plantarum* (20%). *Gluconobacter asaii* comprised 92% of the isolates from the acetic acid group. *Leuconostoc* rotted more root tissue than the other bacteria or yeast inoculated individually or in combination with *Gluconobacter* (Table 3). These pathogenicity tests and subsequent isolations prove the presence of a previously undescribed bacterial complex which leads to the loss of sugar through impurities, fermentation, and breakdown of sugarbeet roots. This complex of bacteria and yeast likely further manifest themselves in storage piles. Extracellular substances such as dextran produced by the bacteria may also lead to factory processing issues.

Table 1. Isolations were made from 225 and 308 sugarbeet roots with fungal rot in 2004 and 2005, respectively. The roots were collected from 29 piling grounds throughout southern Idaho and southeastern Oregon.

Fungus ^z	Number of isolates			Percentage by growing area		
	2004	2005	Total	Treasure Valley	Magic Valley	American Falls
<i>Fusarium oxysporum</i>	45	60	105	62	33	2
<i>Rhizoctonia solani</i>	40	26	66	48	50	2
<i>Fusarium acuminatum</i>	18	47	65	77	20	3
<i>Rhizopus spp.</i>	26	33	59	22	71	7
<i>Phoma betae</i>	7	19	26	12	84	4
Oomycetes	18	2	20	35	55	10
<i>Fusarium culmorum</i>	9	2	11	80	20	0
<i>Fusarium equiseti</i>	9	1	10	20	80	0

^z 68 were *Geotrichum candidum* and 129 other miscellaneous fungal cultures were isolated which would be considered saprophytic fungi.

Table 2. Bacteria and yeast isolated from sugarbeet root rots in 2004 and 2005 from recently harvested roots throughout southern Idaho and southeastern Oregon.

Bacteria and yeast ^z	Number of isolates			Percent of total
	2004	2005	Total	
Lactic acid bacteria	25	136	161	41
Acetic acid bacteria	53	61	114	29
Enteric bacteria	23	43	66	17
<i>Pichia spp.</i>	11	34	45	11
<i>Candida spp.</i>	4	4	8	2
<i>Pseudomonas spp.</i>	1	1	2	1
Total	117	279	396	

^z The primary species associated with the lactic acid bacteria were *Leuconostoc mesenteroides* subsp. *dextranicum* (80% of the isolates from this group) and *Lactobacillus plantarum* (20%). The primary species associated with the acetic acid group were *Gluconobacter asaii* (92% of isolates from this group) but some *Acetobacter lovaniensis* were also present. The primary species from the Enterobacteriaceae group were *Enterobacter spp.* (82% of the isolates from this group), but *Serratia plymuthica*, *Erwinia carotovora* subsp. *betavascularum*, and *Escherichia hermannii* were also found. The primary *Pichia spp.* found were *P. fermentans* and *P. membranifaciens*. The primary *Candida spp.* found were *C. oleophila* and *C. quercitrusa*. The *Pseudomonas spp.* found were *P. fluorescens* C (bt) and *P. putida*.

Table 3. Rot tests using bacteria and yeast isolated from the advancing margin of bacterial-like rot in recently harvested sugarbeets from throughout southern Idaho and southeastern Oregon. Rot tests were conducted in an incubator at 30°C on root disks from sugarbeet cultivar Beta 8600.

Bacterial and yeast species	Diameter of infected area (mm)	
	24 h	48 h
<i>Leuconostoc mesenteroides</i> subsp. <i>dextranicum</i>	15.5 a	31.8 a
<i>L. mesenteroides</i> + <i>G. asaii</i>	14.3 ab	30.0 a
<i>L. mesenteroides</i> + <i>E. cancerogenus</i>	8.0 cd	16.5 b
<i>L. mesenteroides</i> + <i>G. asaii</i> + <i>P. fermentans</i>	9.8 bc	16.3 b
<i>Gluconobacter asaii</i>	4.8 cde	12.0 bc
<i>L. mesenteroides</i> + <i>P. fermentans</i>	7.5 cd	11.7 bc
<i>L. mesenteroides</i> + <i>G. asaii</i> + <i>E. cancerogenus</i>	5.7 cde	9.3 bc
<i>Enterobacter cancerogenus</i>	3.3 de	3.8 c
<i>Pichia fermentans</i>	2.3 e	2.7 c
Noninoculated check	2.0 e	2.0 c
$P > F$	<0.0001	0.0004
LSD ($P \leq 0.05$)	5.1	12.3

Conclusions

- *Rhizoctonia*, considered the primary root rot organism in the IMW, was found in similar frequency as a number of other fungi. Pathogenicity studies will need to be conducted to establish the virulence of these fungal isolates. Pathogenic groups of concern will be investigated for genetic diversity. Upon the completion of these studies, we should have a better understanding of root rots in the IMW.
- *Leuconostoc* was the primary bacterial pathogen isolated from a previously undescribed bacteria complex. This complex leads to fermentation and breakdown of beets in the field but also likely leads to storage and processing problems as well.
- These studies have characterized and provided fungal and bacterial isolates for resistance screening efforts, helped guide the search for novel sources of resistance in breeding efforts, and advanced our scientific knowledge of root rots in sugarbeets.

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RHIZOMANIA RESISTANCE BREEDING *(Project 320)*

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Rhizomania in sugarbeets caused by *Beet necrotic yellow vein virus* (BNYVV) can lead to major reductions in root yield and quality (Rush 2003, Rush et al. 2006). In the United States, BNYVV was first discovered in 1984 in California but has since spread to all major production areas in the country. Control of rhizomania is largely achieved through the use of resistant cultivars. However, the primary resistance gene, *Rz1*, in commercial cultivars does not provide complete resistance. Thus, there is considerable selection pressure present to select for genetic variants which can overcome the resistance gene. In fields with little or no crop rotation, growers appear to have already selected for strains of BNYVV which can overcome the *Rz1* gene (Liu et al. 2005, Ward et al. 2007). Some cultivars contain minor genes for resistance and also *Rz2*. However, none of the gene combinations allow for complete resistance. Therefore, new sources of resistance to rhizomania are urgently needed. In order to combat this problem, we have initiated a breeding program to identify novel sources resistance to rhizomania, establish genetic markers closely linked to the resistance genes, and cross the new sources of resistance into agronomically superior germplasm.

We initiated this research by screening germplasm from both the Salinas and East Lansing USDA-ARS breeding programs in a rhizomania nursery located in Heyburn, ID during the 2006 growing season. Unfortunately, only four of the eight replications had considerable disease pressure. Based on those four replications with disease pressure, the Disease Index (DI) values for the Salinas materials ranged from 13 to 34 (Table 1). These values are considerably lower than the range of 22 to 62 obtained in the 2005 nursery. In the California materials, lines 4842(iso) and Y383 performed well in both the 2006 and 2005 nurseries. The low value of 13 was associated with one of the check cultivars, Beta 4430R. We were not able to detect significant differences between lines from East Lansing (Table 2). The low disease pressure likely explains the lack of significant differences since DI values only ranged from 15 to 28.

The materials in this field were also influenced by *Verticillium dahliae* which is the causal agent of Verticillium wilt. Verticillium wilt was uniformly distributed across the field allowing for separation between materials in all replications (Table 3 and 4). Roots from 30 plants scattered throughout the field were evaluated for the presence of *Verticillium* and *Fusarium*. All 30 plants contained *Verticillium dahliae* and five also contained *Fusarium oxysporum*. These data represent the first screening of germplasm for resistance to Verticillium wilt.

To facilitate future screening for rhizomania, efforts have been made to establish a 20 acre area for a rhizomania nursery on the BSDF farm. Symptoms were evident in the field last year but inoculum levels need to be higher and more uniform before the field can host a screening nursery. To aid these efforts, sprinkler equipment has been purchased for this field. Additional screening of materials from all breeding programs should continue in order to identify additional resistance genes for the control of rhizomania. None of the current sources of

resistance in commercial and experimental germplasm provides for complete resistance. Thus, research to establish superior germplasm with resistance to rhizomania and novel management options continues to be priority.

Table 1. Results of 2006 rhizomania nursery for entries submitted from Robert Lewellen's program in Salinas, CA. Significant differences were found among the entries for Disease Index (DI).

Entry	Replications scored	Mean DI
Beta4430R - (res. check)	4	12.9
Beta4430R (res. check)	4	14.3
R540	4	16.4
4842(iso)	4	17.3
P528	4	17.9
R537-302H5	4	18.4
N412(Sp)	4	18.8
Y577H5	3	19.0
R539H5	4	19.1
R521H5	4	19.8
Y375-311	4	19.8
Y577	4	19.8
Y375-305	3	19.9
Y595	4	20.3
R522H5	4	20.3
P530	4	20.4
05-FC1036	4	20.4
Roberta (sus. check)	3	20.4
5944	4	20.5
05-FC1019	4	20.6
Y393	4	20.6
R4541/2H5	3	20.8
Beta GO17R (<i>Rz2</i> check)	4	21.0
4931	3	21.0
Roberta (sus. check)	4	21.2
4921	4	21.6
R540H5	4	21.6
R537-302	4	21.6
R524-2/3H5	3	21.7
Angelina (<i>Rz1/Rz2</i> check)	4	21.7
4941	4	21.9
Angelina (<i>Rz1/Rz2</i> check)	4	22.0
2992RZ (<i>Rz1</i> check)	3	22.1
Phoenix (sus. check)	4	22.2
R481-22	4	22.3
Y591	4	22.4
P507/8	4	22.6
R539	4	22.6
R5324-302H5	4	22.7

Entry	Replications scored	Mean DI
R524-2/3	4	22.7

Table 1 continued.

Entry	Replications scored	Mean DI
P531CTH5	3	23.0
P529	4	23.3
05-FC1022	4	23.5
Z510	4	23.6
R541/2	4	23.6
Y371(C72)	3	23.7
P531CT(iso)	4	23.7
R578(iso)	3	23.9
Z425	3	24.0
Y5977H5	3	24.0
R522	3	24.3
R521	4	24.3
Y591H50	4	24.4
Phoenix (sus. check)	3	24.4
Beta GO17R (Rz2 check)	4	24.6
05-FC1018	4	25.0
Y590-40(iso)	3	25.1
CR411	4	25.8
2992RZ (Rz1 check)	4	25.9
R578H5	4	26.5
N472(Sp)	4	26.5
4943	4	26.5
N524	4	27.2
EL-SP7322-0 (sus. check)	3	27.4
05-C37	4	27.4
R525-301H5	3	27.4
05-FC1030-16(Sp)	3	27.5
5933	3	27.6
05-FC1030-15(Sp)	4	27.7
R525H5	4	28.0
R424/5	4	28.7
P527	4	29.0
05-US75	4	29.8
R525	3	30.1
R525-301	4	31.5
R524-302	3	32.1
P518-6	3	32.7
05-US22/3	3	34.0
LSD ($P \leq 0.05$)		7.7

Table 2. Results of 2006 rhizomania nursery for entries submitted from the program of Mitch McGrath in East Lansing, MI. No significant differences were found among the entries for Disease Index (DI).

Entry	Replications scored	Mean DI
EL-A006056	4	14.74
EL-A014986	4	16.54
EL-A019308	4	17.22
EL-A019278	4	17.22
EL-A013507	4	17.45
EL-A014204	4	18.10
EL-A014972	4	18.33
EL-A010208	4	18.33
EL-A014208	3	18.39
EL-A014216	4	18.92
EL-A013511	4	18.99
EL-A015027	4	19.12
EL-A013499	3	19.37
EL-A014964	3	19.75
EL-A013521	4	20.03
EL-A007108	4	20.36
EL-A013487	4	20.56
EL-A015024	4	20.72
EL-A006851	4	20.76
EL-A015025	4	21.03
EL-A014971	4	21.18
EL-A014970	4	21.45
EL-A013500	4	21.59
EL-A010150	4	21.62
EL-A007563	4	21.79
EL-A014215	4	21.82
EL-A005467	4	22.04
EL-A013485	2	22.23
EL-A014211	4	22.44
EL-A014981	4	22.44
EL-A014210	4	22.77
EL-A014207	4	23.01
EL-A015029	4	23.16
EL-A007110	4	23.65
EL-A012858	4	24.92
EL-A013698	4	24.95
EL-A006835	4	25.02
EL-A014214	4	25.92
EL-A014206	3	26.41
EL-A014205	4	27.35
EL-A014209	4	27.42
EL-A014963	4	28.44

Table 3. Entries submitted to the 2006 rhizomania nursery from Robert Lewellen's program in Salinas, CA were also evaluated for their response to *Verticillium dahliae*.

Entry	Description	<i>Verticillium</i> symptomatic plants (%)
2992RZ	Hilleshog variety - Rz1 control	1
Y591	IRZM-% Y391	3
05-US75	Inc. 03-US75	5
R540	IRZM-% R940, R840, R740	5
Y577	IRZM-% Y277, Y375	5
R522H5	C833-5CMS x IRZM R522(Sp)	5
P518-6	PMR-RZM P418-6, CP08	7
N412(Sp)	N312, N212-#(C) aa x A, CN12	7
Y375-311	Inc. Y575-311	7
Y371(C72)	C37 bkg., RZM-ER-% Y171	8
R541/2	IRZM-% 12641, R642 (WB169, 258)	9
N472(Sp)	N372, N272-#(C) aa x A, CN72	9
Y375-305	Inc. Y575-305	9
Beta GO17R	Betaseeds - Rz2 variety	9
05-FC1019	RZM-ER-% 20031019 (FC712 x C931)	10
05-FC1030-16(Sp)	03-FC1030-16 aa x A	10
Y590-40(iso)	RZM Y390-40	10
R537-302H5	C833-5CMS x R337-302	10
2992RZ	Hilleshog variety - Rz1 control	10
P529	PMR-RZM P429, (CP05)	11
Y595	RZM Y95 (C)	11
R522	IRZM-% R522(sp)	11
R525	IRZM-% R325, R324, R324/5. R337	11
R424/5	R424/5 (C79-2/3)	11
R5324-302H5	C833-5CMS x IRZM-% R324-302, -306	12
R525-301H5	C833-5CMS x R525-301, 302	12
R525H5	C833-5CMS x IRZM-% R325, R324, R324/5. R337	12
P507/8	PMR-RZM P407/8, CP07	12
P528	PMR-RZM P528, CP04	12
05-FC1018	RZM-ER-% 20031078 (C931 x FC709-2)	12
N524	Inc. N424(g)	12
5933	933(C) aa x A	12
4931	RZM 3931aa x A, C931	12
4941	RZM 3941aa x A, C941	12
R537-302	INC. R337-302 (WB151)	12
Y577H5	C833-5CMS x IRZM Y277, Y375	12
Y5977H5	C833-5CMS x IRZM Y95(C)	12
R540H5	C833-5CMS x IRZM-% R940, R840, R740	12
R539H5	C833-5CMS x R039, (C39R)	12
4921	RZM-ER-% 2921	12
05-US22/3	Inc. 03-US22/3	13
R481-22	RZM R181-22, (C81-22)	13
R521	IRZM-% R321, R021	13
05-FC1022	RZM-ER-% 20031022 (C931 x FCRhizoc)	13
CR411	RZM CR311 aa x A, CR11	13
R524-302	Inc. R324-302, -306 (WB41)	13
R521H5	C833-5CMS x IRZM-% R321, R021	13
Beta GO17R	Betaseeds - Rz2 variety	13

Table 3 continued.

Entry	Description	<i>Verticillium</i> symptomatic plants (%)
P527	PMR-RZM P427, CP03	15
R539	Inc. R039, C39R	15
05-FC1030-15(Sp)	03-FC1030-15 aa x A	15
R4541/2H5	C833-5CMS x IRZM-% R641, R642	15
4842(iso)	C842	15
Phoenix	Holly Hybrids, 3-10-06	15
05-C37	Inc. 04-C37	16
R525-301	Inc. R325-301, -302 (WB42)	16
Y393	Recombine FS-#(C)	16
EL-SP7322-0	Inc. SP22-0	17
P530	PMR-RZM P430, CP06	17
Phoenix	Holly Hybrids, 3-10-06	17
R524-2/3	Inc. R324-213, -215, -222, -223 (WB41, 42)	18
P531CTH5	C833-5CMS x P431CT, (CP09CT)	18
Z510	Inc. Z210	19
05-FC1036	RZM 04-FC1028, 1037, 1038 aa x A, (LSR)	19
Y591H50	C790-15cms x IRZ-% Y391	19
P531CT(iso)	PMR-RZM P431CT	20
5944	S1(C1,2,3) aa x A	20
R578H5	C833-5CMS x R378, (C78/3)	21
R524-2/3H5	C833-5CMS x R324-213, -215, -222, -223	22
Roberta	Betaseed 3/06 pelleted	22
Beta4430R	Betaseed 8-21-03/	24
Z425	RZM Z325 aa x A, CZ25/2	25
R578(iso)	RZM R378(iso), (C78/3)	26
Roberta	Betaseed 3/06 pelleted	27
4943	RZM 3943 aa x A	28
Beta4430R	Betaseed 8-21-03/	28
Angelina	Betaseed 3/06 pelleted	37
Angelina	Betaseed 3/06 pelleted	43
LSD ($P \leq 0.05$)		12

Table 4. Entries submitted to the 2006 rhizomania nursery from Mitch McGrath's program in East Lansing, MI were also evaluated for their response to *Verticillium dahliae*.

Entry	Description	<i>Verticillium</i> symptomatic plants (%)
ELID06-24	EL-A014214	9
ELID06-5	EL-A006056	11
ELID06-27	EL-A015025	11
ELID06-34	EL-A014963	12
ELID06-22	EL-A006851	12
ELID06-21	EL-A006835	13
ELID06-11	EL-A005467	14
ELID06-32	EL-A013507	14
ELID06-10	EL-A019308	16
ELID06-13	EL-A014206	16
ELID06-25	EL-A014205	16
ELID06-29	EL-A013511	16
ELID06-19	EL-A014215	17
ELID06-36	EL-A014970	17
ELID06-20	EL-A014216	18
ELID06-41	EL-A013698	18
ELID06-12	EL-A014204	19
ELID06-14	EL-A014207	20
ELID06-16	EL-A014209	20
ELID06-30	EL-A013499	20
ELID06-35	EL-A014964	20
ELID06-1	EL-A007108	21
ELID06-2	EL-A007110	21
ELID06-9	EL-A010150	21
ELID06-15	EL-A014208	21
ELID06-17	EL-A014210	21
ELID06-42	EL-A012858	21
ELID06-26	EL-A015024	22
ELID06-8	EL-A013485	23
ELID06-23	EL-A007563	23
ELID06-33	EL-A013521	23
ELID06-4	EL-A010208	24
ELID06-7	EL-A014986	24
ELID06-39	EL-A014981	24
ELID06-6	EL-A015027	25
ELID06-37	EL-A014971	25
ELID06-38	EL-A014972	26
ELID06-40	EL-A015029	26
ELID06-18	EL-A014211	27
ELID06-3	EL-A013487	30
ELID06-31	EL-A013500	32
ELID06-28	EL-A019278	34
LSD ($P \leq 0.05$)		12

Conclusions

- Screening of materials from all breeding programs should continue in order to identify additional resistance genes for the control of rhizomania. None of the current sources of resistance in commercial and experimental germplasm provides for complete resistance.
- Materials from both the Salinas and East Lansing programs varied in response to *Verticillium dahliae*. If *Verticillium* wilt becomes a widespread disease problem, we now have a start on locating sources of resistance.
- To facilitate future screening for rhizomania, efforts have been made to establish a 20 acre area for a rhizomania nursery on the BSDF farm. Symptoms were evident in the field last year but inoculum levels need to be higher and more uniform before the field can host a screening nursery. To aid these efforts, sprinkler equipment has been purchased for this field.

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